

XX Claim 35; Page 15; 58pp; English.

XX The present sequence is a PCR primer for the CYP3A4 polymorphism of the

CC cytochrome P450 gene. CYP3A4 is a xenobiotic-metabolising enzyme. Along

CC with allele-specific probes, this primer can be used to determine the

CC genotype of an individual at the cytochrome P450 locus, and thus

CC determine their susceptibility to toxicity associated with carcinogens,

CC steroid hormones and drugs

XX

SQ Sequence 18 BP; 3 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 18;

Best Local Similarity 93.3%; Pred. No. 1e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1457 CCACGAGGAGAGC 1471

DB 15 CCAAGGTGGAGAGC 1

|||||

RESULT 1513

AAC60756

ID AAC60756 standard; DNA; 18 BP.

XX

AC AAC60756;

XX

DT 30-JAN-2001 (first entry)

XX

DE Human psoriasis-linked S gene polymorphism PCR primer SEQ ID NO: 19.

XX

KW Human; psoriasis; S gene; corneodesmosin; polymorphism; probe;

KW PCR primer; ss.

XX

OS Homo sapiens.

XX

FN WO200058506-A2.

XX

PD 05-OCT-2000.

XX

PF 27-MAR-2000; 200WO-GB001152.

XX

PR 26-MAR-1999; 99GB-00006993.

XX

PA (UYLE-) UNIV LEICESTER.

PA (UNLO) KINGS COLLEGE LONDON.

XX

PI Trembath RC, Barker JWN;

XX

DR WPI; 2000-664928/64.

XX

PT Novel S gene encoding corneodesmosin protein useful for diagnosing and

PT treating psoriasis.

XX

XX Example 2; Page 32; 34pp; English.

XX

CC The present invention is concerned with the diagnosis and treatment of

CC psoriasis in humans. It provides a number of primers and probes (one of

CC which is shown here) which can be used to detect polymorphisms in the S

CC gene, which encodes corneodesmosin. Different polymorphisms in the S gene

CC have been linked to different levels of susceptibility to psoriasis, and

CC these primers can predict an individual's risk of developing the disease

XX

SQ Sequence 18 BP; 1 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 18;

Best Local Similarity 93.3%; Pred. No. 1e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1985 TGCTGCTCTCTCTCT 1999

DB 4 TGCTGCTCTCTCTCT 18

|||||

XX OS Homo sapiens.
XX PI WO200206525-A2.
XX PN 24-JAN-2002.
XX PD 28-JUN-2001; 2001WO-1B001477.
XX PF 18-JUL-2000; 2000US-0219704P.
XX PR (GEST) GENSET.
XX PA Cohen D, Blumenfeld M, Chumakov I, Abderrahim H, Bihain B;
XX PI WPI; 2002-155043/20.
XX DR Set of novel map-related biallelic markers, preferably located on obesity
XX PT disorder-associated chromosomal regions on chromosomes 3, 10 and 19,
XX PF useful, for e.g. detecting statistical correlations between marker allele
XX PI and a phenotype.
XX PS Example 2; Page 238; 31pp; English.
XX CC The invention relates to a set of novel map-related biallelic markers,
XX CC preferably located on obesity disorder-associated chromosomal regions on
XX CC chromosomes 3, 10 and 19. The markers are useful for genotyping or
XX CC estimating the frequency of an allele in a population, for detecting an
XX CC association between a genotype or haplotype and a phenotype, e.g. a
XX CC disease involving drug responses, obesity or disorders related to
XX CC obesity, such as hyperuricaemia, digestive pathology, hepatic function
XX CC disorders, cancer, cardiovascular disease, hypertension, hyperlipidaemia,
XX CC insulin disorders, atheromatous disease and cardiac insufficiency. The
XX CC markers are useful for detecting a statistical correlation between a
XX CC biallelic marker allele and a phenotype and/or between a biallelic marker
XX CC haplotype and a phenotype. This sequence represents a PCR primer used to
XX CC amplify a human obesity-associated biallelic marker
XX SQ Sequence 18 BP; 4 A; 6 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1;
QY 1692 GAGCCACCTTGCCAC 1706
Db 4 GAGCCACATGCCAC 18
RESULT 1516
ABT05027
ID ABT05027 standard; DNA; 18 BP.
XX AC ABT05027;
XX DT 11-OCT-2002 (first entry)
XX DE TNFR1 expression modulation related antisense oligo SEQ ID No 57.
XX KW Antisense compound; tumour necrosis factor receptor 1; liver disease;
XX KW TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;
XX KW human; ds.
XX OS Homo sapiens.
XX PN WO200248168-A1.
XX PD 20-JUN-2002.
XX PF 22-OCT-2001; 2001WO-US051224.
XX PR 24-OCT-2000; 2000US-00695451.
XX CC The invention relates to an antisense compound 8 to 30 nucleotides in

PA (ISIS-) ISIS PHARM INC.
XX Baker BF, Cowser LM, Zhang H, Dean NM;
XX PI WPI; 2002-583481/62.
XX DR Novel antisense compound targeted to nucleic acid molecule encoding tumor
XX PT necrosis factor receptor 1 (TNFR1), useful for treating humans having
XX PF disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
XX PS Example 10; Page 45; 121pp; English.
XX CC The invention relates to an antisense compound 8 to 30 nucleotides in
XX CC length targeted to nucleic acid molecule encoding tumour necrosis factor
XX CC receptor 1 (TNFR1), where the antisense compound inhibits expression of
XX CC TNFR1. The antisense compound is useful for inhibiting the expression of
XX CC TNFR1 in cells or tissues. The antisense compound is also useful for
XX CC treating an animal (preferably human) having a disease or condition
XX CC associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver
XX CC injury) or a hyperproliferative disorder such as cancer, by inhibiting
XX CC the expression of TNFR1. The antisense compound is useful for
XX CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
XX CC This polynucleotide sequence represents a human oligonucleotide relating
XX CC to the TNFR1 of the invention
XX SQ Sequence 18 BP; 8 A; 1 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1;
QY 1332 TGAAGAGGAGGGAGA 1346
Db 4 TGAAGAGGAGGGAGA 18
RESULT 1517
ABT05099
ID ABT05099 standard; DNA; 18 BP.
XX AC ABT05099;
XX DT 11-OCT-2002 (first entry)
XX DE TNFR1 expression modulation related antisense oligo SEQ ID No 129.
XX KW Antisense compound; tumour necrosis factor receptor 1; liver disease;
XX KW TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;
XX KW human; ds.
XX OS Homo sapiens.
XX PN WO200248168-A1.
XX PD 20-JUN-2002.
XX PF 22-OCT-2001; 2001WO-US051224.
XX PR 24-OCT-2000; 2000US-00695451.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Baker BF, Cowser LM, Zhang H, Dean NM;
XX PI WPI; 2002-583481/62.
XX PT Novel antisense compound targeted to nucleic acid molecule encoding tumor
XX PT necrosis factor receptor 1 (TNFR1), useful for treating humans having
XX PT disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
XX PS Example 18; Page 56; 121pp; English.
XX CC The invention relates to an antisense compound 8 to 30 nucleotides in

CC length targeted to nucleic acid molecule encoding tumour necrosis factor
 CC receptor 1 (TNFR1), where the antisense compound inhibits expression of
 CC TNFR1. The antisense compound is useful for inhibiting the expression of
 CC TNFR1 in cells or tissues. The antisense compound is also useful for
 CC treating an animal (preferably human) having a disease or condition
 CC associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver
 CC injury) or a hyperproliferative disorder such as cancer, by inhibiting
 CC the expression of TNFR1. The antisense compound is useful for
 CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
 CC This polynucleotide sequence represents a human oligonucleotide relating
 CC to the TNFR1 of the invention
 SQ Sequence 18 BP; 9 A; 0 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 1e+03; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1332 TGAAGAGGAGGAGGA 1346
 |||||
 Db 2 TGAAGAGGAGGAGGA 16

RESULT 1518
 ACA60585/c
 ID ACA60585 standard; DNA; 18 BP.
 XX
 AC ACA60585;

DT 11-JUN-2003 (first entry)
 XX

DE Antisense inhibition of human cyclin D2 related oligonucleotide #22.

KW Human; cyclin D2; diagnostic; therapeutic; prophylaxis;
 KW cyclin 2 inhibition; ss.

OS Homo sapiens.

XX US6492173-B1.

PN 10-DEC-2002.

PF 01-AUG-2001; 2001US-00920760.

PR 01-AUG-2001; 2001US-00920760.

PA (ISIS-) ISIS PHARM INC.

PI Cowsert LM;

DR WPI; 2003-361492/34.

XX Novel antisense compound useful for treating diseases associated with
 XX Cyclin D2 expression, comprises an oligonucleotide comprising up to 50
 XX nucleobases in length, which inhibits expression of Cyclin D2 in cells or
 XX tissues in vitro.

PS Example 15; Col 45-46; 40pp; English.

CC The invention describes a compound (I) of up to 50 nucleobases in length,
 CC which inhibits the expression of Cyclin D2. (I) is useful for inhibiting
 CC the expression of Cyclin D2 in cells or tissues in vitro. (I) is thus
 CC useful for treating disease associated with Cyclin D2 expression. (I) is
 CC useful for diagnostics, therapeutics, prophylaxis and as research
 CC reagents and kits. This sequence represents human cyclin D2 inhibition
 CC associated oligonucleotide

SQ Sequence 18 BP; 2 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 1e+03; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 ACCGCTCCGAGAGC 754
 |||||
 Db 18 ACCTGCTCCGAGAGC 4

RESULT 1519
 ACC48899/c
 ID ACC48899 standard; DNA; 18 BP.
 XX
 AC ACC48899;

XX 11-AUG-2003 (first entry)
 XX
 DT Rhodococcus ruber eth gene cluster region PCR primer gt2.

DE Cytochrome P450; eth gene; fuel; ether; ethyl tert-butyl ether; ETBE;
 XX degradation; bioremediation; soil decontamination; pollutant; biosensor;
 KW PCR; primer; ss.

XX Rhodococcus ruber.

XX EF1270722-A1.

PN 02-JAN-2003.

XX 22-JUN-2001; 2001EP-00401667.

XX 22-JUN-2001; 2001EP-00401667.

XX (INSP) INST PASTEUR.

PA (INSP) INST FRANCAIS DU PETROLE.

PI Chauvaux S, Miras I, Beguin P;

XX WPI; 2003-334761/32.

XX New Rhodococcus ruber nucleic acid, useful for transforming bacteria for
 XX depolluting soil contaminated with ethyl tert-butyl ether comprises the
 XX cytochrome P-450 gene cluster involved in cleavage of ethyl tert-butyl
 XX ether.
 XX Disclosure; Page 8; 58pp; English.

XX The present sequence is primer gr2, which was used with primer gtl (see
 XX ACC48899) in the PCR amplification of Rhodococcus ruber strain CNCM I-
 XX 1889 DNA to obtain an eth gene cluster region (see ACC48894) encoding a
 XX cytochrome P450 system involved in the cleavage of ether fuel additives.
 XX Expression of the eth gene cluster is induced by ethyl tert-butyl ether
 XX (ETBE). The identification of the eth gene cluster allows the
 XX construction of probes and biosensors for detecting pollution by an ether
 XX fuel and for assessing the potential of a contaminated soil or effluent
 XX to cleave the ether fuel. Also provided are recombinant cells comprising
 XX a vector encoding the eth genes and which are capable of ETBE
 XX degradation, for use in ether fuel bioremediation of a contaminated soil
 XX or effluent

SQ Sequence 18 BP; 1 A; 7 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 1e+03; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AGCGAGCCGCGGC 16
 |||||
 Db 16 AGCGAGCCGCGGC 2

RESULT 1520
 ACA98740
 ID ACA98740 standard; DNA; 19 BP.
 XX
 AC ACA98740;

DT	28-JUL-2003	(first entry)	
XX	Human CYP2C8 SNP detection PCR primer #180.		
XX	Cytochrome P450 polypeptide 2C8; CYP2C8; arachidonic acid metabolism;		
DE	cancer; cardiovascular disease; cytosstatic; cardiovascular; gene therapy;		
XX	single nucleotide polymorphism detection; SNP detection; PCR; primer; ss.		
KW	Homo sapiens.		
KW	WO200299099-A2.		
XX	12-DEC-2002.		
XX	31-MAY-2002; 2002WO-EP006000.		
XX	01-JUN-2001; 2001EP-00112899.		
XX	(EPID-) EPIDAUS BIOTECHNOLOGIE AG.		
XX	Penger A, Sprenger R, Brinkmann U;		
XX	WPI; 2003-167344/16.		
XX	New polymorphic variants of the gene encoding Cytochrome P450 polypeptide		
XX	2C8 (CYP2C8), useful for diagnosing or treating a disease, e.g.		
XX	arachidonic acid metabolism, cancer or cardiovascular diseases.		
XX	Claim 1; Page 52; 178pp; English.		
XX	The invention describes a new polynucleotide comprises a polynucleotide:		
XX	(a) having any of 101 nucleic acid sequences with 18-19 bp fully defined		
XX	in the specification; (b) encoding any of seven polypeptides having 7		
XX	amino acids, or a polypeptide with 3 amino acids; (c) capable of		
XX	hybridising to a Cytochrome P450 polypeptide 2C8 (CYP2C8) gene; (d)		
XX	encoding a molecular CYP2C8 variant polypeptide or its fragment. The		
XX	polynucleotide, gene, vector, polypeptide or antibody is useful for		
XX	diagnosing or treating a disease, or for preparing a pharmaceutical composition		
XX	for diagnosing a disease, or for preparing a pharmaceutical composition		
XX	for treating a disease. This disease includes arachidonic acid		
XX	metabolism, cancer or cardiovascular diseases. This sequence represents a		
XX	primer used to isolate regions of the human cytochrome P450 polypeptide		
XX	2C8 gene (CYP2C8) in order to identify the single nucleotide polymorphism		
XX	(SNP) in that region of different individuals useful in disease diagnosis		
XX	Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;		
XX	Query Match 0.6%; Score 13.4; DB 1; Length 19;		
XX	Best Local Similarity 93.3%; Pred. No. 1.1e+03;		
XX	Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1600 ATTTATATAAAATT 1614		
DB	3 ATTTATATAAAATT 17		
RESULT 1521			
AC	ACA98737/c		
XX	28-JUL-2003 (first entry)		
XX	Human CYP2C8 SNP detection PCR primer #177.		
XX	Cytochrome P450 polypeptide 2C8; CYP2C8; arachidonic acid metabolism;		
XX	cancer; cardiovascular disease; cytosstatic; cardiovascular; gene therapy;		
XX	single nucleotide polymorphism detection; SNP detection; PCR; primer; ss.		
XX	Homo sapiens.		
XX	WO200299099-A2.		


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XX
PT Detection of a target neoplastic nucleic acid and treatment of tumours -
PT provides a rapid and accurate detection of mutant sequences.
XX
PS Example 1; Page 39; 126pp; English.
XX
CC AAQ96305-Q96363 are p53 gene hybridisation probes, used in the
CC development of a new method for the detection of mutant nucleotide
CC sequences associated with primary tumours. The method may be used to
CC screen high risk populations, and to monitor patients undergoing
CC chemoprevention or chemotherapy
XX
SQ Sequence 19 BP; 9 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match          0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1584 TTCTATTTCCTGTG 1598
DB 16 TTCTTTTCTGTG 2

RESULT 1523
AAQ95237
ID AAQ95237 standard; DNA; 19 BP.
XX
AC AAQ95237;
XX
DT 09-FEB-1996 (first entry)
XX
DE Simple tandem repeat (STR) PCR primer 2811*.
XX
KW Simple tandem repeat; STR; treatment; genetic; diagnosis;
KW characterisation; mapping; linkage studies; analysis; alleles;
KW PCR primer 2811*; wgid1; ss.
XX
OS Synthetic.
XX
PN WO9517522-A2.
XX
PD 29-JUN-1995.
XX
PF 21-DEC-1994; 94WO-GB002789.
XX
PR 21-DEC-1993; 93GB-00026052.
XX
PA (UYLE-) UNIV LEICESTER.
XX
PI Jeffreys AJ, Armour J;
XX
DR WPI; 1995-240682/31.
XX
PT Identifying simple tandem repeat loci in DNA - by screening DNA library
PT to enrich for fragments contg. the repeats before cloning and
PT rescreening, also simple tandem repeats for treatment or diagnosis.
XX
PS Claim 25; Page 36; 51pp; English.
XX
CC AAQ95236 and AAQ95237 are a primer pair for the PCR amplification of the
CC simple tandem repeat (STR) corresponding to wgid1. The STR can be used
CC for treatment and diagnosis in human and veterinary medicine, partic. for
CC genetic characterisation, mapping, linkage studies and analysis/diagnosis
CC of acquired disease alleles
XX
SQ Sequence 19 BP; 6 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

Query Match          0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1747 AGGTCTGGGTGAAG 1761
DB 16 TTCTTTTCTGTG 2

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Db 1 AGGTCTGGGTGACAG 15

RESULT 1524
AAV36331
ID AAV36331 standard; DNA; 19 BP.
XX
AC AAV36331;
XX
DT 28-SEP-1998 (first entry)
XX
DE Human BRCA1 gene promoter primer 120.3.
XX
KW BRCA1 gene; promoter; polymorphism; human; breast cancer; ovary cancer;
KW 1A1.3B gene; LBRCA1 gene; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO9823779-A1.
XX
PD 04-JUN-1998.
XX
PF 25-NOV-1997; 97WO-US021358.
XX
PR 26-NOV-1996; 96US-0031102P.
XX
PA (UTAH ) UNIV UTAH RES FOUND.
XX
PI Barker DF, Liu X;
XX
DR WPI; 1998-322752/28.
XX
PT New human LBRCA1 gene - used in, e.g. method(s) to aid diagnosis of
PT breast and ovarian cancer.
XX
PS Claim 5; Page 14; 55pp; English.
XX
CC Primer 120.3 and primer 120.2 (see AAV36330) are designed for
CC amplification of the BRCA1 promoter region (see AAV36328). Primer 120.3
CC corresponds to a region of near-identity in the 1A1.3B gene with its
CC cognate; 120-2 is BRCA1-specific. A claimed method for specifically
CC amplifying a portion of the BRCA1 gene or cDNA, while not amplifying the
CC new LBRCA1 (like BRCA1, see AAV36329) gene or cDNA, utilises primer pair
CC 120.2/120.3. The invention relates to partial duplication of the BRCA1
CC gene and to some polymorphic allelic forms which can be useful in
CC tracking the chromosomal arrangement of this gene. Evidence is provided
CC that the BRCA1 promoter and the 1A1.3B gene promoter are parallel
CC elements of a genomic duplication at 17q21. New hypotheses for genetic
CC mechanisms that may be involved in breast and ovarian cancer aetiology
CC are raised by the identification of this duplicated genetic structure
XX
SQ Sequence 19 BP; 5 A; 9 C; 1 G; 4 T; 0 U; 0 Other;

Query Match          0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1557 CTTCCTCCCAACCCCTC 1571
DB 5 CTTCCTCCCAACCCCTC 19

RESULT 1525
AAA85488/c
ID AAA85488 standard; DNA; 19 BP.
XX
AC AAA85488;
XX
DT 04-DEC-2000 (first entry)
XX
DE Cyclin A1 ribozyme binding site #110.

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XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX Mammalia.
XX WO200032765-A2.
XX 08-JUN-2000.
XX 06-DEC-1999; 99WO-US028772.
XX 04-DEC-1998; 98US-0110954P.
XX (IMMU-) IMMUSOL INC.
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX Disclosure; Page 93; 109pp; English.
XX The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX Sequence 19 BP; 5 A; 0 C; 11 G; 3 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1555 TTCTTCCCAACCCC 1569
DB 19 TTCTTCCCAACCTC 5
RESULT 1526
AA82721/C
ID AAA82721 standard; DNA; 19 BP.
AC AAA82721;
XX 04-DEC-2000 (first entry)
XX cdk3 ribozyme binding site #6.
DE Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX Mammalia.
XX WO200032765-A2.
XX 08-JUN-2000.
XX 06-DEC-1999; 99WO-US028772.
XX 04-DEC-1998; 98US-0110954P.
XX (IMMU-) IMMUSOL INC.
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX Disclosure; Page 50; 109pp; English.
XX The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX Sequence 19 BP; 5 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 618 GGCCTTCTACACAC 632
DB 17 GGCCTTGTACACAC 3
RESULT 1527
AAZ71467
ID AAZ71467 standard; DNA; 19 BP.
AC AAZ71467;
XX 10-SEP-2001 (first entry)
XX Human biallelic marker upstream amplification primer SEQ ID NO:5823.
DE Human genome; biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX amplification; single nucleotide polymorphism; SNP; PCR primer;
XX diagnosis; ss.
XX Homo sapiens.
XX WO9954500-A2.
XX 28-OCT-1999.
XX 21-APR-1999; 99WO-IB000822.
XX 21-APR-1998; 98US-0082614P.
XX 23-NOV-1998; 98US-0109732P.
XX (GEST) GENSET.
XX Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-013267/01.
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome.
XX Claim 8; Page 1472; 2745pp; English.
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the invention
XX have a variety of uses: they can be used for high density mapping of the
XX human genome, and in complex association studies and haplotyping studies
XX which are useful in determining the genetic basis for disease states.
XX Compositions and methods of the invention can also be useful for the
XX identification of the targets for the development of pharmaceutical
XX agents and diagnostic methods, as well as the characterisation of the

CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention

XX Sequence 19 BP; 1 A; 5 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 1.1e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1877 CACCTGTTTTTCA 1891

DB 2 CTTCTGTTTTTCA 16

RESULT 1528
 AAH60650/C
 ID AAH60650 standard; DNA; 19 BP.

XX AAH60650;

DT 10-SEP-2001 (first entry)

XX Cyclin A1 ribozyme binding site SEQ ID NO:3074.

XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnery;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytosolic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.

XX Homo sapiens.
 OS Synthetic.

XX WO200130362-A2.

XX 03-MAY-2001.

XX 26-OCT-2000; 2000WO-US029500.

XX 26-OCT-1999; 99US-0161532P.

XX (IMMU-) IMMUSOL INC.

XX Robbins JM, Tritz R;

XX WPI; 2001-300427/31.

PT Treating proliferative skin or eye diseases and scarring, using ribozymes
 PT that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.

PS Example 1; Page 295; 408pp; English.

XX The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
 CC dermatological, cytosolic, antiseborrheic, antidiabetic, antisickling,
 CC ophthalmological, vulnery, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,

CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention

SQ Sequence 19 BP; 5 A; 0 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 1.1e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 TTCTTCCCAACCC 1569

DB 19 TTCTTCCCAACCTC 5

RESULT 1529
 AAH57883/C
 ID AAH57883 standard; DNA; 19 BP.

XX AAH57883;

DT 10-SEP-2001 (first entry)

XX Cell-cycle dependent kinase cdk3 ribozyme binding site SEQ ID NO:307.

XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnery;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytosolic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.

XX Homo sapiens.
 OS Synthetic.

XX WO200130362-A2.

XX 03-MAY-2001.

XX 26-OCT-2000; 2000WO-US029500.

XX 26-OCT-1999; 99US-0161532P.

XX (IMMU-) IMMUSOL INC.

XX Robbins JM, Tritz R;

XX WPI; 2001-300427/31.

PT Treating proliferative skin or eye diseases and scarring, using ribozymes
 PT that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.

PS Example 1; Page 94; 408pp; English.

XX The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
 CC dermatological, cytosolic, antiseborrheic, antidiabetic, antisickling,
 CC ophthalmological, vulnery, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used

CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
XX Sequence 19 BP; 5 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 618 GGCTTCTACACCAC 632
DB 17 GGCTTGTACACCAC 3
RESULT 1530
AAL47744/C
ID AAL47744 standard; DNA; 19 BP.
XX
XX AAL47744;
AC
XX 18-SEP-2002 (first entry)
DT
XX
XX Ras gene PCR primer SEQ ID NO: 40.
DE
XX K-ras; N-ras; H-ras; ras; oncogene; mutation detection; PCR; primer;
KW probe; restriction mediated selection PCR; cancer; ss.
XX
XX Unidentified.
OS
XX WO200229005-A2.
PN
XX 11-APR-2002.
PD
XX 02-OCT-2001; 2001WO-US042422.
PF
XX 02-OCT-2000; 2000US-0237416P.
PR
XX (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
PA
XX Belly RT, Todd AV, Fuary CJ;
FI
XX WPI; 2002-479599/51.
DR
XX Amplifying and determining mutant sequences in DNA sample using
PT thermostable restriction enzyme so that during thermocycling mutant
PT sequences are enriched while wild-type sequences and/or primer induced
PT sites are cleaved.
XX
XX Claim 1; Page 79; 116pp; English.
PS
XX The present invention relates to a method of amplifying and determining
CC target mutant Ras sequences in a DNA sample, involving the use of a
CC thermostable restriction enzyme and primers shown in AAL47705-AAL47771.
CC The method used is designated restriction mediated selection polymerase
CC chain reaction (REMS-PCR). The method can be used to detect H-ras, K-ras
CC and N-ras mutations, which may lead to cancer. The present sequence is a
CC PCR primer useful in the method of the invention
XX
XX Sequence 19 BP; 2 A; 4 C; 7 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1251 GGACGAGACGACCC 1265
|||||

Db 19 GGACGAGTACGACCC 5
RESULT 1531
ABL99370/C
ID ABL99370 standard; DNA; 19 BP.
XX
XX ABL99370;
AC
XX 02-JUL-2002 (first entry)
DT
XX Left PCR primer used to target metallothionein 2 canine gene.
DE
XX Canine gene array; toxicological response; ss.
KW
XX Canis sp.
OS
XX WO200208453-A2.
PN
XX 31-JAN-2002.
PD
XX 23-JUL-2001; 2001WO-US023311.
PF
XX 21-JUL-2000; 2000US-0220057P.
PR
XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY.
PA
XX Farr SB, Pickett GG, Neft RE, Dunn RT;
FI
XX WPI; 2002-217063/27.
DR
XX Identifying toxicologically relevant canine gene to determine
PT toxicological responses of agents, by obtaining and comparing gene
PT expression profiles of untreated canine cells and canine cells treated
PT with an agent.
XX
XX Example 5; Page 48; 140pp; English.
PS
XX This invention relates to identifying a toxicologically relevant canine
CC gene and the generation of an array of toxicologically relevant canine
CC genes. The gene array is useful for obtaining a gene expression profile,
CC by exposing a population of cells to an agent, obtaining cDNA from the
CC population of cells, labeling the cDNA, and contacting the cDNA with the
CC gene array. The relevant gene is useful for making and using arrays to
CC determine toxicological responses to various agents, and also useful for
CC identifying novel gene sequences and novel canine genes. The method for
CC analysing toxicological responses using the canine gene array is rapid
CC and efficient. The present sequence is related to the canine gene array
XX
XX Sequence 19 BP; 2 A; 10 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1850 AGAAGGGGTGCTGG 1864
|||||
Db 19 AGAAGGGGTGCTGG 5
RESULT 1532
AAH77178
ID AAH77178 standard; DNA; 19 BP.
XX
XX AAH77178;
AC
XX 24-JAN-2002 (first entry)
DT
XX Hoxa9 primer 2 for amplification of RNA extracted from MTE cells.
DE
XX PCR primer; Mullerian tract epithelial cell; ovarian cancer; infertility;
KW human Mullerian duct-derived epithelial cell; immunogen; immune response;
KW human tissue model; cell therapy; cervical cancer; endometriosis; RT-PCR;
KW

KW uterine cancer; ectopic pregnancy; ovarian cyst; uterine fibroid; Hoxa9;
KW MTE cell; bioassay; ss.
XX Homo sapiens.
OS WO200177298-A2.
PN 18-OCT-2001.
XX 04-APR-2001; 2001WO-US010998.
XX 07-APR-2000; 2000US-00545435.
XX (RAVE-) RAVEN BIOTECHNOLOGIES INC.
PA Li R, Mather JP;
XX WPI; 2002-010902/01.
XX Isolated Mullerian duct-derived epithelial cells capable of
PT differentiating into oviductal, cervical and vaginal cells are useful as
PT an immunogens and drug targets and to create a human tissue models.
PS Example 4; Page 26; 34pp; English.
XX The polynucleotide sequence represents the Hoxa9 specific primer 2 used
CC for RT-PCR amplification of RNA extracted from MTE (Mullerian tract
CC epithelial) cells. The invention relates to a substantially pure
CC population of human Mullerian duct-derived epithelial cells. By carefully
CC manipulating the microenvironment in which the Mullerian duct-derived
CC epithelial cells are grown, multiple passages are attainable wherein the
CC Mullerian duct-derived epithelial cells are capable of becoming uterine,
CC cervical, vaginal, and oviductal cells. In addition, there are several
CC uses of human Mullerian duct-derived epithelial cells and cells
CC differentiating therefrom. The Mullerian tract epithelial cells can be
CC used as an immunogen to modulate overall immune response. The cells may
CC be used to produce human tissue models, as targets for drug
CC discovery/development and as a source of nucleic acids or protein for use
CC in bioassays. The cells may also be used for cell therapy;
CC transplantation of MTE cells and cells derived therefrom being one such
CC example. The research of the invention is based on addressing women's
CC health issues. These health issues include: cervical cancer, infertility,
CC uterine fibroids. In a specific example the invention could greatly
CC benefit the research relating to ovarian cancers, uterine cancer, uterine
CC fibroids, or endometriosis by the use of human tissue models of the
CC cervix, uterus, oviduct (fallopian tube), and vagina
SQ Sequence 19 BP; 6 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.1e-03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1134 GTACTGTGAGAGAT 1148
Db 5 GTACTGTGAGACGAT 19
RESULT 1533
ACC62358
ID ACC62358 standard; DNA; 19 BP.
XX ACC62358;
XX 23-JUN-2003 (first entry)
XX Human NOV5 forward PCR primer SEQ ID NO:233.
DE Human; NOVX; antiatherosclerotic; hypotensive; cardiant; dermatological;
KW anorectic; immunosuppressive; cyostatic; antidiabetic; antinfertility;
KW haemostatic; antinflammatory; antiaesthatic; anti-HIV; immunomodulator;
KW neuroprotective; nootropic; antiparkinsonian; metabolic; antilipaemic;

gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma;
congenital heart defect; aortic stenosis; valve disease; transplantation;
tuberos sclerosis; obesity; congenital adrenal hyperplasia; diabetes;
prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer;
fertility; haemophilia; hypercoagulation; graft versus host disease;
idiopathic thrombocytopenic purpura; AIDS; bronchial asthma; anorexia;
Crohn's disease; multiple sclerosis; infectious disease; cancer;
cancer-associated cachexia; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia;
metabolic syndrome X; PCR primer; ss.

Homo sapiens.
OS Synthetic.
XX WO2003023001-A2.
XX 20-MAR-2003.

09-SEP-2002; 2002WO-US028538.
07-SEP-2001; 2001US-0318120P.
07-SEP-2001; 2001US-0318184P.
10-SEP-2001; 2001US-0318430P.
17-SEP-2001; 2001US-0322636P.
17-SEP-2001; 2001US-0322781P.
17-SEP-2001; 2001US-0322816P.
17-SEP-2001; 2001US-0322817P.
19-SEP-2001; 2001US-0323519P.
20-SEP-2001; 2001US-0323631P.
20-SEP-2001; 2001US-0323636P.
25-SEP-2001; 2001US-0324969P.
25-SEP-2001; 2001US-0325094P.
26-SEP-2001; 2001US-0324990P.
14-DEC-2001; 2001US-0341144P.
26-FEB-2002; 2002US-0359599P.
05-MAR-2002; 2002US-0361663P.
03-MAY-2002; 2002US-0377908P.
17-MAY-2002; 2002US-0381483P.
29-MAY-2002; 2002US-0383863P.
02-JUL-2002; 2002US-0393332P.
17-JUL-2002; 2002US-0396412P.
13-AUG-2002; 2002US-0403517P.
06-SEP-2002; 2002US-00236417.

(CURA-) CURAGEN CORP.

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Zerhusen BD, Zhong M;
WPI; 2003-313241/30.

Novel human proteins and nucleic acid encoding the proteins, useful for
diagnosis, treatment and prevention of disorders involving the human
protein or nucleic acid e.g. cardiac and neurological disorders.

Example C; Page 301; 460pp; English.

The present invention describes isolated human NOVX proteins, where X is
1 to 42. ACC62236 to ACC62345 encode the human NOVX proteins given in
ABR54167 to ABR54276. NOVX sequences have antiatherosclerotic, cardiant,
hypotensive, dermatological, anorectic, immunosuppressive, cytostatic,
antidiabetic, antinfertility, haemostatic, antinflammatory, anti-HIV,
antiaesthatic, metabolic, immunomodulator, neuroprotective, nootropic,
antiparkinsonian and antilipaemic activities, and can be used in gene
therapy. NOVX proteins are useful for treating or preventing a pathology
associated with a NOVX protein in humans and for treating a syndrome

CC associated with the human disease. NOVX nucleic acids, proteins and
CC antibodies can be used in the treatment and diagnosis of cardiomyopathy,
CC atherosclerosis, hypertension, congenital heart defects, aortic stenosis,
CC valve disease, tuberous sclerosis, scleroderma, obesity, transplantation,
CC congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic
CC disorders, neoplasm, lymphoma, uterus cancer, fertility, haemophilia,
CC hypercoagulation, idiopathic thrombocytopenic purpura, graft versus host
CC disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC Alzheimer's disease, Parkinson's disease, immune disorders,
CC haematopoietic disorders, dyslipidaemias, and metabolic syndrome X.
CC ACC2346 to ACC62465 represent PCR primers and probes for human NOVX
CC sequences, which are used in examples from the present invention.
CC ABR54277 represents a human trypsinogen protein given in comparison with
CC the human NOV35b protein in the exemplification of the present invention
XX
SQ Sequence 19 BP; 6 A; 3 C; 9 G; 1 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1132 GAGTACCTGGAGAG 1146
||| ||||| |||||
Db 5 GAGGACCTGGAGAG 19

RESULT 1534
ADA25493/C
ID ADA25493 standard; RNA; 19 BP.
XX
AC ADA25493;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human PKC-alpha short interfering nucleic acid SEQ ID NO:224.
XX
KW short interfering nucleic acid; siNA; protein kinase C alpha; PKC-alpha;
KW RNA interference; cytostatic; vasotropic; nephrotropic; modulation;
KW inhibition; cancer; breast cancer; ovarian cancer; lung cancer;
KW prostate cancer; glioblastoma; proliferative disease; restenosis;
KW polycystic kidney disease; human; ribozyme; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003070983-A1.
XX
PD 28-AUG-2003.
XX
PF 11-FEB-2003; 2003WO-US004034.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 18-SEP-2002; 2002US-0411707P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L;
XX
XX WPI; 2003-679891/64.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer and restenosis, downregulates expression of the
PT protein kinase C-alpha gene.
XX
XX Example 3; Page 120; 143pp; English.
PS
XX

CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of a protein kinase C-alpha (PKC-alpha)
CC gene by RNA interference. Also described: (1) a siNA that modulates
CC expression and/or activity of genes for other isoforms of PKC or genes
CC involved in the PKC pathway; (2) kits for in vitro or in vivo delivery of
CC siNA; (3) conjugates and/or complexes of siNA; and (4) vectors that
CC express siNA. The siNA sequences have cytostatic, vasotropic and
CC nephrotropic activities, and can be used in the modulation (inhibition)
CC of expression of the PKC-alpha gene by RNA interference. The siNA can be
CC used to modulate expression of PKC-alpha genes. They are potentially
CC useful in treating a variety of cancers including e.g. breast cancer,
CC cancers of the head and neck, ovarian cancer, lung cancer, prostate
CC cancer, and glioblastoma and for treating other proliferative diseases
CC and conditions, such as restenosis and polycystic kidney disease. The
CC siNA may also be useful for diagnosis, drug screening, target
CC identification and validation, genetic engineering, studying gene
CC function, and for gene mapping (e.g. of single-nucleotide polymorphisms).
CC The present sequence represents a human PKC-alpha siNA, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 10 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 466 TGGGCTGGGGGCTG 480
||||| |||||
Db 15 TGGGCTGGGGGCTG 1

RESULT 1535
ADA25368
ID ADA25368 standard; RNA; 19 BP.
XX
AC ADA25368;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human PKC-alpha short interfering nucleic acid target SEQ ID NO:99.
XX
KW short interfering nucleic acid; siNA; protein kinase C alpha; PKC-alpha;
KW RNA interference; cytostatic; vasotropic; nephrotropic; modulation;
KW inhibition; cancer; breast cancer; ovarian cancer; lung cancer;
KW prostate cancer; glioblastoma; proliferative disease; restenosis;
KW polycystic kidney disease; human; ribozyme; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003070983-A1.
XX
PD 28-AUG-2003.
XX
PF 11-FEB-2003; 2003WO-US004034.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 18-SEP-2002; 2002US-0411707P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L;
XX
XX WPI; 2003-679891/64.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer and restenosis, downregulates expression of the
PT protein kinase C-alpha gene.
XX
XX Example 3; Page 120; 143pp; English.
PS
XX

PT protein kinase C-alpha gene.
 XX Example 3; Page 120; 143pp; English.
 CC The present invention describes a short interfering nucleic acid (siNA)
 CC that downregulates expression of a protein kinase C-alpha (PKC-alpha)
 CC gene by RNA interference. Also described: (1) a siNA that modulates
 CC expression and/or activity of genes for other isoforms of PKC or genes
 CC involved in the PKC pathway; (2) kits for in vitro or in vivo delivery of
 CC siNA; (3) conjugates and/or complexes of siNA; and (4) vectors that
 CC express siNA. The siNA sequences have cytostatic, vasotropic and
 CC nephrotropic activities, and can be used in the modulation (inhibition)
 CC of expression of the PKC-alpha gene by RNA interference. The siNA can be
 CC used to modulate expression of PKC-alpha genes. They are potentially
 CC useful in treating a variety of cancers including e.g. breast cancer,
 CC cancers of the head and neck, ovarian cancer, lung cancer, prostate
 CC cancer, and glioblastoma and for treating other proliferative diseases
 CC and conditions, such as restenosis and polycystic kidney disease. The
 CC siNA may also be useful for diagnosis, drug screening, target
 CC identification and validation, genetic engineering, studying gene
 CC function, and for gene mapping (e.g. of single-nucleotide polymorphisms).
 CC The present sequence represents a human PKC-alpha siNA target, which is
 CC used in the exemplification of the present invention.
 XX Sequence 19 BP; 0 A; 5 C; 10 G; 0 T; 4 U; 0 Other;
 SQ Query Match 0.6%; Score 13.4; DB 1; Length 19;
 XX Best Local Similarity 73.3%; Pred. No. 1.1e+03;
 PS Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 CC
 QY 466 TGGGCTGGGGGCTG 480
 DB :||||:|||||:
 5 UGGGCTUGGGGCTG 19
 RESULT 1536
 ADC56821/c
 ID ADC56821 standard; DNA; 19 BP.
 XX AC ADC56821;
 XX DT 18-DEC-2003 (first entry)
 XX DE Mouse neuromedin PCR primer 1.
 KW Mouse; oestrogen; hippocampus; gene expression; calmodulin I; chimaerin;
 KW neuromedin; T-Rec-alpha rel.; 3B-HSD related protein; ATP-binding cass.;
 KW chaperonin; HCNp; histone-like protein; ZW10; vitronectin; gene; ds.
 XX OS Mus sp.
 XX JN JP2003139771-A.
 PD 14-MAY-2003.
 XX PF 02-NOV-2001; 2001JP-00338515.
 XX PR 02-NOV-2001; 2001JP-00338515.
 PA (EISA) EISAI CO LTD.
 XX DR WPI; 2003-818084/77.
 XX Screening for estrogen analog, by administering test compound to rodents,
 PT isolating hippocampus, monitoring for the expression of a particular gene
 PT in hippocampus, and selecting compound that alters gene expression.
 PS Disclosure; Fig 2; 16pp; Japanese.
 CC The invention relates to screening for an oestrogen analogue, comprising
 CC administering a test compound to rodents, isolating hippocampus from
 CC rodents, monitoring for the expression level of a gene comprising mouse
 CC calmodulin I, chimaerin, neuromedin, T-Rec-alpha rel., 3B-HSD related

CC protein, ATP-binding cass., chaperonin, HCNp, histone-like protein,
 CC unknown, ZW10, vitronectin or unknown encoding genes (SEQ ID NO 1-13) in
 CC the hippocampus and selecting a compound that alters the gene expression
 CC as oestrogen analogue. The method is useful for screening for oestrogen
 CC analogues. The identified compound is useful for studying the effect of
 CC oestrogen on the brain. The present sequence is that of a PCR primer used
 CC to measure mouse gene expressed in the hippocampus and disclosed in the
 CC invention.
 XX Sequence 19 BP; 2 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.4; DB 1; Length 19;
 XX Best Local Similarity 93.3%; Pred. No. 1.1e+03;
 PS Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC
 QY 60 CAAGATGGCGCAGAC 74
 DB |||||||||
 18 CAAGATGGCGCTGAC 4
 RESULT 1537
 ADD24344
 ID ADD24344 standard; DNA; 19 BP.
 XX AC ADD24344;
 XX DT 15-JAN-2004 (first entry)
 XX DE CD2 binding protein 1 (CD2BP1) primer #13.
 KW human; CD2 binding protein; CD2BP1; genetic marker; autoimmune disorder;
 KW PAPA syndrome; familial recurrent arthritis; FRA syndrome; ss; PCR;
 KW primer.
 XX OS Homo sapiens.
 XX JN US2003104404-A1.
 PD 05-JUN-2003.
 XX PF 04-FEB-2002; 2002US-00067076.
 XX PR 08-NOV-2000; 2000US-00710693.
 PR 01-MAY-2001; 2001US-0287893P.
 XX (WISE/) WISE C A.
 PA Wise CA;
 PI WPI; 2003-801229/75.
 DR Novel isolated nucleic acid molecule useful as genetic markers for
 PT autoimmune disorder such as PAPA syndrome.
 XX Example 2; SEQ ID NO 16; 22pp; English.
 CC The invention relates to an isolated nucleic acid molecule where the
 CC molecule encodes CD2 binding protein (CD2BP1). The nucleic acid is useful
 CC as genetic markers for autoimmune disorder such as PAPA syndrome which is
 CC a combination of familial recurrent arthritis (FRA) syndrome and PAPA
 CC syndrome. The present sequence is used in the exemplification of the
 CC present invention.
 XX Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.4; DB 1; Length 19;
 XX Best Local Similarity 93.3%; Pred. No. 1.1e+03;
 PS Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC
 QY 1302 AATTGCCTGTGAGGA 1316
 DB |||||||||
 4 AATGCCTGTGAGGA 18

RESULT 1539
ADE27548/c
ID ADE27548 standard; RNA; 19 BP.
XX
AC ADE27548;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:492.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytosolic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
XX WPI; 2003-721687/68.
XX
DR New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearyl-CoA desaturase gene.
XX
XX Example 3; SEQ ID NO 492; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 4 C; 4 G; 0 T; 6 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1162 TTTCAGACCTTAGA 1176
DB 17 TTTCAGACCTTAGA 3
RESULT 1540

RESULT 1538
ADE27258
ID ADE27258 standard; RNA; 19 BP.
XX
AC ADE27258;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:202.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytosolic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
XX WPI; 2003-721687/68.
XX
DR New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearyl-CoA desaturase gene.
XX
XX Example 3; SEQ ID NO 202; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1162 TTTCAGACCTTAGA 1176
DB 3 UUUGAGACCUUGA 17

AAQ20654
 ID AAQ20654 standard; DNA; 20 BP.
 XX
 AC AAQ20654;
 XX
 DT 10-APR-1992 (first entry)
 XX
 DE Detection probe #1 for detecting ras oncogene DNA.
 XX
 KW Capture probe; sandwich hybridisation assay; cancer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9119812-A.
 XX
 PD 26-DEC-1991.
 XX
 PF 11-JUN-1990; 90FR-00007249.
 XX
 PR 11-JUN-1990; 90FR-00007249.
 XX
 PA (INMR) BIO MERIEUX.
 XX
 PI Cros P, Allibert P, Mallet F, Mabilat C, Mandrand B;
 XX
 DR WPI; 1992-024428/03.
 XX
 XX
 XX Sandwich hybridisation of single strand nucleic acid - using short
 PT immobilised capture probe and detection probe with non-radioactive label,
 PT for diagnosing e.g. human papilloma virus or HIV.
 XX
 PS Claim 56; Page 41; Sipp; French.
 XX
 CC Target DNA corresponding to the ras oncogene is detected using capture
 CC probe(s) AAQ20652 and/or AAQ20653 fixed passively to a solid support and
 CC detection probe(s) AAQ20654 and AAQ20655 labelled with a non-radioactive
 CC marker. The capture and detection probes are able to hybridise to non-
 CC overlapping segments of the target sequence. See AAQ20389-Q20420 and
 CC AAQ20630-Q20663
 XX
 SQ Sequence 20 BP; 2 A; 5 C; 3 G; 10 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1589 TTCTCTGTGTATTT 1603
 Db 1 TTCCTCTGTGTATTT 15
 RESULT 1541
 AAQ48910/c
 ID AAQ48910 standard; DNA; 20 BP.
 XX
 AC AAQ48910;
 XX
 DT 25-MAR-2003 (revised)
 DT 16-MAR-1994 (first entry)
 XX
 DE Cross-linking oligonucleotide 6 (anti-sense).
 XX
 KW Crosslink; ON; oligonucleotide; hairpin loop; stem loop; interior loop;
 KW bulge; fixation; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_binding 9
 FT /*tag= e
 FT /note= "crosslinked to base 9 of (AAQ48922) via an oxime
 FT linkage as in example 13b; The ONs also bind by
 FT hybridisation"
 FT

FT misc_binding 9
 FT /*tag= c
 FT /note= "crosslinked to base 9 of (AAQ48908) via O-(CH2)5-
 FT N-CH2- as in example 13a; The ONs also bind by
 FT hybridisation"
 FT
 FT modified_base 9
 FT /*tag= a
 FT /mod_base= pentylamino_functional_adenosine
 FT /note= "ref: example 4-A"
 FT
 FT misc_binding 18
 FT /*tag= f
 FT /note= "crosslinked to base 18 of (AAQ48922) via an oxime
 FT linkage as in example 13b; The ONs also bind by
 FT hybridisation"
 FT
 FT misc_binding 18
 FT /*tag= d
 FT /note= "crosslinked to base 18 of (AAQ48908) via O-(CH2)5
 FT -N-CH2- as in example 13a; The ONs also bind by
 FT hybridisation"
 FT
 FT modified_base 18
 FT /*tag= b
 FT /mod_base= pentylamino_functional_adenosine
 FT /note= "ref: example 4-A"
 FT
 FT WO9318052-A1.
 PN
 XX
 XX 16-SEP-1993.
 PD
 XX
 PF 05-MAR-1993; 93WO-US002059.
 XX
 PR 05-MAR-1992; 92US-00846376.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX
 PI Cook PD, Manoharan M, Bruice T;
 XX
 DR WPI; 1993-303395/38.
 XX
 XX New covalently crosslinked oligo-nucleotide(s) - used to fix duplex
 PT structures or hairpin loop, stem loop, interior loop, bulge or other
 PT structures.
 PT
 XX Disclosure; Page 63; 145pp; English.
 PS
 XX Sequences (AAQ48905-28) consist of novel crosslinked oligo-nucleotides. A
 CC number of crosslinking methods are claimed, which are used to fix
 CC separate ON strands in duplex structures or to fix a single ON strand in
 CC a hairpin loop, stem loop, interior loop, bulge or other similar higher-
 CC order structures. Fixing a strand or strands in a duplex structure also
 CC can disrupt the normal function of a single stranded nucleic acid-binding
 CC protein by forming nuclease resistant mimics of the protein binding
 CC receptors. The ONs have diagnostic, therapeutic and prophylactic
 CC applications as well as being used as research agents. (Updated on 25-MAR
 CC -2003 to correct PN field.)
 XX
 SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1332 TGAAGAGGAGGGAGA 1346
 Db 18 TGAAGAGGATGGAGA 4
 RESULT 1542
 AAQ34983
 ID AAQ34983 standard; DNA; 20 BP.
 XX
 AC AAQ34983;
 XX
 DT 25-MAR-2003 (revised)
 DT

DT	26-MAY-1993	(first entry)	
XX			
DE	PCR primer PV4(3')		
XX			
KW	Amplification; cervical cancer; HPV-16; human papillomavirus; ss.		
XX			
OS	Synthetic.		
XX			
PN	EP524808-A2.		
XX			
PD	27-JAN-1993.		
XX			
PF	22-JUL-1992;	92EP-00306701.	
XX			
PR	23-JUL-1991;	91US-00733419.	
XX			
PA	(HOFF) HOFFMANN LA ROCHE & CO AG F.		
PA	(UINY) UNIV NEW YORK STATE RES FOUND.		
XX			
PI	Bloch W, Nuovo GJ;		
XX			
XX			
DR	WPI; 1993-028856/04.		
XX			
PT	Compen. for in situ polymerase chain reaction on fixed cells - involves		
PT	preventing reaction until start of thermal cycling, and providing higher		
PT	sensitivity and selectivity.		
XX			
PS	Example 1; Page 10; 14pp; English.		
XX			
CC	The PCR primer PV4(3') correspond to an oligomer starting at nucleotide		
CC	956 of human papillomavirus type 16. The primer is used to demonstrate a		
CC	novel in situ PCR method comprising fixed cells, a subset of PCR reagents		
CC	and opt. a binding protein for single stranded DNA, or fixed cells, a		
CC	complete set of PCR reagents and the binding protein. The method is used		
CC	to perform PCR on cells present in histochemical sections or cytochemical		
CC	smears, e.g. for biological, forensic or pathological studies. The primer		
CC	was one of a pair used to amplify papillomavirus DNA from human cervical		
CC	cancer cells SiHa. A 449 bp PCR prod. was obtd. by this method whereas		
CC	multiple primer pairs were needed for the same result using conventional		
CC	PCR methods. See also AAQ34980-6. (Updated on 25-MAR-2003 to correct PN		
CC	field.)		
XX			
SQ	Sequence 20 BP; 2 A; 6 C; 1 G; 11 T; 0 U; 0 Other;		
Query Match 0.6%; Score 13.4; DB 1; Length 20;			
Best Local Similarity 93.3%; Pred. No. 1.2e+03;			
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	1875	ATCTCCTGTTT TTTT 1889	
Db	1	ATCCCTGTTT TTTT 15	
RESULT 1543			
AAQ40527/C			
ID	AAQ40527 standard; RNA; 20 BP.		
XX			
AC	AAQ40527;		
XX			
DT	25-MAR-2003	(revised)	
DT	12-AUG-1993	(first entry)	
XX			
DE	2' protected functionalised oligomer 10.		
XX			
KW	Linked; nucleoside; functionalised; 2'; steroid; reporter; protein;		
KW	non-aromatic; lipophilic; molecule; enzyme; peptide; metal chelator;		
KW	water soluble; vitamin; RNA cleaving complex; cholic acid; pyrene;		
KW	porphyrin; alkylator; hybrid; photo-nuclease; intercalator; agent;		
KW	aryl azide; photo-crosslinking; folic acid; heterocyclic base;		
KW	inter-strand; ss.		
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	modified_base	9	
FT		/*tag= a	
FT		/note= "Nucleotide functionalised to incorporate a pentyl	
FT		-N-phthalimido functionality acid linked to the 5'	
FT		position of the nucleoside"	
XX			
PN	WO9307893-A1.		
XX			
PD	29-APR-1993.		
XX			
PF	23-OCT-1992;	92WO-US009196.	
XX			
PR	24-OCT-1991;	91US-00782374.	
XX			
PA	(ISIS-) ISIS PHARM INC.		
XX			
PI	Manoharan M, Cook PD, Bennett CF;		
XX			
DR	WPI; 1993-152175/18.		
XX			
PT	linked nucleoside(s) in which at least one nucleoside is functionalised -		
PT	used as anti-sense diagnostic or therapeutic agents with enhanced		
PT	activity.		
XX			
PS	Disclosure; Page 24; 73pp; English.		
XX			
CC	The sequences given in AAQ40518-61 are oligonucleosides which comprise		
CC	linked nucleosides at least one of which is functionalised at its 2'.		
CC	position by attachment of a molecule selected from a steroid molecule, a		
CC	reporter molecule, a non-aromatic lipophilic molecule, a reporter enzyme,		
CC	a peptide, a protein, a water soluble vitamin, an RNA cleaving complex, a		
CC	metal chelator, a porphyrin, an alkylator, a hybrid photo-		
CC	nuclease/intercalator and an aryl azide photo-crosslinking agent. The		
CC	oligonucleosides may also comprise a 2' functionalised nucleoside having		
CC	cholic acid, pyrene, or folic acid linked to the 2' position of the		
CC	nucleoside, a heterocyclic base functionalised nucleoside having cholic		
CC	acid or folic acid linked to the heterocyclic base of the nucleoside, a		
CC	5' or 3' terminal nucleoside having cholic acid, pyrene or folic acid		
CC	linked to the 5' or 3' position of the nucleoside respectively, or an		
CC	inter-strand nucleoside having cholic acid, pyrene or folic acid linked		
CC	to an inter-nucleotide linkage linking the inter- strand nucleoside to an		
CC	adjacent nucleoside. (Updated on 25-MAR-2003 to correct PN field.)		
XX			
SQ	Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;		
Query Match 0.6%; Score 13.4; DB 1; Length 20;			
Best Local Similarity 93.3%; Pred. No. 1.2e+03;			
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	1332	TGAAGAGGAGGAGA 1346	
Db	18	TGAAGAGGATGGAGA 4	
RESULT 1544			
AAQ40548/C			
ID	AAQ40548 standard; DNA; 20 BP.		
XX			
AC	AAQ40548;		
XX			
DT	25-MAR-2003	(revised)	
DT	12-AUG-1993	(first entry)	
XX			
DE	BPV-1 functionalised oligomer 31.		
XX			
KW	Linked; nucleoside; functionalised; 2'; steroid; reporter; protein;		
KW	non-aromatic; lipophilic; molecule; enzyme; peptide; metal chelator;		
KW	water soluble; vitamin; RNA cleaving complex; cholic acid; pyrene;		
KW	porphyrin; alkylator; hybrid; photo-nuclease; intercalator; agent;		
KW	aryl azide; photo-crosslinking; folic acid; heterocyclic base;		
KW	inter-strand; ss.		
OS			
XX			

OS Synthetic.
 PN WO9307883-AL.
 XX 29-APR-1993.
 XX 23-OCT-1992; 92WO-US009196.
 XX 24-OCT-1991; 91US-00782374.
 XX (ISIS-) ISIS PHARM INC.
 PA Manoharan M, Cook PD, Bennett CF;
 PI WPI; 1993-152175/18.
 DR Linked nucleoside(s) in which at least one nucleoside is functionalised -
 XX used as anti-sense diagnostic or therapeutic agents with enhanced
 PT activity.
 XX Disclosure; Page 39; 73pp; English.
 PS The sequences given in AAQ0518-61 are oligonucleosides which comprise
 XX linked nucleosides at least one of which is functionalised at its 2',
 CC position by attachment of a molecule selected from a steroid molecule, a
 CC reporter molecule, a non-aromatic lipophilic molecule, a reporter enzyme,
 CC a peptide, a protein, a water soluble vitamin, an RNA cleaving complex, a
 CC metal chelator, a porphyrin, an alkylator, a hybrid photo-
 CC nuclease/intercalator and an aryl azide photo-crosslinking agent. The
 CC oligonucleosides may also comprise a 2' functionalised nucleoside having
 CC cholic acid, pyrene, or folic acid linked to the 2' position of the
 CC nucleoside, a heterocyclic base functionalised nucleoside having cholic
 CC acid or folic acid linked to the heterocyclic base of the nucleoside, a
 CC 5' or 3' terminal nucleoside having cholic acid, pyrene or folic acid
 CC linked to the 5' or 3' position of the nucleoside respectively, or an
 CC inter-strand nucleoside having cholic acid, pyrene or folic acid linked
 CC to an inter-nucleotide linkage linking the inter- strand nucleoside to an
 CC adjacent nucleoside. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1332 TGAAGAGGAGGAGA 1346
 Db |||||
 18 TGAAGAGGATGGAGA 4
 RESULT 1545
 AAQ0540/c
 ID AAQ0540 standard; DNA; 20 BP.
 XX AAQ0540;
 XX 25-MAR-2003 (revised)
 DT 12-AUG-1993 (first entry)
 XX 2' functionalised oligomer 23.
 DE
 XX Linked; nucleoside; functionalised; 2'; steroid; reporter; protein;
 KW non-aromatic; lipophilic; molecule; enzyme; peptide; metal chelator;
 KW water soluble; vitamin; RNA cleaving complex; cholic acid; pyrene;
 KW porphyrin; alkylator; hybrid; photo-nuclease; intercalator; agent;
 KW aryl azide; photo-crosslinking; folic acid; heterocyclic base;
 KW inter-strand; ss.
 XX Synthetic.
 OS Key Location/Qualifiers
 PH modified_base 9 /*tag= a
 FT

FT /note= "Incorporates a SV40 peptide functionality linked
 XX via a 2'-O-pentyl-amino-sulpho-SMCC (sulphosuccinimidyl-4
 FT -(N-maleimidomethyl)- cyclohexane-1-carboxylate) linking
 FT group to the 2' position of the nucleotide"
 XX WO9307883-AL.
 PN 29-APR-1993.
 XX 23-OCT-1992; 92WO-US009196.
 XX 24-OCT-1991; 91US-00782374.
 XX (ISIS-) ISIS PHARM INC.
 PA Manoharan M, Cook PD, Bennett CF;
 PI WPI; 1993-152175/18.
 DR Linked nucleoside(s) in which at least one nucleoside is functionalised -
 XX used as anti-sense diagnostic or therapeutic agents with enhanced
 PT activity.
 XX Disclosure; Page 31; 73pp; English.
 PS The sequences given in AAQ0518-61 are oligonucleosides which comprise
 XX linked nucleosides at least one of which is functionalised at its 2',
 CC position by attachment of a molecule selected from a steroid molecule, a
 CC reporter molecule, a non-aromatic lipophilic molecule, a reporter enzyme,
 CC a peptide, a protein, a water soluble vitamin, an RNA cleaving complex, a
 CC metal chelator, a porphyrin, an alkylator, a hybrid photo-
 CC nuclease/intercalator and an aryl azide photo-crosslinking agent. The
 CC oligonucleosides may also comprise a 2' functionalised nucleoside having
 CC cholic acid, pyrene, or folic acid linked to the 2' position of the
 CC nucleoside, a heterocyclic base functionalised nucleoside having cholic
 CC acid or folic acid linked to the heterocyclic base of the nucleoside, a
 CC 5' or 3' terminal nucleoside having cholic acid, pyrene or folic acid
 CC linked to the 5' or 3' position of the nucleoside respectively, or an
 CC inter-strand nucleoside having cholic acid, pyrene or folic acid linked
 CC to an inter-nucleotide linkage linking the inter- strand nucleoside to an
 CC adjacent nucleoside. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1332 TGAAGAGGAGGAGA 1346
 Db |||||
 18 TGAAGAGGATGGAGA 4
 RESULT 1546
 AAQ0536/c
 ID AAQ0536 standard; DNA; 20 BP.
 XX AAQ0536;
 XX 25-MAR-2003 (revised)
 DT 12-AUG-1993 (first entry)
 XX 2' functionalised oligomer 19.
 DE
 XX Linked; nucleoside; functionalised; 2'; steroid; reporter; protein;
 KW non-aromatic; lipophilic; molecule; enzyme; peptide; metal chelator;
 KW water soluble; vitamin; RNA cleaving complex; cholic acid; pyrene;
 KW porphyrin; alkylator; hybrid; photo-nuclease; intercalator; agent;
 KW aryl azide; photo-crosslinking; folic acid; heterocyclic base;
 KW inter-strand; ss.
 XX Synthetic.

FH Key Location/Qualifiers
FT modified_base 9
FT /*tag= a
FT /note= "Incorporates a fluorescein functionality linked
FT via a 2'-O-pentyl-amino linking group"
FT 18
FT modified_base 18
FT /*tag= a
FT /note= "Incorporates a fluorescein functionality linked
FT via a 2'-O-pentyl-amino linking group"
XX
XX WO9307883-A1.
XX
XX
XX 29-APR-1993.
XX
XX 23-OCT-1992; 92WO-US009196.
XX
XX 24-OCT-1991; 91US-00782374.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD, Bennett CF;
XX
XX WPI; 1993-152175/18.
XX
XX Linked nucleoside(s) in which at least one nucleoside is functionalised -
XX PT used as anti-sense diagnostic or therapeutic agents with enhanced
XX PT activity.
XX
XX Disclosure; Page 28; 73pp; English.
XX
XX The sequences given in AAQ40518-61 are oligonucleosides which comprise
XX linked nucleosides at least one of which is functionalised at its 2',
XX position by attachment of a molecule selected from a steroid molecule, a
XX reporter molecule, a non-aromatic lipophilic molecule, a reporter enzyme,
XX a peptide, a protein, a water soluble vitamin, an RNA cleaving complex, a
XX metal chelator, a porphyrin, an alkylator, a hybrid photo-
XX nuclease/intercalator and an aryl azide photo-crosslinking agent. The
XX oligonucleosides may also comprise a 2' functionalised nucleoside having
XX cholic acid, pyrene, or folic acid linked to the 2' position of the
XX nucleoside, a heterocyclic base functionalised nucleoside having cholic
XX acid or folic acid linked to the heterocyclic base of the nucleoside, a
XX 5' or 3' terminal nucleoside having cholic acid, pyrene or folic acid
XX linked to the 5' or 3' position of the nucleoside respectively, or an
XX inter-strand nucleoside having cholic acid, pyrene or folic acid linked
XX to an inter-nucleotide linkage linking the inter- strand nucleoside to an
XX adjacent nucleoside. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.4; DB 1; Length 20;
XX Best Local Similarity 93.3%; Pred. No. 1.2e+03;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1332 TGAAGAGGAGGGAGA 1346
XX |||||
XX Db 18 TGAAGAGGATGGAGA 4
XX
XX RESULT 1547
XX AAQ40537/C
XX ID AAQ40537 standard; DNA; 20 BP.
XX
XX AC AAQ40537;
XX
XX 25-MAR-2003 (revised)
XX 12-AUG-1993 (first entry)
XX
XX 2' functionalised oligomer 20.
XX
XX Linked; nucleoside; functionalised; 2'; steroid; reporter; protein;
XX non-aromatic; lipophilic; molecule; enzyme; peptide; metal chelator;
XX water soluble; vitamin; RNA cleaving complex; cholic acid; pyrene;
XX porphyrin; alkylator; hybrid; photo-nuclease; intercalator; agent;

KW aryl azide; photo-crosslinking; folic acid; heterocyclic base;
KW inter-strand; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 9
FT /*tag= a
FT /note= "Incorporates a cholic acid functionality linked
FT via a 2'-O-pentyl-amino linking group"
XX
XX WO9307883-A1.
XX
XX 29-APR-1993.
XX
XX 23-OCT-1992; 92WO-US009196.
XX
XX 24-OCT-1991; 91US-00782374.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD, Bennett CF;
XX
XX WPI; 1993-152175/18.
XX
XX Linked nucleoside(s) in which at least one nucleoside is functionalised -
XX PT used as anti-sense diagnostic or therapeutic agents with enhanced
XX PT activity.
XX
XX Disclosure; Page 28; 73pp; English.
XX
XX The sequences given in AAQ40518-61 are oligonucleosides which comprise
XX linked nucleosides at least one of which is functionalised at its 2',
XX position by attachment of a molecule selected from a steroid molecule, a
XX reporter molecule, a non-aromatic lipophilic molecule, a reporter enzyme,
XX a peptide, a protein, a water soluble vitamin, an RNA cleaving complex, a
XX metal chelator, a porphyrin, an alkylator, a hybrid photo-
XX nuclease/intercalator and an aryl azide photo-crosslinking agent. The
XX oligonucleosides may also comprise a 2' functionalised nucleoside having
XX cholic acid, pyrene, or folic acid linked to the 2' position of the
XX nucleoside, a heterocyclic base functionalised nucleoside having cholic
XX acid or folic acid linked to the heterocyclic base of the nucleoside, a
XX 5' or 3' terminal nucleoside having cholic acid, pyrene or folic acid
XX linked to the 5' or 3' position of the nucleoside respectively, or an
XX inter-strand nucleoside having cholic acid, pyrene or folic acid linked
XX to an inter-nucleotide linkage linking the inter- strand nucleoside to an
XX adjacent nucleoside. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.4; DB 1; Length 20;
XX Best Local Similarity 93.3%; Pred. No. 1.2e+03;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1332 TGAAGAGGAGGGAGA 1346
XX |||||
XX Db 18 TGAAGAGGATGGAGA 4
XX
XX RESULT 1548
XX AAQ40538/C
XX ID AAQ40538 standard; DNA; 20 BP.
XX
XX AC AAQ40538;
XX
XX 25-MAR-2003 (revised)
XX 12-AUG-1993 (first entry)
XX
XX 2' functionalised oligomer 21.
XX
XX Linked; nucleoside; functionalised; 2'; steroid; reporter; protein;
XX non-aromatic; lipophilic; molecule; enzyme; peptide; metal chelator;
XX water soluble; vitamin; RNA cleaving complex; cholic acid; pyrene;

KW porphyrin; alkylator; hybrid; photo-nuclease; intercalator; agent;
 KW aryl azide; photo-crosslinking; folic acid; heterocyclic base;
 XX inter-strand; ss.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 9
 FT /*tag= a
 FT /note= "Incorporates a cholic acid functionality linked
 FT via a 2'-O-pentyl-amino linking group"
 FT modified_base 18
 FT /*tag= b
 FT /note= "Incorporates a cholic acid functionality linked
 FT via a 2'-O-pentyl-amino linking group"
 XX
 XX
 PN WO9307883-A1.
 XX
 XX
 PD 29-APR-1993.
 XX
 XX 23-OCT-1992; 92WO-US009196.
 XX
 XX 24-OCT-1991; 91US-00782374.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 XX Manoharan M, Cook PD, Bennett CF;
 PI
 XX WPI; 1993-152175/18.
 DR
 XX
 XX Linked nucleoside(s) in which at least one nucleoside is functionalised -
 PT used as anti-sense diagnostic or therapeutic agents with enhanced
 PT activity.
 XX
 PS Disclosure; Page 29; 73pp; English.
 XX
 CC The sequences given in AAQ0518-61 are oligonucleosides which comprise
 CC linked nucleosides at least one of which is functionalised at its 2'
 CC position by attachment of a molecule selected from a steroid molecule, a
 CC reporter molecule, a non-aromatic lipophilic molecule, a reporter enzyme,
 CC a peptide, a protein, a water soluble vitamin, an RNA cleaving complex, a
 CC metal chelator, a porphyrin, an alkylator, a hybrid photo-
 CC nuclease/intercalator and an aryl azide photo-crosslinking agent. The
 CC oligonucleosides may also comprise a 2' functionalised nucleoside having
 CC cholic acid, pyrene, or folic acid linked to the 2' position of the
 CC nucleoside, a heterocyclic base functionalised nucleoside having cholic
 CC acid or folic acid linked to the heterocyclic base of the nucleoside, a
 CC 5' or 3' terminal nucleoside having cholic acid, pyrene or folic acid
 CC linked to the 5' or 3' position of the nucleoside respectively, or an
 CC inter-strand nucleoside having cholic acid, pyrene or folic acid linked
 CC to an inter-nucleotide linkage linking the inter- strand nucleoside to an
 CC adjacent nucleoside. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1332 TGAAGAGGAGGAGA 1346
 Db |||||
 18 TGAAGAGGAGGAGA 4
 RESULT 1549
 AAQ0561/C
 ID AAQ0561 standard; DNA; 20 BP.
 XX
 AC AAQ0561;
 XX
 XX 25-MAR-2003 (revised)
 DT 12-AUG-1993 (first entry)
 XX
 XX 2' protected functionalised oligomer 11.
 XX
 XX Linked; nucleoside; functionalised; 2'; steroid; reporter; protein;
 KW non-aromatic; lipophilic; molecule; enzyme; peptide; metal chelator;
 KW water soluble; vitamin; RNA cleaving complex; cholic acid; pyrene;
 KW porphyrin; alkylator; hybrid; photo-nuclease; intercalator; agent;
 KW aryl azide; photo-crosslinking; folic acid; heterocyclic base;
 KW inter-strand; ss.

DE 2' functionalised oligomer 44.
 XX
 KW Linked; nucleoside; functionalised; 2'; steroid; reporter; protein;
 KW non-aromatic; lipophilic; molecule; enzyme; peptide; metal chelator;
 KW water soluble; vitamin; RNA cleaving complex; cholic acid; pyrene;
 KW porphyrin; alkylator; hybrid; photo-nuclease; intercalator; agent;
 KW aryl azide; photo-crosslinking; folic acid; heterocyclic base;
 KW inter-strand; ss.
 XX
 XX Synthetic.
 OS
 XX
 PN WO9307883-A1.
 XX
 XX 29-APR-1993.
 PD
 XX 23-OCT-1992; 92WO-US009196.
 PF
 XX 24-OCT-1991; 91US-00782374.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Manoharan M, Cook PD, Bennett CF;
 PI
 XX WPI; 1993-152175/18.
 DR
 XX
 XX Linked nucleoside(s) in which at least one nucleoside is functionalised -
 PT used as anti-sense diagnostic or therapeutic agents with enhanced
 PT activity.
 XX
 PS Disclosure; Page 55; 73pp; English.
 XX
 CC The sequences given in AAQ0518-61 are oligonucleosides which comprise
 CC linked nucleosides at least one of which is functionalised at its 2'
 CC position by attachment of a molecule selected from a steroid molecule, a
 CC reporter molecule, a non-aromatic lipophilic molecule, a reporter enzyme,
 CC a peptide, a protein, a water soluble vitamin, an RNA cleaving complex, a
 CC metal chelator, a porphyrin, an alkylator, a hybrid photo-
 CC nuclease/intercalator and an aryl azide photo-crosslinking agent. The
 CC oligonucleosides may also comprise a 2' functionalised nucleoside having
 CC cholic acid, pyrene, or folic acid linked to the 2' position of the
 CC nucleoside, a heterocyclic base functionalised nucleoside having cholic
 CC acid or folic acid linked to the heterocyclic base of the nucleoside, a
 CC 5' or 3' terminal nucleoside having cholic acid, pyrene or folic acid
 CC linked to the 5' or 3' position of the nucleoside respectively, or an
 CC inter-strand nucleoside having cholic acid, pyrene or folic acid linked
 CC to an inter-nucleotide linkage linking the inter- strand nucleoside to an
 CC adjacent nucleoside. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1332 TGAAGAGGAGGAGA 1346
 Db |||||
 18 TGAAGAGGAGGAGA 4
 RESULT 1550
 AAQ0528/C
 ID AAQ0528 standard; RNA; 20 BP.
 XX
 AC AAQ0528;
 XX
 XX 25-MAR-2003 (revised)
 DT 12-AUG-1993 (first entry)
 XX
 XX 2' protected functionalised oligomer 11.
 XX
 XX Linked; nucleoside; functionalised; 2'; steroid; reporter; protein;
 KW non-aromatic; lipophilic; molecule; enzyme; peptide; metal chelator;
 KW water soluble; vitamin; RNA cleaving complex; cholic acid; pyrene;


```

FT modified_base 16. .17
FT /tag= p
FT /note= "Phosphorothioate inter-nucleotide backbone
FT linkage"
FT modified_base 17. .18
FT /tag= q
FT /note= "Phosphorothioate inter-nucleotide backbone
FT linkage"
FT modified_base 18. .19
FT /tag= r
FT /note= "Phosphorothioate inter-nucleotide backbone
FT linkage"
FT modified_base 19. .20
FT /tag= s
FT /note= "Phosphorothioate inter-nucleotide backbone
FT linkage"
FT modified_base 20
FT /tag= t
FT /note= "Nucleotide functionalised to include a cholic
FT acid linked to the 5' position of the nucleoside"
FT
FT
PN WO9307883-A1.
XX
XX
PD 29-APR-1993.
XX
XX
PF 23-OCT-1992; 92WO-US009196.
XX
XX
PR 24-OCT-1991; 91US-00782374.
XX
XX
PA (ISIS-) ISIS PHARM INC.
XX
XX
PI Manoharan M, Cook PD, Bennett CF;
XX
XX
DR WPI; 1993-152175/18.
XX
XX
PT Linked nucleoside(s) in which at least one nucleoside is functionalised -
PT used as anti-sense diagnostic or therapeutic agents with enhanced
PT activity.
XX
XX
PS Disclosure; Page 20; 73pp; English.
XX
XX
CC The sequences given in AAQ40534-61 are oligonucleosides which comprise
CC linked nucleosides at least one of which is functionalised at its 2'
CC position by attachment of a molecule selected from a steroid molecule, a
CC reporter molecule, a non-aromatic lipophilic molecule, a reporter enzyme,
CC a peptide, a protein, a water soluble vitamin, an RNA cleaving complex, a
CC metal chelator, a porphyrin, an alkylator, a hybrid photo-
CC nuclease/intercalator and an aryl azide photo-crosslinking agent. The
CC oligonucleosides may also comprise a 2' functionalised nucleoside having
CC cholic acid, pyrene, or folic acid linked to the 2' position of the
CC nucleoside, a heterocyclic base functionalised nucleoside having cholic
CC acid or folic acid linked to the heterocyclic base of the nucleoside, a
CC 5' or 3' terminal nucleoside having cholic acid, pyrene or folic acid
CC linked to the 5' or 3' position of the nucleoside respectively, or an
CC inter-strand nucleoside having cholic acid, pyrene or folic acid linked
CC to an inter-nucleotide linkage linking the inter- strand nucleoside to an
CC adjacent nucleoside. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1332 TGAAGAGGAGGAGA 1346
DB 18 TGAAGAGGAGGAGA 4
RESULT 1552
AAQ40534/c
ID AAQ40534 standard; DNA; 20 BP.
XX

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AC AAQ40534;
XX
XX
DT 25-MAR-2003 (revised)
DT 12-AUG-1993 (first entry)
XX
XX
DE 2' functionalised oligomer 17.
XX
XX
KW Linked; nucleoside; functionalised; 2'; steroid; reporter; protein;
KW non-aromatic; lipophilic; molecule; enzyme; peptide; metal chelator;
KW water soluble; vitamin; RNA cleaving complex; cholic acid; pyrene;
KW porphyrin; alkylator; hybrid; photo-nuclease; intercalator; agent;
KW aryl azide; photo-crosslinking; folic acid; heterocyclic base;
KW inter-strand; ss.
XX
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 9
FT /tag= a
FT /note= "Incorporates a biotin functionality linked via a
FT 2'-O-pentyl-amino linking group"
XX
XX
PN WO9307883-A1.
XX
XX
PD 29-APR-1993.
XX
XX
PF 23-OCT-1992; 92WO-US009196.
XX
XX
PR 24-OCT-1991; 91US-00782374.
XX
XX
PA (ISIS-) ISIS PHARM INC.
XX
XX
PI Manoharan M, Cook PD, Bennett CF;
XX
XX
DR WPI; 1993-152175/18.
XX
XX
PT Linked nucleoside(s) in which at least one nucleoside is functionalised -
PT used as anti-sense diagnostic or therapeutic agents with enhanced
PT activity.
XX
XX
PS Disclosure; Page 26; 73pp; English.
XX
XX
CC The sequences given in AAQ40518-61 are oligonucleosides which comprise
CC linked nucleosides at least one of which is functionalised at its 2'
CC position by attachment of a molecule selected from a steroid molecule, a
CC reporter molecule, a non-aromatic lipophilic molecule, a reporter enzyme,
CC a peptide, a protein, a water soluble vitamin, an RNA cleaving complex, a
CC metal chelator, a porphyrin, an alkylator, a hybrid photo-
CC nuclease/intercalator and an aryl azide photo-crosslinking agent. The
CC oligonucleosides may also comprise a 2' functionalised nucleoside having
CC cholic acid, pyrene, or folic acid linked to the 2' position of the
CC nucleoside, a heterocyclic base functionalised nucleoside having cholic
CC acid or folic acid linked to the heterocyclic base of the nucleoside, a
CC 5' or 3' terminal nucleoside having cholic acid, pyrene or folic acid
CC linked to the 5' or 3' position of the nucleoside respectively, or an
CC inter-strand nucleoside having cholic acid, pyrene or folic acid linked
CC to an inter-nucleotide linkage linking the inter- strand nucleoside to an
CC adjacent nucleoside. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1332 TGAAGAGGAGGAGA 1346
DB 18 TGAAGAGGAGGAGA 4
RESULT 1553
AAQ40535/c
ID AAQ40535 standard; DNA; 20 BP.
XX

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XX AAQ40535;
AC
XX 25-MAR-2003 (revised)
DT 12-AUG-1993 (first entry)
XX
DE 2' functionalised oligomer 18.
XX
KW Linked; nucleoside; functionalised; 2'; steroid; reporter; protein;
KW non-aromatic; lipophilic; molecule; enzyme; peptide; metal chelator;
KW water soluble; vitamin; RNA cleaving complex; cholic acid; pyrene;
KW porphyrin; alkylator; hybrid; photo-nuclease; intercalator; agent;
KW aryl azide; photo-crosslinking; folic acid; heterocyclic base;
KW inter-strand; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 9 /*tag= a
FT /note= "Incorporates a biotin functionality linked via a
FT 2'-O-pentyl-amino linking group"
FT modified_base 15
FT /*tag= a
FT /note= "Incorporates a biotin functionality linked via a
FT 2'-O-pentyl-amino linking group"
XX
PN WO9307883-A1.
XX
XX 29-APR-1993.
XX
XX 23-OCT-1992; 92WO-US009196.
XX
XX 24-OCT-1991; 91US-00782374.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD, Bennett CF;
XX WPI; 1993-152175/18.
XX
XX Linked nucleoside(s) in which at least one nucleoside is functionalised -
XX used as anti-sense diagnostic or therapeutic agents with enhanced
XX activity.
XX
XX Disclosure; Page 27; 73pp; English.
XX
XX The sequences given in AAQ40518-61 are oligonucleosides which comprise
XX linked nucleosides at least one of which is functionalised at its 2'
XX position by attachment of a molecule selected from a steroid molecule, a
XX reporter molecule, a non-aromatic lipophilic molecule, a reporter enzyme,
XX a peptide, a protein, a water soluble vitamin, an RNA cleaving complex, a
XX metal chelator, a porphyrin, an alkylator, a hybrid photo-
XX nuclease/intercalator and an aryl azide photo-crosslinking agent. The
XX oligonucleosides may also comprise a 2' functionalised nucleoside having
XX cholic acid, pyrene, or folic acid linked to the 2' position of the
XX nucleoside, a heterocyclic base functionalised nucleoside having cholic
XX acid or folic acid linked to the heterocyclic base of the nucleoside, a
XX 5' or 3' terminal nucleoside having cholic acid, pyrene or folic acid
XX linked to the 5' or 3' position of the nucleoside respectively, or an
XX inter-strand nucleoside having cholic acid, pyrene or folic acid linked
XX to an inter-nucleotide linkage linking the inter- strand nucleoside to an
XX adjacent nucleoside. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1332 TGAAGAGGAGGAGA 1346
Db 18 TGAAGAGGATGAGA 4

RESULT 1554
AAQ40539/c
ID AAQ40539 standard; DNA; 20 BP.
XX
XX AC AAQ40539;
AC
XX 25-MAR-2003 (revised)
DT 12-AUG-1993 (first entry)
XX
DE 2' functionalised oligomer 22.
XX
KW Linked; nucleoside; functionalised; 2'; steroid; reporter; protein;
KW non-aromatic; lipophilic; molecule; enzyme; peptide; metal chelator;
KW water soluble; vitamin; RNA cleaving complex; cholic acid; pyrene;
KW porphyrin; alkylator; hybrid; photo-nuclease; intercalator; agent;
KW aryl azide; photo-crosslinking; folic acid; heterocyclic base;
KW inter-strand; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 9 /*tag= a
FT /note= "Incorporates a digoxigenin functionality linked
FT via a 2'-O-pentyl-amino linking group to the 2' position
FT of the nucleotide"
XX
PN WO9307883-A1.
XX
XX 29-APR-1993.
XX
XX 23-OCT-1992; 92WO-US009196.
XX
XX 24-OCT-1991; 91US-00782374.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD, Bennett CF;
XX WPI; 1993-152175/18.
XX
XX Linked nucleoside(s) in which at least one nucleoside is functionalised -
XX used as anti-sense diagnostic or therapeutic agents with enhanced
XX activity.
XX
XX Disclosure; Page 29; 73pp; English.
XX
XX The sequences given in AAQ40518-61 are oligonucleosides which comprise
XX linked nucleosides at least one of which is functionalised at its 2'
XX position by attachment of a molecule selected from a steroid molecule, a
XX reporter molecule, a non-aromatic lipophilic molecule, a reporter enzyme,
XX a peptide, a protein, a water soluble vitamin, an RNA cleaving complex, a
XX metal chelator, a porphyrin, an alkylator, a hybrid photo-
XX nuclease/intercalator and an aryl azide photo-crosslinking agent. The
XX oligonucleosides may also comprise a 2' functionalised nucleoside having
XX cholic acid, pyrene, or folic acid linked to the 2' position of the
XX nucleoside, a heterocyclic base functionalised nucleoside having cholic
XX acid or folic acid linked to the heterocyclic base of the nucleoside, a
XX 5' or 3' terminal nucleoside having cholic acid, pyrene or folic acid
XX linked to the 5' or 3' position of the nucleoside respectively, or an
XX inter-strand nucleoside having cholic acid, pyrene or folic acid linked
XX to an inter-nucleotide linkage linking the inter- strand nucleoside to an
XX adjacent nucleoside. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1332 TGAAGAGGAGGAGA 1346
Db 18 TGAAGAGGATGAGA 4

XX DE Oligonucleotide used in amine containing therapeutic.

XX KW Oligonucleotide; analogue; antisense; therapy; diagnosis; identification;

XX KW retention; therapeutic; amine; lipophile; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT misc_feature 9

XX FT /*tag= a

XX FT /note= "2'-O-aminopentoxo-2'-deoxyadenosine."

XX PN WO9406815-A1.

XX PD 31-MAR-1994.

XX PF 03-SEP-1993; 93WO-US008367.

XX PR 11-SEP-1992; 92US-00943516.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Manoharan M, Cook PD;

XX PI WPI; 1994-118388/14.

XX DR Nucleotide and oligo-nucleotide (poly)amine analogues - used in anti-

XX DR sense therapy, diagnosis, and identification, amino gp. enhances cell

XX DR uptake and retention.

XX PS Example 4; Page 31; 93pp; English.

XX CC The sequence is used in the production of an amine analogue. The analogue

XX CC may be used in antisense therapy. The analogue may also have enhanced

XX CC cellular uptake, increased lipophilicity, cause greater cellular

XX CC retention and demonstrate increased distribution. (Updated on 25-MAR-2003

XX CC to correct PN field.)

XX SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;

Best Local Similarity 93.3%; Pred. No. 1.2e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1332 TGAAGAGGAGGAGAGA 1346

Db 18 TGAAGAGGATGGAGA 4

RESULT 1558

AAQ45151/c

ID AAQ45151 standard; DNA; 20 BP.

XX AC AAQ45151;

XX DT 25-MAR-2003 (revised)

XX DT 31-OCT-1994 (first entry)

XX DE Oligonucleotide used in amine containing therapeutic.

XX KW Oligonucleotide; analogue; antisense; therapy; diagnosis; identification;

XX KW retention; therapeutic; amine; lipophile; ss.

XX OS Synthetic.

XX PN WO9406815-A1.

XX PD 31-MAR-1994.

XX PF 03-SEP-1993; 93WO-US008367.

XX PR 11-SEP-1992; 92US-00943516.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Manoharan M, Cook PD;

XX PI WPI; 1994-118388/14.

XX XX Nucleotide and oligo-nucleotide (poly)amine analogues - used in anti-

XX PT sense therapy, diagnosis, and identification, amino gp. enhances cell

XX PT uptake and retention.

XX PS Example 4; Page 31; 93pp; English.

XX CC The sequence is used in the production of an amine analogue. The analogue

XX CC may be used in antisense therapy. The analogue may also have enhanced

XX CC cellular uptake, increased lipophilicity, cause greater cellular

XX CC retention and demonstrate increased distribution. (Updated on 25-MAR-2003

XX CC to correct PN field.)

XX SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;

Best Local Similarity 93.3%; Pred. No. 1.2e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1332 TGAAGAGGAGGAGAGA 1346

Db 18 TGAAGAGGATGGAGA 4

RESULT 1559

AAQ85800/c

ID AAQ85800 standard; DNA; 20 BP.

XX AC AAQ85800;

XX DT 25-MAR-2003 (revised)

XX DT 03-NOV-1995 (first entry)

XX DE Alkylamino chemical functionality-containing oligomer #12.

XX KW Alkylamino group; ribofuranosyl sugar; antisense therapy; virus; HIV;

XX KW herpes; papilloma; antiviral; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT misc_feature 9

XX FT /*tag= a

XX FT /note= "contains a pentyl-N-phthalimido functional group"

XX FT misc_feature 18

XX FT /*tag= a

XX FT /note= "optionally contains a pentyl-N-phthalimido

XX FT functional group"

XX PN WO9506659-A1.

XX PD 09-MAR-1995.

XX PF 02-SEP-1994; 94WO-US010131.

XX PR 03-SEP-1993; 93US-00117363.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Cook PD, Manoharan M, Guinasso CJ;

XX PI WPI; 1995-115397/15.

XX DR New amine-derivatised nucleoside(s) and oligo-nucleoside(s) - useful as

XX PT diagnostics, therapeutics and research reagents, partic. in anti-sense

XX PT therapy.

PS Example 1; Page 16; 117pp; English.

XX The sequence of a oligonucleotide sequence with a nucleotide
 CC incorporating an alkylamino functional group e.g. pentyl-N- phthalimido
 CC function. This oligonucleotide is an antisense sequence targeted to the
 CC E2 region of the bovine papilloma virus-1. This is an example of a
 CC compound (see AAQ85799-Q85839 for other examples) e.g. a nucleoside or
 CC oligonucleoside, which contains a ribofuranosyl sugar portion and a base
 CC portion, such that at least one of the nucleoside contains a substitution
 CC at a 2'-O-, 3'-O- or 5'-O-position. (See AAQ85799 for details of the
 CC substitutions). The compounds are useful in diagnostics, therapeutics and
 CC as research reagents particularly in antisense therapy for killing cells
 CC and viruses such as HIV, herpes or papilloma viruses. (Updated on 25-MAR-
 CC 2003 to correct PN field.)

XX Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1332 TGAAGAGGAGGAGGA 1346
 |||||
 DB 18 TGAAGAGGAGGAGGA 4

RESULT 1561
 AAQ85803/C
 ID AAQ85803 standard; DNA; 20 BP.
 XX AC AAQ85803;
 XX 25-MAR-2003 (revised)
 DT 03-NOV-1995 (first entry)
 XX Alkylamino chemical functionality-containing oligomer #19.
 DE Alkylamino group; ribofuranosyl sugar; antisense therapy; virus; HIV;
 KW herpes; papilloma; antiviral; ss.
 XX Synthetic.

Key Location/Qualifiers
 FT misc_feature 9
 FT /tag= a
 FT /note= "contains a biotin, fluorescein or cholic acid
 FT functional group linked via a 2'-O-pentyl amino group to
 FT the 2' position"
 FT misc_feature 18
 FT /tag= a
 FT /note= "contains a biotin, fluorescein or cholic acid
 FT functional group linked via a 2'-O-pentyl amino group to
 FT the 2' position"

XX W09506659-Al.
 XX 09-MAR-1995.
 XX 02-SEP-1994; 94WO-US010131.
 XX 03-SEP-1993; 93US-00117363.
 XX (ISIS-) ISIS PHARM INC.
 XX Cook PD, Manoharan M, Guinasso CJ;
 XX WPI; 1995-115397/15.
 XX New amine-derivatised nucleoside(s) and oligo-nucleoside(s) - useful as
 PT diagnostics, therapeutics and research reagents, partic. in anti-sense
 PT therapy.

XX Example 2; Page 18; 117pp; English.

XX The sequence of a oligonucleotide sequence with a nucleotide
 CC incorporating a biotin group at position 9. This is an example of a
 CC compound (see AAQ85799-Q85839 for other examples) e.g. a nucleoside or
 CC oligonucleoside, which contains a ribofuranosyl sugar portion and a base
 CC portion, such that at least one of the nucleoside contains a substitution
 CC at a 2'-O-, 3'-O- or 5'-O-position. (See AAQ85799 for details of the
 CC substitutions). The compounds are useful in diagnostics, therapeutics and
 CC as research reagents particularly in antisense therapy for killing cells
 CC and viruses such as HIV, herpes or papilloma viruses. (Updated on 25-MAR-
 CC 2003 to correct PN field.)

XX Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1332 TGAAGAGGAGGAGGA 1346
 |||||
 DB 18 TGAAGAGGAGGAGGA 4

RESULT 1561
 AAQ81117/C
 ID AAQ81117 standard; DNA; 20 BP.
 XX AC AAQ81117;
 XX 25-MAR-2003 (revised)
 DT 28-SEP-1995 (first entry)
 XX Peptide nucleic acid.
 DE Peptide nucleic acid; gene therapy; transcription arrest; diagnosis;
 KW prophylaxis; ss.
 XX Synthetic.

Key Location/Qualifiers
 FT modified_base 20
 FT /tag= a
 FT /note= "amidated"

XX W09501370-Al.
 XX 12-JAN-1995.
 XX 28-JUN-1994; 94WO-US007319.
 XX 02-JUL-1993; 93US-00088658.
 XX (ISIS-) ISIS PHARM INC.
 XX Buchardt O, Egholm M, Nielsen PE, Berg RH, Ecker DJ;
 XX Mollegaard NE;
 XX WPI; 1995-060949/08.
 XX Use of oligonucleotide analogues, partic. peptide nucleic acids - for
 PT binding to ssDNA, dsDNA or RNA for use in therapy, diagnosis and
 PT prophylaxis.
 XX Example 1; Page 28; 139pp; English.
 XX AAQ81117 is a peptide nucleic acid (PNA), which binds a target sequence.
 CC The binding of the PNA prevents the transcription of the target sequence
 CC by RNA polymerase. The ability of the PNA to arrest transcription makes
 CC it useful in gene therapy, and in diagnostic and prophylactic methods.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1332 TGAAGAGGAGGAGA 1346
|||||
DB 18 TGAAGAGGATGGAGA 4

QY 1332 TGAAGAGGAGGAGA 1346
|||||
DB 18 TGAAGAGGATGGAGA 4

RESULT 1563
AAQ95776/c
ID AAQ95776 standard; DNA; 20 BP.
XX
AC AAQ95776;
XX
DT 20-FEB-1996 (first entry)
XX
DE Primer B (Group 8, set C) for marker D17S793, chromosome 17.
XX
KW primer; polymerase chain reaction; PCR; linkage study; locus;
KW microsatellite marker sequence; automated genotyping; allele;
KW polymorphism; detection; Homo sapiens; ss.
XX
OS Synthetic.
XX
PN WO9515400-A1.
XX
PD 08-JUN-1995.
XX
PF 05-DEC-1994; 94WO-US013945.
XX
PR 03-DEC-1993; 93US-00160837.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Levitt RC;
XX
DR WPI; 1995-215278/28.
XX
PT Kit for automated genotyping contg. pairs of PCR primers - designed to
PT amplify polymorphic nucleotide repeat sequences, arranged in sets each
PT with a characteristic fluorescence label, useful e.g. in detection of
PT disease related genetic rearrangement.
XX
PS Disclosure; Fig 7H-3; 104pp; English.

RESULT 1562
AAT01738/c
ID AAT01738 standard; DNA; 20 BP.
XX
AC AAT01738;
XX
DT 17-DEC-1995 (first entry)
XX
DE Peptide nucleic acid targeting HPV E2 translation initiation codon.
XX
KW peptide nucleic acid; PNA; cytomegalovirus; CMV; papillomavirus;
KW antiviral; diagnostic; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..20
FT /*tag= a
FT /note= "at least one (and preferably all) of the backbone
FT subunits are composed of amide units, so that the
FT oligomer consists of the nucleobases attached covalently
FT to a polyamide backbone"
XX
PN WO9504748-A1.
XX
PD 16-FEB-1995.
XX
PF 09-AUG-1994; 94WO-US009039.
XX
PR 09-AUG-1993; 93US-00104438.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Anderson KP, Crooke ST, Mirabelli CK, Becker DJ, Cowseert LM;
XX
DR WPI; 1995-090841/12.
XX
PT New peptide nucleic acid oligomers hybridisable to cytomegalovirus or
PT papilloma-virus - are stable anti-sense molecules with high affinity for
PT single stranded DNA, used for treating infections.
XX
PS Claim 10; Page 52; 65pp; English.

The method aims to provide a collection of highly reproducible
microsatellite marker sequences (MMS) at approx. 10-50 cm intervals
throughout the human genome which can be detectably labelled. The MMS are
polymorphic, simple sequence repeats and can be used in automated
genotyping. esp. fluorescence-based. The primers correspond to the unique
DNA sequence surrounding each marker, and PCR is used to detect each
polymorphism. When the MMS show considerable polymorphism (ie. a
difference in the number of repeats) between individuals, the markers can
be particularly informative. The MMS can be ideal for linkage studies.
Kits comprise at least 4 groups, of at least 3 sets, each comprising
labelled primers for PCR amplification of the DNA. Group 8 primer pairs
are shown in AAQ95735-76. The published size range of the D17S793 allele
is 95-109 bp, and the degree of heterozygosity in the population is about
70%
XX
SQ Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

New oligomers are claimed which (A) have at least one peptide nucleic
acid (PNA) subunit and (B) have a sequence hybridisable to AUG region, 5'
untranslated region, intron/exon (I/E) junction or coding sequence of
cytomegalovirus gene selected from DNA polymerase, I β 1 and I β 2, or
hybridisable to the E, E4, E5, E6, E7, L1 or L2 reading frames of a
papillomavirus. The PNAs can be used to target RNA and single stranded
DNA (ssDNA) to produce antisense-type gene regulation moieties. Hence
they may be used therapeutically for modulating cytomegalovirus and
papillomavirus processes and also as diagnostics (e.g., as probes for
specific mRNAs). PNA oligomers have high affinity for complementary
single stranded DNA. They are also able to form triple helices in which a
first PNA strand binds with RNA or ssDNA and a second PNA strand binds
with the resulting double helix or with the first PNA strand. The PNAs
possess no significant charge and are water soluble, which facilitates
cellular uptake. Further, since they contain amides of non-biological
amino acids, they are biostable and resistant to enzymatic degradation by
proteases. The present sequence targets papillomavirus E2 translation
initiation codon
XX
SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1747 AGGTCCTGGTCAAG 1761
|||||
DB 16 AGGTCCTGGTCAAG 2

QY 1747 AGGTCCTGGTCAAG 1761
|||||
DB 16 AGGTCCTGGTCAAG 2

RESULT 1564

```

AAV06684/c
ID  AAV06684 standard; DNA; 20 BP.
AC
XX
AC  AAV06684;
XX
XX  25-MAR-2003 (revised)
DT  26-MAY-1998 (first entry)
XX
XX  Oligonucleotide used in covalently cross-linked nucleic acid.
DE
XX
XX  Covalent cross-link; RNA mimic; spatial configuration; abasic site; ss.
KW
XX
XX  Synthetic.
OS
XX
XX  Key
FH  modified_base 9 Location/Qualifiers
FT  /*tag= a
FT  /*note= "pentylamino-adenosine"
FT  18
FT  modified_base
FT  /*tag= b
FT  /*note= "pentylamino-adenosine"
XX
XX  US5543507-A.
XX
XX  06-AUG-1996.
XX
XX  02-MAR-1994; 94US-00205507.
XX
XX  05-MAR-1992; 92US-00846376.
XX  05-MAR-1993; 93WO-US002059.
XX
XX  (ISIS-) ISIS PHARM INC.
XX
XX  Bruce T, Manoharan M, Cook PD;
XX
XX  WPI; 1996-370682/37.
XX
XX  Crosslinked nucleic acids and oligo:nucleotide(s) - used as RNA mimics
XX  that are fixed in specific spatial configurations.
XX
XX  Example 9; Col 40; 44pp; English.
XX
XX  This sequence represents an oligonucleotide shown in the specification. A
XX  crosslinked nucleic acid comprises: a 1st nucleotide (N1) located on a
XX  1st oligonucleotide (ON) strand; a 1st bond means (B1) located on a sugar
XX  moiety of N1, a 2nd nucleotide (N2) located on a 2nd ON strand; a 2nd
XX  bond means (B2) located on a sugar moiety of N2; and a covalent cross-
XX  linkage (CCL) between B1 and B2; provided that at least one of B1 and B2
XX  is located at a non-terminal nucleotide and further provided that CCL is
XX  not between the 3' carbon of a sugar moiety of N1 and the 5' carbon of a
XX  sugar moiety of N2; is not between the 3' carbon of a sugar group of N2
XX  and the 5' carbon of a sugar gp. of N1; and does not include a
XX  nucleosidic base. The oligonucleotides can be used as RNA mimics that are
XX  fixed in specific spatial conformations via crosslinking covalent bonds.
XX  The covalently crosslinked ON's have the same sequence as known nuclease-
XX  resistant mimics of binding receptors for nucleic acid binding proteins.
XX  (Updated on 25-MAR-2003 to correct PR field.)
XX
XX  Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
XX
XX  Query Match 0.6%; Score 13.4; DB 1; Length 20;
XX  Best Local Similarity 93.3%; Pred. No. 1.2e+03;
XX  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX  QY 1332 TGAAGAGAGGAGGA 1346
XX  18 TGAAGAGGATGGAGA 4
XX
XX  Db
XX
XX  RESULT 1565
XX  AAT37933/c
XX  ID AAT37933 standard; cDNA; 20 BP.
XX
XX

```

```

AC
XX  AAT37933;
XX
XX  30-APR-1997 (first entry)
XX
XX  VEGF-B exon 1 boundary 1.
DE
XX
XX  Endothelial cell; proliferation; vascular endothelial growth factor; VPF;
XX  VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
XX  vascular permeability factor; cell mitogen; angiogenesis; cell growth;
XX  embryonic development; wound healing; tissue reorganisation; antibody;
XX  cancer; metastatic risk; tumour cell; human; ss.
XX
XX  Homo sapiens.
XX
XX  WO9626736-A1.
XX
XX  06-SEP-1996.
XX
XX  01-MAR-1996; 96WO-US002957.
XX
XX  01-MAR-1995; 95US-00397651.
XX  06-JUN-1995; 95US-00469427.
XX  06-DEC-1995; 95US-00569063.
XX
XX  (LUDW-) LUDWIG INST CANCER RES.
XX  (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
XX  Eriksson U, Olofsson B, Alitalo K, Pajusola K;
XX
XX  WPI; 1996-412582/41.
XX
XX  Vascular endothelial growth factor VEGF-B proteins - useful to accelerate
XX  angiogenesis in wound healing, also related nucleic acid and antibodies
XX  for cancer diagnosis.
XX
XX  Example 7; Page 28; 107pp; English.
XX
XX  AAT37933-T37946 represent the intron/exon boundaries for the human
XX  vascular endothelial growth factor (VEGF) proteins of the invention (see
XX  AA04829, and AA04831), which promote endothelial or mesodermal cell
XX  proliferation. VEGF is also a glycosylated cationic dimer, and is
XX  sometimes referred to as vascular permeability factor (VPF). VEGF has
XX  diverse effects, depending on the specific biological context in which it
XX  is found. VEGF is a potent endothelial cell mitogen, and directly
XX  contributes to induction of angiogenesis in vivo by promoting endothelial
XX  cell growth during normal embryonic development, wound healing, and
XX  tissue regeneration/reorganisation. The VEGF proteins of the invention
XX  share the angiogenic and other properties of VEGF, but are distributed
XX  and expressed in tissues differently to VEGF. The proteins can therefore
XX  be used to accelerate angiogenesis in wound healing. Antibodies against
XX  the proteins can be used for inhibiting angiogenesis. The antibodies can
XX  also be used diagnostically to quantitatively detect VEGF-B. Primers
XX  complementary to the coding sequences for the proteins of the invention
XX  can also be used to detect VEGF-B coding sequences. Quantification of
XX  VEGF-B in cancer biopsy specimens may be useful as an indicator of
XX  metastatic risk. VEGF-B expression in a cell can be retarded using
XX  antisense sequences direct against the VEGF coding sequences, this is
XX  especially useful in retarding VEGF expression in tumour cells
XX
XX  Sequence 20 BP; 2 A; 9 C; 7 G; 2 T; 0 U; 0 Other;
XX
XX  Query Match 0.6%; Score 13.4; DB 1; Length 20;
XX  Best Local Similarity 93.3%; Pred. No. 1.2e+03;
XX  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX  QY 1183 CCGCAGCAGCAGCTGGG 1197
XX  20 CCGCAGCTACCTGGG 6
XX
XX  Db
XX
XX  RESULT 1566
XX  AAT11263
XX  ID AAT11263 standard; DNA; 20 BP.
XX

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PF 12-JUL-1996; 96WO-US011688.
XX
PR 14-JUL-1995; 95US-0001148P.
PR 11-JUL-1996; 96US-00680326.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
PI Rose TM, Bosch ML, Strand K, Todaro GJ;
XX WPI; 1997-132644/12.
XX
XX Herpes virus DNA polymerase and corresponding nucleotide sequence - used
PT in the detection and treatment of herpes virus infection.
XX
XX Claim 26; Page 92; 132pp; English.
XX
XX The present sequence represents oligonucleotide SLYPSQA which is specific
CC for polynucleotides encoding DNA polymerases from herpes virus (Type 1).
CC The oligonucleotide may be used for detecting viral DNA or RNA in a
CC sample of primate origin, especially in the diagnosis of herpes viral
CC infection. Herpes virus DNA polymerases of this invention, may be used in
CC vaccines for the protection against infection by a herpes virus of the
CC RFHV/KSHV family. They may also be used in the design and screening of
CC anti-viral drugs. Antibodies raised against the polymerase or fragments
CC of it, may be used in the detection of herpes virus infection and for
CC drug targeting for the therapy of herpes virus infection
XX
SQ Sequence 20 BP; 3 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 708 GGCTGGCAAGCA 722
DB 16 GGCTGGCAAGTCAA 2
RESULT 1569
AAV33260
ID AAV33260 standard; DNA; 20 BP.
XX
AC AAV33260;
XX
XX 25-MAR-2003 (revised)
DT 07-DEC-1998 (first entry)
XX
XX HPV type 16 gene amplifying 3' primer PV4.
XX
XX Human papillomavirus; HPV; human; cervical cancer cell line; SiHa;
KW thermal cycler sample compartment; veterinary; thermal conductivity;
KW in situ PCR; nucleic acid detection; PCR primer; ss.
XX
OS Synthetic.
OS Human papillomavirus.
XX
XX EP863213-A1.
XX
XX 09-SEP-1998.
XX
XX 22-JUL-1992; 98EP-00200769.
XX
XX 23-JUL-1991; 91US-00733419.
XX 22-JUL-1992; 92EP-00306701.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (UYN ) UNIV NEW YORK STATE RES FOUND.
XX Bloch W, Nuovo GJ;
XX
XX WPI; 1998-522852/45.
XX
XX New thermal cycler for in-situ PCR on microscope slides - and device for
PT
PT protecting microscope slides from fluid or vapour.
XX
XX Example 1; Page 10; 16pp; English.
XX
XX Sequences shown in AAV33263 represent primers used for the
CC PCR amplification of the human papillomavirus (HPV) type 16 genome
CC contained in the human cervical cancer cell line SiHa. The invention
CC provides a thermal cycler sample compartment optimised for holding and
CC controlling the temperature of one or more microscopes which facilitates
CC thermal cycling. It also contains a device (barrier) for protecting a
CC microscope slide from fluid or vapour when the slide is sealed in the
CC device, comprising a plastics material that has high thermal
CC conductivity, and is impervious to fluid or vapour, and is dimensioned so
CC as to receive the slide. The new thermal cycling compartment is useful
CC for performing in situ PCR for detection of target nucleic acid sequences
CC directly from cells fixed onto a microscope slide, used in the field of
CC cell biology, forensic science and clinical, veterinary and plant
CC pathology. The modified heat blocks increase the speed and reliability of
CC in situ PCR performed on microscope slides by accelerating and rendering
CC more uniform the heat transfer which occurs during thermal cycling.
CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
CC correct PR field.)
XX
SQ Sequence 20 BP; 2 A; 6 C; 1 G; 11 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1875 ATCTCTGTTTTTTT 1889
DB 1 ATCCCTGTTTTTTT 15
RESULT 1570
AAV07421/c
ID AAV07421 standard; DNA; 20 BP.
XX
AC AAV07421;
XX
XX 10-SEP-1998 (first entry)
DT
DE Oligonucleotide containing carbamate-derivatised nucleoside.
XX
XX Carbamate-derivatised nucleoside; therapy; protein production;
KW DNA degradation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 9 /*tag= a
FT /*note= "Nucleotide functionalised with a carbamate-2'-
FT aminolinker moiety"
XX
XX WO9811123-A1.
XX
XX 19-MAR-1998.
XX
XX 10-SEP-1997; 97WO-US015970.
XX
XX 13-SEP-1996; 96US-00713742.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cook PD, Manoharan M;
XX
XX WPI; 1998-271659/24.
XX
XX Nucleoside compounds - which contain carbamate moiety at 2'-O or 3'-O
XX position of sugar or at 5-position of pyrimidine base.
XX
XX Example 34; Page 30; 49pp; English.
PS

```

XX The invention relates to nucleoside compounds which contain carbamate moiety at 2'-O or 3'-O position of sugar or at 5-position of pyrimidine base. The may be incorporated into oligonucleosides or oligonucleotides for use in diagnostics, research and therapy. The nucleoside or oligonucleoside or oligonucleotide can be used, e.g. for modulating production of certain proteins by an organism (and treatment of diseases related to production of these proteins), for inducing degradation of particular regions of double stranded DNA, for killing cells or viruses, or for detecting the presence or absence of RNA in biological samples. The present sequence represents an example of an oligonucleotide containing a nucleotide functionalised with a carbamate-2'-aminolinker moiety

SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1332 TGAAGAGGAGGAGA 1346
| | | | | | | | | |
Db 18 TGAAGAGGATGGAGA 4

RESULT 1571
AAV85773/c
ID AAV85773 standard; DNA; 20 BP.
XX AAV85773;
AC AAV85773;
XX 10-FEB-1999 (first entry)
DT LRP5 exon primer 58-3 lf.
XX LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;
KW insulin dependent diabetes mellitus; autoimmune disease;
KW glomerulonephritis; inflammation; viral infection; osteoporosis;
KW hypercholesterolemia; Alzheimer's disease; low density lipoprotein;
KW PCR primer; ss.
XX Synthetic.
OS Homo sapiens.
XX WO9846743-A1.
XX 22-OCT-1998.
XX 15-APR-1998; 98WO-GB001102.
XX 15-APR-1997; 97US-0043553P.
XX 05-JUN-1997; 97US-0048740P.
XX (WELL) WELLCOME TRUST LTD.
XX (MERI) MERCK & CO INC.
XX Todd JA, Hess JW, Caskey CT, Cox RD, Gerhold D, Hammond H;
PI Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y;
PI Phillips MS, Twells RCU;
XX WPI; 1998-594573/50.
XX New isolated LDL-receptor related protein - used to develop products for treating, e.g. elevated triglyceride levels, diabetes, autoimmune disorders, inflammation or Alzheimer's disease.
PS Claim 12; Page 105; 200pp; English.
XX The present invention describes LRP5 (low density lipoprotein (LDL) receptor related protein, previously designated LRP-3). AAV85587 to AAV85822 represent exon primers used for obtaining LRP5 cDNA. Nucleic acid molecules (NAMS) encoding LRP5 can be used for determining if an individual is susceptible to insulin dependent diabetes mellitus (IDDM).

CC The NAMS or proteins can be used for reducing triglyceride levels in the serum of an individual. Therapies that affect LRP5 may also be useful in the treatment of autoimmune diseases such as glomerulonephritis, diseases and disorders involving disruption of endocytosis and/or antigen presentation, cytokine clearance and/or inflammation, viral infection, pathogenic bacterial toxin contamination, elevation of free fatty acids or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's disease and cardiovascular disease. Products from the present invention can also be used for detection, diagnosis and drug screening

XX Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1305 TGCTGTGTGAGGAAGA 1319
| | | | | | | | | |
Db 18 TCCTGTGTGAGGAAGA 4

RESULT 1572
AAV8581/c
ID AAV8581 standard; DNA; 20 BP.
XX AAV8581;
AC AAV8581;
XX 10-FEB-1999 (first entry)
DT LRP5 SNP primer 58-3 lf.
XX LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;
KW insulin dependent diabetes mellitus; autoimmune disease;
KW glomerulonephritis; inflammation; viral infection; osteoporosis;
KW hypercholesterolemia; Alzheimer's disease; low density lipoprotein;
KW PCR primer; ss.
XX Synthetic.
OS Homo sapiens.
XX WO9846743-A1.
XX 22-OCT-1998.
XX 15-APR-1998; 98WO-GB001102.
XX 15-APR-1997; 97US-0043553P.
XX 05-JUN-1997; 97US-0048740P.
XX (WELL) WELLCOME TRUST LTD.
XX (MERI) MERCK & CO INC.
XX Todd JA, Hess JW, Caskey CT, Cox RD, Gerhold D, Hammond H;
PI Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y;
PI Phillips MS, Twells RCU;
XX WPI; 1998-594573/50.
XX New isolated LDL-receptor related protein - used to develop products for treating, e.g. elevated triglyceride levels, diabetes, autoimmune disorders, inflammation or Alzheimer's disease.
PS Claim 12; Page 110; 200pp; English.
XX The present invention describes LRP5 (low density lipoprotein (LDL) receptor related protein, previously designated LRP-3). AAV85823 to AAV85900 represent SNP primers used for obtaining LRP5 cDNA. Nucleic acid molecules (NAMS) encoding LRP5 can be used for determining if an individual is susceptible to insulin dependent diabetes mellitus (IDDM). The NAMS or proteins can be used for reducing triglyceride levels in the serum of an individual. Therapies that affect LRP5 may also be useful in the treatment of autoimmune diseases such as glomerulonephritis, diseases and disorders involving disruption of endocytosis and/or antigen

CC presentation, cytokine clearance and/or inflammation, viral infection,
CC pathogenic bacterial toxin contamination, elevation of free fatty acids
CC or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's
CC disease and cardiovascular disease. Products from the present invention
CC can also be used for detection, diagnosis and drug screening
XX
SQ Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1305 TGCCTGTGAGGAGA 1319
| | | | | | | | | |
Db 18 TCCTGTGAGGAGA 4
RESULT 1573
AAV06674/C
ID AAV06674 standard; DNA; 20 BP.
XX
AC AAV06674;
XX
XX 25-MAR-2003 (revised)
DT 21-MAY-1998 (first entry)
XX
DE Modified oligonucleotide in covalently cross-linked nucleic acid.
XX
KW Covalent cross-link; modified oligonucleotide; abasic site;
KW space spanning group; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 9
FT /*tag= a
FT /note= "nucleotide modified to incorporate a pentylamino
FT functionality"
XX
PN US5719271-A.
XX
PD 17-FEB-1998.
XX
PF 30-AUG-1994; 94US-00295743.
XX
PR 05-MAR-1992; 92US-00846376.
PR 05-MAR-1993; 93WO-US002059.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Manoharan M, Bruice T, Cook PD;
XX
XX WPI; 1998-158831/14.
XX
XX Covalently cross-linked nucleic acids - in which 2'- or 3'-hydroxy groups
PT on sugar moieties of nucleotide(s), on one or more oligonucleotide
PT strands, are linked by a non-phosphorus linkage.
XX
PS Example 4; Col 37; 36pp; English.
XX
XX This sequence represents an oligonucleotide shown in the patent. The
CC invention relates to a cross-linked nucleic acid, which comprises: (a) a
CC first nucleotide located on a first oligonucleotide strand having a first
CC bond site located on either a 2'- or 3'-OH of the sugar moiety; (b) a
CC second nucleotide located on a second oligonucleotide strand having a
CC second bond site located on either a 2'- or 3'-OH of the sugar moiety.
CC The first strand is linked to the second strand via a non-phosphorus
CC covalent cross-linkage between the first and second bond sites, where not
CC both sites may be on a 3'-OH or a terminal nucleotide. The cross-linked
CC nucleic acids include materials in which oligonucleotide strands are
CC covalently cross-linked to themselves or to other strands. Such materials
CC can be used, e.g., as RNA mimics which are fixed in specific spatial
CC conformations. These materials may be used as therapeutic agents,...

CC research reagents and diagnostic agents. (Updated on 25-MAR-2003 to
CC correct PR field.)
XX
SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1332 TGAAGAGGAGGAGA 1346
| | | | | | | | | |
Db 18 TGAAGAGGAGGAGA 4
RESULT 1574
AAV54680
ID AAV54680 standard; DNA; 20 BP.
XX
AC AAV54680;
XX
DT 13-NOV-1998 (first entry)
XX
DE Human papillomavirus (HPV) gene amplifying primer PV4.
XX
KW Human papillomavirus; HPV; thermal cycling device; ceramic sample plate;
KW biological sample; thermal sensor; heater; cooler; thermal cycling;
KW rapid heat transfer; microscope slide; PCR amplification; hybridisation;
KW target nucleic acid; PCR primer; ss.
XX
OS Synthetic.
OS Human papillomavirus.
XX
XX WO9839479-A1.
XX
PD 11-SEP-1998.
XX
PF 03-MAR-1998; 98WO-US004041.
XX
PR 03-MAR-1997; 97US-00810641.
XX
PA (MINU) UNIV MINNESOTA.
XX
PI Blumenfeld M, Chaplin J;
XX
XX WPI; 1998-495869/42.
XX
PT Thermal device for PCR amplification or hybridisation of target nucleic
PT acid on microscope slide - has ceramic sample plate supporting flat
PT substrate for sample and heater and cooler controlled to maintain or
PT rapidly cycle temperature of sample.
XX
PS Example 2; Page 34; 58pp; English.
XX
XX Sequences shown in AAV54677 to AAV54683 represent primers used for the
CC PCR amplification of the Human papillomavirus (HPV) gene contained in the
CC human cervical cancer cell line SHa. These are used in the course of the
CC invention which provides a thermal cycling device comprising a ceramic
CC sample plate. This device has a ceramic sample plate supporting a flat
CC substrate carrying a biological sample and a thermal sensor, a heater
CC thermally coupled to the plate and a cooler for the substrate. The device
CC either maintains the temperature of the sample or subjects it to thermal
CC cycling. The thin ceramic plate permits very rapid heat transfer to a
CC sample on a microscope slide and this thermal cycling device can be used
CC for PCR amplification or hybridisation of target nucleic acid on
CC microscope slide
XX
SQ Sequence 20 BP; 2 A; 6 C; 1 G; 11 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1875 ATCTCTGTTTTTTT 1889

Db	1	ATCCCTGTGTTTTT	15
Db	1682	GCTCTTCCAGGAGCC	1696
Db			
Db		20	GATCTTCCAGGAGCC 6
RESULT 1575			
AAV22456/c			
ID	AAV22456	standard; DNA; 20 BP.	
XX	AAV22456;		
XX	08-JUL-1998	(first entry)	
XX	Antisense oligonucleotide	designed to target the R2 message.	
XX	R2 subunit; ribonucleotide	reductase; ras pathway; cell proliferation;	
KW	tumour cell; antisense;	growth; inhibition; sensitivity; hydroxyurea;	
KW	chemotherapeutic drug;	methotrexate; PALA; treatment; phosphorothioate;	
KW	ss.		
XX	Synthetic.		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
FT	modified_base	1..20	
FT		/tag= a	
FT		/note= "contains phosphorothioate bonds between the	
FT		nucleotides"	
XX	WO9805769-A2.		
XX	12-FEB-1998.		
XX	01-AUG-1997;	97WO-CA000540.	
XX	02-AUG-1996;	96US-0023040P.	
PR	07-MAR-1997;	97US-0039959P.	
XX	(GENE-) GENESENSE TECHNOLOGIES INC.		
XX	Wright JA, Young AH;		
XX	WPI; 1998-145609/13.		
XX	Antisense oligonucleotides	to ribonucleotide reductase genes - used to	
PT	modulate tumour growth	and inhibit tumour cell proliferation.	
XX	Claim 4; Page 39; 79pp;	English.	
XX	AAV2429-530	represent antisense oligonucleotides which are targeted	
CC	against the mRNA of the R2	subunit sequence of ribonucleotide reductase.	
CC	Aberrant expression of the	R2 gene can determine the malignant	
CC	characteristics of cells.	Altered R2 expression was found to cooperate	
CC	with ras in mechanisms of	malignant progression, and recombinant R2	
CC	expression resulted in	increased membrane associated Raf-1 protein. These	
CC	results suggest that R2	cooperates with Raf-1 and Rac-1, thereby	
CC	affecting ras pathways	and cell proliferation. Suppression of R2 gene	
CC	expression was found to	reduce transformed properties of tumour cells.	
CC	The antisense oligonucleotides	can be used for modulating tumour cell	
CC	growth, or for inhibiting	tumour cell proliferation. They can also be	
CC	used for increasing the	sensitivity of neoplastic cells to	
CC	chemotherapeutic drugs	(especially to hydroxyurea, methotrexate (MTX),	
CC	and PALA). The antisense	oligonucleotides may be used to treat	
CC	proliferative disorders	including leukaemias, lymphomas, sarcomas,	
CC	melanomas, various other	forms of cancer, papillomas, arthrosclerosis,	
CC	psoriasis, polythemia,	mastocytosis, autoimmune diseases, angiogenesis,	
CC	bacterial infections	and viral infections (including HIV hepatitis, or	
CC	herpes infections)		
XX	Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	
	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
XX	1335	AGAGGAGGAGGAGG	1349
XX	Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;		
SQ	Query Match	0.6%; Score 13.4; DB 1; Length 20;	
	Best Local Similarity	93.3%; Pred. No. 1.2e+03;	


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OS Synthetic.
OS Chlamydia trachomatis.
PN WO9928475-A2.
PD 10-JUN-1999.
XX
XX 27-NOV-1998; 98WO-IB001939.
PF
XX 28-NOV-1997; 97FR-00015041.
PR 17-DEC-1997; 97FR-00015034.
PR 04-NOV-1998; 98US-0107077P.
XX
XX (GEST ) GENSET.
XX
XX Griffais R;
XX
XX WPI; 1999-371125/31.
XX
XX Genome sequence of Chlamydia trachomatis.
XX Disclosure; Page 1445; 1755pp; English.
XX
XX PCR primers AAZ01426-Z06209 were used to amplify open reading frames
XX (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
XX encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
XX against Chlamydia trachomatis. Antisense and ribozyme sequences can also
XX be used to control growth of the microorganism. Chlamydia trachomatis is
XX responsible for a large number of diseases, e.g. eye diseases such as
XX conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
XX conjunctivitis; genital diseases such as nongonococcal urethritis,
XX epididymitis, cervicitis, salpingitis, perihepatitis, Bartholinitis;
XX pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
XX The polypeptides of the invention may be of use in treating these
XX diseases
XX
XX SQ Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.4; DB 1; Length 20;
XX Best Local Similarity 93.3%; Pred. No. 1.2e+03;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1315 GAAGAGTTCCTCCGAT 1329
DB 16 GAAGAGTTCCTCCGAT 2
XX
RESULT 1580
AAZ01588
ID AAZ01588 standard; DNA; 20 BP.
XX
XX AAZ01588;
XX
XX 07-OCT-1999 (first entry)
XX
XX PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
XX paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
XX nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
XX Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
XX Synthetic.
XX OS Chlamydia trachomatis.
XX
XX WO9928475-A2.
XX
XX 10-JUN-1999.
XX
XX 27-NOV-1998; 98WO-IB001939.
XX
XX 28-NOV-1997; 97FR-00015041.
XX
XX 17-DEC-1997; 97FR-00015034.
XX

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PR 04-NOV-1998; 98US-0107077P.
XX
XX (GEST ) GENSET.
XX
XX Griffais R;
XX
XX WPI; 1999-371125/31.
XX
XX Genome sequence of Chlamydia trachomatis.
XX Disclosure; Page 1455; 1755pp; English.
XX
XX PCR primers AAZ01426-Z06209 were used to amplify open reading frames
XX (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
XX encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
XX against Chlamydia trachomatis. Antisense and ribozyme sequences can also
XX be used to control growth of the microorganism. Chlamydia trachomatis is
XX responsible for a large number of diseases, e.g. eye diseases such as
XX conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
XX conjunctivitis; genital diseases such as nongonococcal urethritis,
XX epididymitis, cervicitis, salpingitis, perihepatitis, Bartholinitis;
XX pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
XX The polypeptides of the invention may be of use in treating these
XX diseases
XX
XX SQ Sequence 20 BP; 5 A; 0 C; 13 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.4; DB 1; Length 20;
XX Best Local Similarity 93.3%; Pred. No. 1.2e+03;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1338 GGAGGGAGAGCGGGG 1352
DB 2 GGAGAGAGAGCGGGG 16
XX
RESULT 1581
AAZ03315/C
ID AAZ03315 standard; DNA; 20 BP.
XX
XX AAZ03315;
XX
XX 07-OCT-1999 (first entry)
XX
XX PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
XX paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
XX nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
XX Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
XX Synthetic.
XX OS Chlamydia trachomatis.
XX
XX WO9928475-A2.
XX
XX 10-JUN-1999.
XX
XX 27-NOV-1998; 98WO-IB001939.
XX
XX 28-NOV-1997; 97FR-00015041.
XX
XX 17-DEC-1997; 97FR-00015034.
XX
XX 04-NOV-1998; 98US-0107077P.
XX
XX (GEST ) GENSET.
XX
XX Griffais R;
XX
XX WPI; 1999-371125/31.
XX
XX Genome sequence of Chlamydia trachomatis.
XX Disclosure; Page 1596; 1755pp; English.
XX
XX PS

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XX PCR primers AAZ01426-Z06209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC be used to control growth of the microorganism. Chlamydia trachomatis is
CC responsible for a large number of diseases, e.g. eye diseases such as
CC conjunctivitis, genital diseases such as nongonococcal urethritis,
CC epididymitis, cervicitis, salpingitis, perihepatitis, Bartholinitis;
CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
CC The polypeptides of the invention may be of use in treating these
CC diseases
XX
SQ Sequence 20 BP; 2 A; 3 C; 8 G; 7 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1353 CCGCAAGAACTCTTC 1367
DB 20 CCGCAGACGCTTC 6
RESULT 1582
AAZ04937
ID AAZ04937 standard; DNA; 20 BP.
XX
XX AAZ04937;
AC
XX
XX 07-OCT-1999 (first entry)
DT
DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
KW Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
OS Synthetic.
OS Chlamydia trachomatis.
XX
XX WO928475-A2.
PN
XX
XX 10-JUN-1999.
PD
XX
XX 27-NOV-1998; 98WO-IB001939.
PF
XX
XX 28-NOV-1997; 97FR-00015041.
PR
XX 17-DEC-1997; 97FR-00016034.
PR
XX 04-NOV-1998; 98US-0107077P.
PR
XX (GEST) GENSET.
PA
XX
XX Griffais R;
PI
XX
XX WPI; 1999-371125/31.
DR
XX
XX Genome sequence of Chlamydia trachomatis.
PT
XX
XX Disclosure; Page 1729; 1755pp; English.
PS
XX
XX PCR primers AAZ01426-Z06209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC be used to control growth of the microorganism. Chlamydia trachomatis is
CC responsible for a large number of diseases, e.g. eye diseases such as
CC conjunctivitis, genital diseases such as nongonococcal urethritis,
CC epididymitis, cervicitis, salpingitis, perihepatitis, Bartholinitis;
CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
CC The polypeptides of the invention may be of use in treating these
CC diseases

CC The polypeptides of the invention may be of use in treating these
CC diseases
XX
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1864 GGTCTTCAGGATCT 1878
DB 6 GCTCTTCAGGATCT 20
RESULT 1583
AAZ06762
ID AAZ06762 standard; DNA; 20 BP.
XX
XX AAZ06762;
AC
XX 26-APR-1999 (first entry)
DT
XX
DE Lymphocyte activation gene 3 (LAG-3) reverse primer R401.
XX
XX Lymphocyte activation gene 3; LAG-3; LAG-3V2; LAG-3V3; splice variant;
KW human; immunomodulator; Hashimoto's thyroiditis;
KW type 1 diabetes mellitus; multiple sclerosis; Crohn's disease;
KW rheumatoid arthritis; allograft rejection; graft-versus-host disease;
KW Grave's ophthalmopathy; abortion; cerebral malaria; Lyme arthritis;
KW reactive arthritis; hepatitis; primary sclerosing colangitis; dermatitis;
KW aplastic anaemia; gastric antritis; therapy; PCR; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO9858059-A1.
PN
XX 23-DEC-1998.
PD
XX
XX 03-JUN-1998; 98WO-EP003307.
PF
XX
XX 18-JUN-1997; 97EP-00401404.
PR
XX (INEM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (INSR) INST ROUSSY GUSTAVE.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
XX Triebel F, Mastrangeli R, Romagnani S;
PI
XX WPI; 1999-080953/07.
DR
XX New lymphocyte activation gene 3 (LAG-3) splice variants - which can be
XX used as immunomodulators.
PT
XX
XX Example 2; Page 15; 49pp; English.
PS
XX
XX Reverse primer R401 was used with forward primer F176 (see AAX06759) in
CC the PCR amplification of cDNA derived from human peripheral blood
CC mononuclear cells. cDNA clones (see AAX06755-56) encoding the human
CC lymphocyte activation gene 3 (LAG-3) splice variants LAG-3V2 and LAG-3V3
CC (see AAW88360-61). The invention provides 3 splice variants (see AAW88359
CC -61) of LAG-3 and nucleotide sequences encoding them (see AAX06754-56).
CC The LAG-3 variants can be used in, or for the manufacture of,
CC compositions used to treat immune-related pathologies (claimed)
XX
XX Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1017 GGCCCTGGATACGGA 1031
|||||

D	b
	1 GGCCCTGGATCCGA 15
	RESULT 1584
AAX25834/c	
ID AAX25834 standard; DNA; 20 BP.	
XX AC AAX25834;	
XX XX	
XX XX	
XX 08-JUN-1999 (first entry)	
DE Primer #2 for bacteriophage lambda bases 32011-32110.	
XX Analysis; mutation; binding reagent; chromatography; separation; genome;	
KW detection; primer; PCR; amplification; bacteriophage; lambda; ss.	
XX Synthetic.	
OS Bacteriophage lambda.	
XX W09909203-A1.	
PEN W09909203-A1.	
XX PD	
XX 25-FEB-1999.	
PF 18-AUG-1998; 98WO-US017062.	
XX PR	
PR 18-AUG-1997; 97US-0055676P.	
FR 14-OCT-1997; 97US-0062413P.	
XX PA (TRAN-) TRANSGENOMIC INC.	
Gjerde DT, Taylor PD;	
WPI; 1999-190174/16.	
Analyzing sample of double stranded DNA - useful for determining genetic mutations.	
Example 3; Page 36; 50pp; English.	
The invention relates to a method for analysing a sample of double stranded DNA to determine the presence of a mutation by:	(a) contacting the sample with a mutation site binding reagent; and
(b) chromotographically separating and detecting the product of (a). Primers AAX25833-X25834 were used to PCR amplify a 100 bp fragment of the bacteriophage lambda genome (bases 32011-32110) which contains an A to C mutation at position 51 (corresponding to base 32061).	
The amplified sequence is used to illustrate the method. The method is useful for the detection of mutations which is important in the field of diagnosing diseases, understanding their origins and the development of potential treatments	
Sequence 20 BP; 7 A; 5 C; 5 G; 3 T; 0 U; 0 Other;	
Query Match 0.6%; Score 13.4; DB 1; Length 20;	
Best Local Similarity 93.3%; Pred. No. 1.2e+03;	Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 640 GTCATGACTGTGCC 654 15 GTCTTGACTGTGCC 1	
Db	
RESULT 1585	
AAX25599/c	
ID AAX25599 standard; DNA; 20 BP.	
AC AAX25599;	
DT 13-SEP-1999 (first entry)	
PCR primer used to amplify an ORF of Chlamydia pneumoniae.	
Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.	
Synthetic. Chlamydophila pneumoniae.	
WO9927105-A2.	
PN WO9927105-A2.	
PD 03-JUN-1999.	
PP 20-NOV-1998; 98WO-IB001890.	
PF 21-NOV-1997; 97FR-00014673.	
PR 04-NOV-1998; 98US-0107078P.	
PA (GEST) GENSET.	
Griffais R;	
WPI; 1999-357842/30.	
Genome sequence of Chlamydia pneumoniae.	
Page 1524; Disclosure; 1912pp; English.	
AAX91991-K97517 represent PCR primers used to amplify open reading frames and other nucleic acid sequences from the genome of Chlamydia pneumoniae (see AAY91990). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotide sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae	
Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 U; 0 Other;	
Query Match 0.6%; Score 13.4; DB 1; Length 20;	
Best Local Similarity 93.3%; Pred. No. 1.2e+03;	Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1034 TCCTAAGTGCCTTC 1048 17 TCCTCAATGAGCTTC 3	
Db	
RESULT 1586	
AAX95370	
ID AAX95370 standard; DNA; 20 BP.	
AC AAX95370;	
DT 13-SEP-1999 (first entry)	
PCR primer used to amplify an ORF of Chlamydia pneumoniae.	
Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.	
Synthetic. Chlamydophila pneumoniae.	
WO9927105-A2.	
PN WO9927105-A2.	
PD 03-JUN-1999.	
PP 20-NOV-1998; 98WO-IB001890.	
PF 21-NOV-1997; 97FR-00014673.	
PR 04-NOV-1998; 98US-0107078P.	
PA	

[illegible]

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XX (GEST ) GENSET.
XX Griffais R;
XX WPI; 1999-357842/30.
XX Genome sequence of Chlamydia pneumoniae.
XX Page 1742; Disclosure; 1912pp; English.
XX AAX91991-X97517 represent PCR primers used to amplify open reading frames
XX and other nucleic acid sequences from the genome of Chlamydia pneumoniae
XX (see AAX91990). C. pneumoniae causes respiratory disease such as
XX pneumonia and bronchitis and is thought to be a contributing factor in
XX heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
XX nodosum or pharyngitis. The polypeptides encoded by the open reading
XX frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
XX in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
XX nucleotide sequences can also be used as immunogenic compositions,
XX especially where the vector directs the expression of a neutralising
XX epitope of C. pneumoniae
XX Sequence 20 BP; 6 A; 4 C; 5 G; 5 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 TAGTAGCTTTGGAAA 1828
Db 5 TAGTAGCTTTGGAAA 19

RESULT 1587
AAX96229
ID AAX96229 standard; DNA; 20 BP.
XX AAX96229;
AC AAX96229;
XX 13-SEP-1999 (first entry)
XX PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
XX sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
XX neutralising epitope; PCR primer; ss.
XX Synthetic.
XX Chlamydothila pneumoniae.
XX WO9927105-A2.
XX 03-JUN-1999.
XX 20-NOV-1998; 98WO-IB001890.
XX 21-NOV-1997; 97FR-00014673.
XX 04-NOV-1998; 98US-0107078P.
XX (GEST ) GENSET.
XX Griffais R;
XX WPI; 1999-357842/30.
XX Genome sequence of Chlamydia pneumoniae.
XX Page 1809; Disclosure; 1912pp; English.
XX AAX91991-X97517 represent PCR primers used to amplify open reading frames
XX and other nucleic acid sequences from the genome of Chlamydia pneumoniae
XX (see AAX91990). C. pneumoniae causes respiratory disease such as

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CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotide sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX Sequence 20 BP; 7 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 889 CTAACATATCAAGGA 903
Db 6 CTAACATATCACAGGA 20

RESULT 1588
AAV63596/c
ID AAV63596 standard; DNA; 20 BP.
XX AAV63596;
AC AAV63596;
XX 29-JAN-1999 (first entry)
XX Human VEGF-B exon E1 exon/intron junction donor site.
XX Vascular endothelial growth factor; VEGF; proliferation; human;
XX endothelial cell; angiogenesis; tissue growth; organ repair; ss.
XX Homo sapiens.
XX US5840693-A.
XX 24-NOV-1998.
XX 01-MAR-1996; 96US-00609443.
XX 01-MAR-1995; 95US-00397651.
XX 06-JUN-1995; 95US-00469427.
XX 06-DEC-1995; 95US-00569063.
XX (LUDW-) LUDWIG INST CANCER RES.
XX (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX Alitalo K, Pajusola K, Eriksson U, Olofsson B;
XX WPI; 1999-034079/03.
XX Vascular endothelial growth factor-B isoforms, and DNA encoding them -
XX useful for inducing angiogenesis and cellular proliferation, and raising
XX antibodies to inhibit activities in e.g. tumours.
XX Example 7; Col 17-18; 52pp; English.
XX AAV63583-608 represent exon/intron junctions for vascular endothelial
XX growth factor (VEGF)-B proteins. VEGF proteins are used for promoting
XX proliferation of endothelial cells and for stimulating angiogenesis (the
XX proliferation of new capillaries form pre-existing blood vessels). These
XX activities are useful for treating tissue growth and repair, including
XX organ repair. This is also useful in pregnancy, in follicle development,
XX as these processes must occur in development of the placenta. The
XX proteins can also be used to raise antibodies, either for use in
XX detection of the proteins or as inhibitors of their action. This is
XX especially useful as angiogenesis is required by tumours as they need new
XX blood supplies to grow and proliferate
XX Sequence 20 BP; 2 A; 9 C; 7 G; 2 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 13.4; DB 1; Length 20;

```


Db 15 CTGTGAATTGGCTG 1

RESULT 1591
AAZ46681
ID AAZ46681 standard; DNA; 20 BP.
XX
AC AAZ46681;
XX
DT 17-MAR-2000 (first entry)
XX
DE Blast disease-resistance (Pi-b) gene specific primer 4.
XX
KW Blast disease; rice; Pi-b gene; blast disease-resistance gene; RT-PCR;
KW primer; ss.
XX
OS Synthetic.
OS Oryza sativa.
XX
PN EP969092-A1.
XX
PD 05-JAN-2000.
XX
PF 11-JUN-1999; 99EP-00111443.
XX
PR 12-JUN-1998; 98JP-00181455.
XX
PA (NORQ) NAT INST AGROBIOLOGICAL RESOURCES.
XX
PI Yano M, Iwamoto M, Katayose Y, Sasaki T, Wang Z, Yamanouchi U;
PI Ishimaru L;
XX
DR WPI; 2000-064864/06.
XX
PT Novel polypeptide and DNA encoding it used to produce plants resistant to
PT fungal blast disease.
XX
PS Example 6; Page 7; 46pp; English.
XX
CC The invention provides a protein which confers resistance to blast
CC disease onto plants. The blast disease-resistance (Pi-b) protein can be
CC expressed by standard recombinant methodology. The novel Pi-b gene is
CC used to produce transgenic plants resistant to the rice blast disease,
CC which will control the disease and increase crop yields. The resistance
CC gene Pi-b is located at the end of the long arm of rice chromosome 2 and
CC displays resistance to blast fungi. Sequences AAZ46681-84 represent RI-
CC PCR primers specific for the rice Pi-b gene
XX
SQ Sequence 20 BP; 9 A; 1 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 209 GAAAAATGGAATCT 223
DB 4 GAAAAATGGAATGT 18

RESULT 1592
AAZ76512/c
ID AAZ76512 standard; DNA; 20 BP.
XX
AC AAZ76512;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:10868.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
XX

diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 9; Page 2547; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 20 BP; 1 A; 5 C; 3 G; 11 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1384 AAGAGAGTCAAAACA 1398
DB 16 AAGAAAGTCAAAACA 2

RESULT 1593
AAZ70540/c
ID AAZ70540 standard; DNA; 20 BP.
XX
AC AAZ70540;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:4896.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX

PF 21-APR-1999; 99WO-IB000822.
 XX
 PR 21-APR-1998; 98US-0082614P.
 PR 23-NOV-1998; 98US-0109732P.
 XX
 XX (GEST) GENSET.
 PA
 XX Cohen D, Blumenfeld M, Chumakov I;
 PI WPI; 2000-013267/01.
 XX
 DR Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome.
 PT
 XX Claim 8; Page 1275; 2745pp; English.
 PS
 XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX
 SQ Sequence 20 BP; 1 A; 5 C; 2 G; 12 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1401 GGATGAAAAAGAGAA 1415
 DB 20 GGATGAAAAAGAAAA 6
 RESULT 1594
 AAAL1870
 ID AAAL1870 standard; DNA; 20 BP.
 AC
 XX AAAL1870;
 DT 16-AUG-2000 (first entry)
 XX
 DE Human MDMX antisense oligonucleotide #31035.
 XX
 KW MDMX; human; antisense; inhibitor; anticarcinogen; antiinflammatory;
 KW antiinfectious; modulation; treatment; disease; diagnosis; primer; ss.
 XX
 OS Homo sapiens.
 XX
 XX US6046320-A.
 XX
 XX 04-APR-2000.
 XX
 PF 09-APR-1999; 99US-00289267.
 XX
 PR 09-APR-1999; 99US-00289267.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Cowser LM;
 XX
 DR WPI; 2000-282710/24.
 XX
 PT New antisense oligonucleotides targeting nucleic acids encoding human

PT MDMX useful for inhibiting MDMX expression and for treating diseases
 PT associated with MDMX expression e.g. tumor formation, inflammation.
 XX
 XX Claim 3; Col 75-76; 51pp; English.
 XX
 CC This invention describes a novel antisense compound (I), 8-30 nucleobases
 CC in length, targeted to a nucleic acid encoding a human MDMX. (I)
 CC specifically hybridizes with and inhibits the expression of human MDMX.
 CC The products of the invention have anticarcinogen, antiinflammatory and
 CC antiinfectious activity. Synthesized chimeric oligonucleotides targeted
 CC to human MDMX, 20 nucleotides in length, composed of a central gap region
 CC consisting of ten 2'-deoxynucleotides flanked on both sides by 5-
 CC nucleotide wings were tested for antisense inhibition of MDMX expression.
 CC Results of real-time quantitative polymerase chain reaction (PCR) showed
 CC 71 out of the 159, 20 base pair sequences, all fully defined in the
 CC specification, demonstrated at least 30% inhibition of MDMX expression.
 CC The antisense oligonucleotides are useful for effective and specific
 CC modulation, particularly inhibition of MDMX expression, and may be used
 CC in treating humans or animals suspected of having or being prone to a
 CC disease or condition associated with expression of MDMX. The antisense
 CC oligonucleotides may also be used as research reagents or kits, and as
 CC diagnostics, e.g. to elucidate the function of a particular gene or to
 CC distinguish between functions of various members of a biological pathway,
 CC and as prophylaxis, e.g. to prevent or delay infection, inflammation or
 CC tumor formation. AAAL1781-A11945 represent antisense oligonucleotides
 CC described in the method of the invention
 XX
 SQ Sequence 20 BP; 7 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1722 TTAACCTTGAACCAT 1736
 DB 2 TTAACCTTGAACCAT 16
 RESULT 1595
 AAZ93986/c
 ID AAZ93986 standard; DNA; 20 BP.
 XX
 AC AAZ93986;
 XX
 XX 29-AUG-2000 (first entry)
 DT
 XX
 DE Sequencing primer (AS2) used to sequence mouse uromodulin promoter.
 KW Uromodulin; promoter; kidney; urine; heterologous gene; treatment;
 KW therapy; gene expression; pharmaceutical; primer; ss.
 XX
 OS Synthetic.
 XX
 XX WO200029608-A1.
 XX
 XX 25-MAY-2000.
 XX
 XX 12-NOV-1999; 99WO-US026870.
 XX
 XX 13-NOV-1998; 98US-0108195P.
 PR 09-JUL-1999; 99US-0142925P.
 XX
 XX (UNY) UNIV NEW YORK STATE.
 PA
 XX Wu X, Sun T;
 PI WPI; 2000-387816/33.
 XX
 XX New kidney-specific promoter useful for production of transgenic animals
 PT as urinary bioreactors, is operably linked to a heterologous gene.
 XX
 PS Example 1; Page 20; 55pp; English.
 XX

XX SQ Sequence 20 BP; 9 A; 6 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 410 GTTCTGTGGAAAGT 424
|||||
Db 15 GTTCTGTGGAAAGT 1

RESULT 1598
AAC92853
ID AAC92853 standard; DNA; 20 BP.
XX
AC AAC92853;
XX
DT 27-MAR-2001 (first entry)
XX
DE Human PI3 kinase p55 gamma antisense oligonucleotide, SEQ ID NO:36.
XX
KW Human phosphatidylinositol 3-kinase p55 gamma regulatory subunit;
KW PI3 kinase p55 gamma; hp55-gamma; PIK3R3; p55PIK;
KW signal transduction; downstream effector; receptor tyrosine kinase;
KW insulin receptor; IR; insulin-like growth factor receptor; IGF1R;
KW cell growth; differentiation; apoptosis; developmental regulation;
KW alternative splicing; tumour formation; cancer; inflammation; infection;
KW expression inhibition; phosphothioate; antisense oligonucleotide; ss.
OS Homo sapiens.
XX
XX US6165790-A.
XX
XX 26-DEC-2000.
XX
XX 03-NOV-1999; 99US-00433694.
XX
XX 03-NOV-1999; 99US-00433694.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Borchers AH, Cowsett LM, Ward DT;
XX WPI; 2001-101697/11.
XX
XX Novel antisense compound targeted to human PI3 kinase p55 gamma
XX specifically hybridizes with and inhibits the expression of human PI3
XX kinase p55 gamma, useful for modulating the expression of PI3 kinase p55
XX gamma in cells.
XX
XX Claim 14; Col 41-42; 39pp; English.
XX
XX Sequences AAC92827-C92906 represent phosphothioate antisense
XX oligonucleotides targeted to the phosphatidylinositol 3-kinase p55 gamma
XX regulatory subunit (PI3 kinase p55 gamma) gene, which inhibit its
XX expression. The antisense oligonucleotides were designed to target
XX different regions of human PI3 kinase p55 mRNA species, and were analysed
XX for their effect on PI3 kinase p55 mRNA levels by quantitative real-time
XX PCR. PI3 kinase p55 gamma (also known as hp55-gamma, PIK3R3
XX and p55PIK) is one of several PI3 kinase regulatory subunits that may
XX associate with the PI3 kinase catalytic subunit to form a heterodimeric
XX PI3 kinase holoenzyme. PI3 kinases act as downstream effectors of
XX receptor tyrosine kinases such as growth factor and hormone receptors and
XX oncogene products, and are found in association with the cytoplasmic
XX domains of such receptors. PI3 kinase p55 gamma is able to interact with
XX both the insulin receptor (IR) and the insulin-like growth factor
XX receptor (IGF1R), which play important roles in growth, differentiation
XX and apoptosis. PI3 kinase p55 gamma is thought to be developmentally
XX regulated, as four distinct mRNA species are found in adult tissues,
XX while only the larger mRNA is expressed in foetal tissues. The
XX oligonucleotides of the invention are useful for diagnosis, prevention
XX and treatment of conditions associated with PI3 kinase p55 expression,

CC such as tumour formation, inflammation and certain infections, and allow
CC expression level modulation of the alternatively spliced forms of PI3
CC kinase p55
XX
SQ Sequence 20 BP; 5 A; 3 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 545 TGGAACTGCTAAAGT 559
|||||
Db 2 TGGAACTGCTGAAGT 16

RESULT 1599
AAC92864/c
ID AAC92864 standard; DNA; 20 BP.
XX
XX AAC92864;
XX
DT 27-MAR-2001 (first entry)
XX
DE Human PI3 kinase p55 gamma antisense oligonucleotide, SEQ ID NO:47.
XX
KW Human phosphatidylinositol 3-kinase p55 gamma regulatory subunit;
KW PI3 kinase p55 gamma; hp55-gamma; PIK3R3; p55PIK;
KW signal transduction; downstream effector; receptor tyrosine kinase;
KW insulin receptor; IR; insulin-like growth factor receptor; IGF1R;
KW cell growth; differentiation; apoptosis; developmental regulation;
KW alternative splicing; tumour formation; cancer; inflammation; infection;
KW expression inhibition; phosphothioate; antisense oligonucleotide; ss.
OS Homo sapiens.
XX
XX US6165790-A.
XX
XX 26-DEC-2000.
XX
XX 03-NOV-1999; 99US-00433694.
XX
XX 03-NOV-1999; 99US-00433694.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Borchers AH, Cowsett LM, Ward DT;
XX WPI; 2001-101697/11.
XX
XX Novel antisense compound targeted to human PI3 kinase p55 gamma
XX specifically hybridizes with and inhibits the expression of human PI3
XX kinase p55 gamma, useful for modulating the expression of PI3 kinase p55
XX gamma in cells.
XX
XX Claim 14; Col 41-42; 39pp; English.
XX
XX Sequences AAC92827-C92906 represent phosphothioate antisense
XX oligonucleotides targeted to the phosphatidylinositol 3-kinase p55 gamma
XX regulatory subunit (PI3 kinase p55 gamma) gene, which inhibit its
XX expression. The antisense oligonucleotides were designed to target
XX different regions of human PI3 kinase p55 mRNA species, and were analysed
XX for their effect on PI3 kinase p55 mRNA levels by quantitative real-time
XX PCR. PI3 kinase p55 gamma (also known as hp55-gamma, PIK3R3
XX and p55PIK) is one of several PI3 kinase regulatory subunits that may
XX associate with the PI3 kinase catalytic subunit to form a heterodimeric
XX PI3 kinase holoenzyme. PI3 kinases act as downstream effectors of
XX receptor tyrosine kinases such as growth factor and hormone receptors and
XX oncogene products, and are found in association with the cytoplasmic
XX domains of such receptors. PI3 kinase p55 gamma is able to interact with
XX both the insulin receptor (IR) and the insulin-like growth factor
XX receptor (IGF1R), which play important roles in growth, differentiation
XX and apoptosis. PI3 kinase p55 gamma is thought to be developmentally
XX regulated, as four distinct mRNA species are found in adult tissues,
XX while only the larger mRNA is expressed in foetal tissues. The
XX oligonucleotides of the invention are useful for diagnosis, prevention
XX and treatment of conditions associated with PI3 kinase p55 expression,

CC While only the larger mRNA is expressed in foetal tissues. The
 CC oligonucleotides of the invention are useful for diagnosis, prevention,
 CC and treatment of conditions associated with P13 kinase p55 expression,
 CC such as tumour formation, inflammation and certain infections, and allow
 CC expression level modulation of the alternatively spliced forms of P13
 CC kinase p55
 XX
 SQ Sequence 20 BP; 9 A; 2 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1283 TGTGCTCCTGTGACA 1297
 DB 19 TGTGATCCTGTGACA 5

RESULT 1600
 AAH44820
 ID AAH44820 standard; DNA; 20 BP.
 XX
 AC AAH44820;
 XX
 DT 31-AUG-2001 (first entry)
 XX
 DE Antisense oligonucleotide targeting murine AChE mRNA.
 XX
 KW Antisense oligonucleotide; acetylcholine esterase; AChE; dystonia;
 KW cholinergic neurotransmission; progressive neuromuscular disorder;
 KW myasthenia gravis; Eaton-Lambert disease; muscular dystrophy; PTSD;
 KW amyotrophic lateral sclerosis; post-traumatic stress disorder;
 KW multiple sclerosis; post-stroke sclerosis; post-injury muscle damage;
 KW excessive re-innervation; mouse; ss.
 XX
 OS Mus musculus.

XX WO200136627-A2.
 XX 25-MAY-2001.
 XX 16-NOV-2000; 2000WO-IL000763.
 XX 16-NOV-1999; 99IL-00132972.
 XX (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 XX Soreq H, Seidman S;
 XX WPI; 2001-336003/35.
 XX
 PT New antisense oligonucleotide targeted to acetylcholine esterase mRNA,
 PT useful for treating or preventing progressive neuromuscular disorders
 PT such as myasthenia gravis.
 XX
 PS Claim 28; Page 92; 124pp; English.

XX Sequences AAH44810 - AAH44822 represent antisense oligonucleotides
 CC targeting the acetylcholine esterase (AChE) mRNA. AChE is involved in the
 CC termination of cholinergic neurotransmission, by hydrolysing the
 CC neurotransmitter acetylcholine. Mammalian AChE is encoded by one gene but
 CC alternative splicing at its 3' end yields three different mRNA
 CC transcripts which encode protein with distinct carboxyl termini. All
 CC three proteins are catalytically active. AChE has morphogenic, non-
 CC catalytic capacities too. AChE antisense oligonucleotides are used in
 CC treating or preventing a progressive neuromuscular disorder. Examples of
 CC disorders which are treatable using the antisense oligonucleotides
 CC include myasthenia gravis, Eaton-Lambert disease, muscular dystrophy,
 CC amyotrophic lateral sclerosis, post-traumatic stress disorder (PTSD),
 CC multiple sclerosis, dystonia, post-stroke sclerosis, post-injury muscle
 CC damage, excessive re-innervation and post-exposure to AChE inhibitors
 XX
 SQ Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1335 AGAGGAGGAGGAGGG 1349
 DB 1 AGAGGAGGAGGAGGG 15

RESULT 1601
 AAC92613/C
 ID AAC92613 standard; DNA; 20 BP.

XX AAC92613;
 AC AAC92613;
 XX
 DT 27-MAR-2001 (first entry)

XX Human nucleolin phosphorothioate antisense oligonucleotide, SEQ ID NO:63.
 XX
 KW Human nucleolin; P92; C23; phosphoprotein; ribosome biogenesis;
 KW ribosome transport; cytokinesis; nucleogenesis; cell proliferation;
 KW cell growth; transcriptional repression; replication;
 KW signal transduction; chromatin decondensation; Ag-NOR family;
 KW nucleolin antibody; systemic connective tissue disease; SLE;
 KW systemic lupus erythematosus;
 KW scleroderma-like chronic graft versus host disease;
 KW expression inhibition; tumour formation; cancer; inflammation;
 KW immune disorder; phosphorothioate; antisense oligonucleotide; ss.
 XX
 OS Homo sapiens.

XX US6165786-A.
 XX 26-DEC-2000.
 XX 03-NOV-1999; 99US-00433699.
 XX 03-NOV-1999; 99US-00433699.

XX (ISIS-) ISIS PHARM INC.
 XX Bennett CF, Cowsett LM;
 XX WPI; 2001-079848/09.
 XX
 PT Novel antisense compound targeted to human nucleolin which specifically
 PT hybridizes with and inhibits the expression of human nucleolin, useful
 PT for modulating the expression of nucleolin in cells.

XX Claim 14; Col 43-44; 41pp; English.
 XX
 CC Sequences AAC92560-C92639 represent antisense oligonucleotides targeted
 CC to the human nucleolin gene, which inhibit its expression. The antisense
 CC oligonucleotides were designed to target different regions of the human
 CC nucleolin mRNA, and were analysed for their effect on nucleolin mRNA
 CC levels by quantitative real-time PCR. Nucleolin (also known as P92 or
 CC C23) is the most abundant nucleolar phosphoprotein in actively growing
 CC cells. Nucleolin primarily participates in ribosome biogenesis and
 CC transport of ribosomal components, being able to transiently bind to pre-
 CC ribosomes in the nucleolus via a ribonucleoprotein consensus sequence.
 CC However, it has also been shown to be involved in cytokinesis, cell
 CC nucleogenesis, cell proliferation and growth, transcriptional repression,
 CC replication, signal transduction, and chromatin decondensation. Nucleolin
 CC is a member of the Ag-NOR (active ribosomal gene located in the nucleolar
 CC organiser region) family of proteins which are markers of active
 CC ribosomal genes, and whose expression is associated with the prediction
 CC of tumour growth rate. The presence of antibodies against nucleolin are
 CC associated with systemic connective tissue diseases such as systemic
 CC lupus erythematosus (SLE) and scleroderma-like chronic graft versus host
 CC disease. The oligonucleotides of the invention are useful for diagnosis,
 CC prevention and treatment of conditions associated with nucleolin
 CC expression, such as tumour formation, immune disorders and inflammation

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XX SQ Sequence 20 BP; 2 A; 6 C; 3 G; 9 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 328 AAGCAGATGCAGAGA 342
Db 17 AAGCTGATGCAGAGA 3

RESULT 1602
AAH41757/c
ID AAH41757 standard; DNA; 20 BP.
XX
AC AAH41757;
XX
DT 29-AUG-2001 (first entry)
XX
DE VEGF receptor gene PCR primer SEQ ID NO:4.
XX
KW Base; string; tape; circular disc; ligand; immobilised; PCR primer;
KW detection; diagnosis; ss.
XX
OS Synthetic.
XX
PN WO200135098-A1.
XX
PD 17-MAY-2001.
XX
PF 24-OCT-2000; 2000WO-JP007415.
XX
PR 05-NOV-1999; 99JP-00315610.
XX
PA (TAKI ) TAKARA SHUZO CO LTD.
XX
PI Kato I, Izu H, Asada K;
XX
DR WPI; 2001-343623/36.
XX
PT String, tape or disk shaped bases with several different immobilized
PT ligands including nucleic acids, sugars, peptides and proteins.
XX
PS Example 1; Page 30; 56pp; Japanese.
XX
CC The present invention describes bases in the shape of a string, tape or
CC circular disc on the surface of which a plural number of different
CC ligands are immobilised respectively in pre-determined domains. Also
CC described are devices for detecting the binding between the ligands and
CC receptors and methods for detection using these bases. The methods are
CC useful for detection in biochemical and diagnostic assays. The ligands
CC are immobilised in line, so the user only needs to determine the presence
CC or absence of receptor binding, without further processing. AAH41754 to
CC AAH41815 represent primers which are used in an example from the present
CC invention
XX
SQ Sequence 20 BP; 9 A; 5 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 458 CTGTGAATTGGCTG 472
Db 15 CTGTGAATTGGCTG 1

RESULT 1603
AAF59911
ID AAF59911 standard; DNA; 20 BP.
XX
AC AAF59911;

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XX 04-MAY-2001 (first entry)
XX Human transferrin receptor PCR primer, SEQ ID NO:5.
XX Human transferrin receptor; immobilised double-stranded DNA; DNA chip;
XX nucleotide array; expression monitoring; complete genome; PCR primer; ss.
XX Homo sapiens.
XX WO200107593-A1.
XX
XX 01-FEB-2001.
XX
XX 17-JUL-2000; 2000WO-JP004791.
XX
XX 23-JUL-1999; 99JP-00209782.
XX (TAKI ) TAKARA SHUZO CO LTD.
XX Asada K, Ueda M, Takayama M, Mineno J, Kimizuka F, Kato I;
XX WPI; 2001-182786/18.
XX
XX New DNA chip with two-stranded DNA immobilized onto a support under
XX denaturing conditions, useful for high sensitivity monitoring of active
XX gene expression from whole genome.
XX Example 2; Page 26; 32pp; Japanese.
XX
XX The invention relates to a novel DNA chip comprising double-stranded DNA
XX immobilised under denaturing conditions and aligned on a predetermined
XX region of the surface of a support. The invention also encompasses a DNA
XX solution for use in the preparation of the chip, which contains the DNA
XX to be immobilised together with a volatile organic acid or its salt; and
XX the preparation of the DNA chip using the solution. The DNA chip is
XX useful for the monitoring of expression of active genes of a complete
XX genome. The chip has a high immobilisation ratio for short chain DNA and
XX a high detection sensitivity. Sequences AAF59909- AAF59915 represent
XX human transferrin receptor PCR primers used in an exemplification of the
XX invention
XX
XX SQ Sequence 20 BP; 4 A; 5 C; 2 G; 9 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1983 TCTGTCGTCTCTC 1997
Db 6 TCTGTCGTCTCTC 20

RESULT 1604
AAH48600/c
ID AAH48600 standard; DNA; 20 BP.
XX
AC AAH48600;
XX
XX 20-SEP-2001 (first entry)
XX
XX Human fascin associated primer SEQ ID 52.
XX
XX Fascin; regulatory sequence; human; dendritic cell; antiviral; tumor;
XX antibacterial; antifungal; antiparasitic; anti-allergic; neurological;
XX immunomodulatory; apoptotic; expression regulator; vaccine; allergen;
XX Creutzfeld-Jakob disease; Alzheimer's disease; gene therapy;
XX autoimmune disease; transplant rejection; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200151631-A2.
XX

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PD 19-JUL-2001.
 PF 12-JAN-2001; 2001WO-EP000362.
 XX
 PF 13-JAN-2000; 2000DE-01001169.
 PR 02-MAR-2000; 2000DE-01010188.
 XX
 PA (RESK/) RESKE-KUNZ A.
 PA (ROSS/) ROSS X.
 PA (ROSS/) ROSS R.
 PA (BROS/) BROS M.
 XX
 PI Reske-Kunz A, Ross X, Ross R, Bros M;
 XX WPI; 2001-451858/48.
 DR
 XX New regulatory sequences from the fascin gene, useful for providing
 PT dendritic cell-specific expression of e.g. antigens, e.g. for vaccination
 PT against tumors and infections.
 XX
 PS Claim 2b; Page 108; 117pp; German.
 XX
 CC This invention describes novel regulatory sequences (A) derived from
 CC human fascin that provide specific expression in dendritic cells (DC) and
 CC which have antiviral, antibacterial, antifungal, antiparasitic, anti-
 CC allergic, neurological, immunomodulatory and apoptotic activity. (A) are
 CC used to regulate expression of antigens, immunoregulators, antisense
 CC sequences etc. in DC-specific fashion. Recombinant DNA, vectors and host
 CC cells that contain (A) are useful: (i) in vaccines against viruses,
 CC bacteria, fungi, parasites, tumors, allergens and plaques in Creutzfeld-
 CC Jakob and Alzheimer's disease; and (ii) for gene therapy of tumors,
 CC allergies, infections, autoimmune diseases and transplant rejection. They
 CC can also be provide specific expression of antigens and immunoregulators
 CC in DC; for isolation and identification of cell factors and cis-elements
 CC from regulatory sequences that mediate DC-specific expression; to
 CC determine the degree of maturity of DC and to block transcription
 CC factors, by providing binding sites in DC. (A) provide DC-specific
 CC expression of nucleic acid under their control, allowing a more specific
 CC regulation of the immune response and eliminating the long and laborious
 CC purification of DC (since a complete leucocyte population may be
 CC transformed), including transformation in vitro. This sequence represents
 CC a primer associated with the human fascin gene described in the invention
 XX
 SQ Sequence 20 BP; 1 A; 10 C; 2 G; 7 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1334 AAGAGGAGGGAGG 1348
 DB 19 AGGAGGAGGGAGG 5
 RESULT 1605
 AAD11744
 ID AAD11744 standard; DNA; 20 BP.
 XX
 AC AAD11744;
 XX
 DT 24-SEP-2001 (first entry)
 XX
 DE Human AAG6 DNA exon 1.10 amplifying reverse PCR primer #10.
 XX
 KW Human; asthma-associated gene; AAG6; antiinflammatory; gene therapy;
 KW obstructive airway disease; asthma; chronic bronchitis; eosinophila;
 KW adult respiratory distress syndrome; ARDS; dyspnoea; emphysema; COPD;
 KW COAD; chronic obstructive or pulmonary disease; pneumoconiosis;
 KW eosinophil related disorder; bronchopulmonary aspergillosis;
 KW Loffler's syndrome; polyarteritis nodosa; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX

PN WO200155214-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 23-JAN-2001; 2001WO-EP000719.
 XX
 PR 25-JAN-2000; 2000US-00490616.
 XX
 XX (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX
 PI Whittaker PA, Jones SJ, Hanley MT;
 XX WPI; 2001-457719/49.
 DR
 XX Novel polypeptide AAG6 useful for treating an inflammatory or obstructive
 PT airways disease, e.g., asthma.
 XX
 XX Example 2; Page 26; 62pp; English.
 XX
 CC The invention relates to human asthma-associated gene designated as AAG6.
 CC AAG6 is used in the diagnosis, prognosis and treatment of inflammatory or
 CC obstructive airway diseases such as asthma, adult respiratory distress
 CC syndrome (ARDS), chronic obstructive or pulmonary disease (COPD or COAD),
 CC chronic bronchitis, dyspnoea, emphysema and pneumoconiosis. AAG6 is also
 CC used in the treatment of eosinophil related disorders such as
 CC eosinophila, eosinophilic pneumonia, Loffler's syndrome, bronchopulmonary
 CC aspergillosis, polyarteritis nodosa and eosinophilic granuloma. AAG6 DNA
 CC is useful in gene therapy. The present sequence is a PCR primer used for
 CC amplifying human AAG6 DNA
 XX
 SQ Sequence 20 BP; 2 A; 7 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1540 CTGAGTCCCTCAGT 1554
 DB 1 CTGAGTCCCTCAGT 15
 RESULT 1606
 AAF85738
 ID AAF85738 standard; DNA; 20 BP.
 XX
 AC AAF85738;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE Human TrkA coding sequence PCR primer #1.
 XX
 KW Human; glial cell line-derived growth factor; GDNF; corneal defect;
 KW epidermal healing; wound healing; wound healing disorder; scarring;
 KW gene therapy; neurturin; persephin; artemin; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200130375-A2.
 XX
 PD 03-MAY-2001.
 XX
 PF 30-OCT-2000; 2000WO-EP010674.
 XX
 PR 29-OCT-1999; 99EP-00121597.
 XX
 PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
 XX
 PI Hanke M, Kruse F, Paulista M, Pohl J;
 XX WPI; 2001-316290/33.
 DR
 XX Use of glial cell line-derived growth factor for epidermal and stromal
 PT

PT wound healing, and treating wound healing or scarring disorders,
 PT particularly for treating corneal defects.
 XX
 PS
 PS Example; Page 28; 60pp; English.
 XX
 CC The present invention describes the use of glial cell line-derived growth
 CC factor (GDNF) or a derivative in the manufacture of pharmaceutical
 CC compositions for epidermal and wound healing, the treatment of epidermal
 CC and stromal wound healing disorders and scarring disorders. In
 CC particular, they are useful for treating corneal defects. Alternatives to
 CC GDNF are neurturin, persephin and artemin. The present sequence is a PCR
 CC primer used to clone the human TrkA gene in the exemplification of the
 CC invention
 XX
 XX SQ Sequence 20 BP; 3 A; 5 C; 10 G; 2 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 951 GATGCTGGAGGCGG 965
 Db 1 GATGCTGGAGGCGG 15
 ||||| |||||
 RESULT 1607
 AAF89396
 ID AAF89396 standard; DNA; 20 BP.
 AC AAF89396;
 XX
 DT 14-AUG-2001 (first entry)
 XX
 DE Unknown base determining method probe #5.
 XX
 KW Base determination; sequencing; probe; ss.
 XX
 OS Synthetic.
 XX
 XX US6228593-B1.
 PN
 XX 08-MAY-2001.
 PD
 XX
 PF 14-JAN-2000; 2000US-00483190.
 XX
 PR 14-SEP-1995; 95US-00528656.
 PR 10-OCT-1997; 97US-00948896.
 XX
 XX (AFFY-) AFFYMETRIX INC.
 PA
 XX Lipshutz RJ, Walker MG;
 PI
 XX WPI; 2001-353685/37.
 DR
 XX
 XX Computer-aided probability base calling for arrays of nucleic acid probes
 PT on chips, useful for evaluating and comparing biological sequences,
 PT comprises inputting base calls each having an associated value for
 PT unknown base.
 XX
 XX Disclosure; Fig 7; 30pp; English.
 PS
 XX The present invention describes a computer implemented method of calling
 CC an unknown base in a sample nucleic acid, involving inputting nucleotide
 CC options where each base has an associated value, and selecting one of the
 CC options depending on the values. The method can be used for evaluating
 CC and comparing biological sequences and for forming arrays of DNA that may
 CC be used to study and detect mutations relevant to cystic fibrosis, the
 CC p53 gene, HIV, and other genetic characteristics. The method may also be
 CC used to analyse hybridization intensity files for a chip containing
 CC hybridized nucleic acid probes, and to analyse other measurements of
 CC hybridization. The present sequence is a probe used in the
 CC exemplification of the invention
 XX

SQ Sequence 20 BP; 7 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 270 CGATGACTACATTAA 284
 Db 4 CGATAACTACATTAA 18
 ||||| |||||
 RESULT 1608
 AAD17619
 ID AAD17619 standard; DNA; 20 BP.
 AC AAD17619;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE Human Hnf-3 gene specific reverse RT-PCR primer.
 XX
 KW Embryonic stem cell; ES; inner cell mass; neural progenitor cell;
 KW glial cell; neurodegenerative disorder; vascular condition; trauma;
 KW autoimmune disorder; congenital disorder; haemangioblast stem cell;
 KW haematopoietic stem cell; reverse transcription PCR; RT-PCR primer;
 KW Hnf-3 gene; neuron; cell therapy; gene therapy; ICM; human; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200168815-A1.
 PN
 XX 20-SEP-2001.
 PD
 XX 14-MAR-2001; 2001WO-AU000278.
 PF
 XX 14-MAR-2000; 2000AU-00006211.
 PR 06-NOV-2000; 2000AU-00001279.
 PR 06-FEB-2001; 2001AU-00002920.
 XX
 XX (MONU) UNIV MONASH.
 PA (UYSI-) UNIV SINGAPORE NAT.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
 PA (REUB-) REUBINOFF.
 XX
 XX Pera MF, Ben-Hur T;
 PI
 XX WPI; 2001-582442/65.
 DR
 XX
 XX Preparing undifferentiated human embryonic stem cells for differentiation
 PT into neural progenitor cells, involves culturing inner cell mass removed
 PT in vitro fertilized human embryo under specific conditions.
 XX
 XX Disclosure; Page 63; 125pp; English.
 PS
 XX The invention relates to a method for preparing undifferentiated human
 CC embryonic stem (ES) cells for differentiation into neural progenitor
 CC cells. The method involves growing an in vitro fertilized human embryo to
 CC blastocyst stage of development; removing inner cell mass (ICM) cells
 CC from the embryo; culturing ICM cells so that extraembryonic
 CC differentiation and cell death is not induced and proliferation of
 CC undifferentiated ES cells is promoted; and recovering ES cells. ES cells
 CC are useful for producing an enriched preparation of human ES- derived
 CC neuronal progenitor cells. The neural progenitor cells when transplanted
 CC into host nervous system are useful for establishing a stable graft and
 CC contributing in the histogenesis of a living host. Production of a stable
 CC graft of neural cells is useful for modifying nervous system of a host
 CC which includes replacing deficient neuronal or glial cell populations,
 CC restoring deficient functions, or activating regenerative and healing
 CC processes in the nervous system. Neural progenitor cells cultured in
 CC spheres for these processes comprise a genetically modified neuronal
 CC progenitor cells which express specific desired genes at the target
 CC organ. Modifying a nervous system of a host is useful for treating a
 CC pathological condition of nervous system, such as neurodegenerative

disorders, vascular conditions, autoimmune disorders, congenital disorders and trauma. ES cells on differentiation forms progenitor cells, preferably neural progenitor cells or mesodermal progenitor cells including haemangioblast or haematopoietic stem cells. Neural progenitor cells on differentiation forms somatic cells such as neurons and/or glial cells. The methods of the invention are useful in cell therapy and gene therapy. The present sequence is human Hnf-3 gene specific (reverse transcription PCR) RT-PCR primer. This primer is used to study the expression of Hnf-3 gene which is used as a marker for characterising neural progenitor cells in the sphere

XX SQ Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1209 GGCATTCTCTGAGGA 1223
 ||| |||||
 Db 4 GGCATTCTCTGAGGA 18

RESULT 1609
 AAH20673
 ID AAH20673 standard; DNA; 20 BP.
 XX AC AAH20673;
 DT 13-AUG-2001 (first entry)
 XX DE Human telomeric repeat binding factor 2 oligonucleotide 111401.
 DE KW Antisense; phosphorothioate; human; telomeric repeat binding factor 2;
 KW inhibitor; premature aging; hyperproliferative disorder; cancer;
 KW Cytostatic; ss.
 XX OS Homo sapiens.

Key Location/Qualifiers
 modified_base 1..20
 /tag= b
 /mod_base= OTHER
 /note= "phosphorothioate backbone"
 modified_base 1..3
 /tag= a
 /mod_base= OTHER
 /note= "2-O-methoxyethyl"
 modified_base 13..20
 /tag= c
 /mod_base= OTHER
 /note= "2-O-methoxyethyl"

WO200143752-A1.
 21-JUN-2001.
 14-DEC-2000; 2000WO-US033954.
 17-DEC-1999; 99US-00467642.
 (ISIS-) ISIS PHARM INC.
 Monia BP, Cowser LM;
 WPI; 2001-398071/42.
 Antisense compounds targeted to nucleic acid encoding telomeric repeat binding factor 2 useful for treating conditions such as premature aging and diseases such as cancer.
 Example 15; Page 80; 108pp; English.
 This invention describes a novel antisense compound (I) 8-30 nucleobases

in length targeted to a polynucleotide encoding human telomeric repeat binding factor 2 (II) which specifically hybridizes with, and inhibits the expression of (II). (I) is useful for treating a human having a disease or condition associated with (II) such as premature aging or a hyperproliferative disorder especially cancer, by inhibiting the expression of (II) in human cells or tissues. (I) is useful for diagnostics, therapeutics, prophylaxis and as research reagents and kits. The products of the invention have cytostatic activity. This sequence represents an antisense oligonucleotide used to illustrate the method of the invention

XX SQ Sequence 20 BP; 3 A; 2 C; 11 G; 4 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 947 TCGTGATGCTGGGAG 961
 ||| |||||
 Db 6 TCGTGATGCTGGGAG 20

RESULT 1610
 ABK86216
 ID ABK86216 standard; DNA; 20 BP.
 XX AC ABK86216;
 DT 24-SEP-2002 (first entry)
 XX DE Probe #5 used in computer based sequence identification method.
 DE KW Probe; human immunodeficiency virus; HIV; nucleic acid analysis; ss.
 XX OS Synthetic.
 XX PN US2002058261-A1.
 PD 16-MAY-2002.
 XX PF 20-MAR-2001; 2001US-00814144.
 XX PR 14-SEP-1995; 95US-00528656.
 PR 10-OCT-1997; 97US-00948896.
 PR 14-JAN-2000; 2000US-00483190.
 XX PA (LIPS/) LIPSHUTZ R J.
 PA (WALK/) WALKER M G.
 XX PI Lipshutz RJ, Walker MG;
 XX DR WPI; 2002-526899/56.

Computer-implemented unknown base calling method for nucleic acid sequence sample analysis, comprises determining probability corresponding to each probe best hybridizes for each probe intensity.

Disclosure; Fig 7; 41pp; English.

The invention relates to a method involving a computer system, for identifying an unknown base in a sample nucleic acid sequence comprising: (a) inputting a number of hybridisation probe intensities, each corresponding to a nucleic acid probe; (b) determining a probability that the corresponding nucleic acid probe best hybridises with the sample nucleic acid; and (c) identifying the unknown base according to the nucleic acid probe with the highest associated probability. Also described is the computer program storing instructions for calling an unknown base. The method is used for calling an unknown base for analysing a nucleic acid sequence sample for analysing DNA or RNA, human immunodeficiency virus (HIV) and other genetic characteristics. The method facilitates analysis of fluorescence and other measurements of hybridisation. Specific mutations in DNA or RNA are identified with improved operation efficiency, by providing high accurate base calling

CC within the dark regions around mutations. The present sequence represents
 CC a probe used in the method of the invention

XX Sequence 20 BP; 7 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 270 CGATGACTACATTAA 284
 ||||| ||||| ||||| |||||
 Db 4 CGATACTACATTAA 18

RESULT 1611
 AAH77195
 ID AAH77195 standard; DNA; 20 BP.

XX AAH77195;
 XX 07-AUG-2003 (revised)
 DT 24-JAN-2002 (first entry)
 XX PCR primer PV4 used to amplify HPV in human cervical cancer cells.

XX Human; Cervical cancer; human papilloma virus; PCR primer; PV4; SiHa;
 KW HPV; Thermal cycling; AIDS; ss.

XX Human papillomavirus.

XX US6300124-B1.

XX 09-OCT-2001.

XX 02-NOV-1999; 99US-00432012.

XX 02-NOV-1999; 99US-00432012.

XX (MINU) UNIV MINNESOTA.

XX Blumenfeld M, Bar-Cohen A, Cibuzar GT, Schiller P, Arik M;

XX WPI; 2002-009526/01.

XX Microscopic slide temperature control apparatus for medical diagnosis
 PT comprises coupling resistive heating element between the connection pads
 PT provided at opposing ends of slide.

XX Example 3; Col 27; 25pp; English.

XX The sequence represents PCR primer PV4. The primer was used in the
 CC invention to amplify DNA from cells of the stable human cervical cancer
 CC cell line SiHa, containing an integrated copy of human papilloma virus
 CC (HPV) type 16 per human genome. The invention relates to a novel thermal
 CC cycling device for regulating the temperature of a biological sample on a
 CC flat substrate. The invention also includes an apparatus comprising the
 CC flat substrate for use in the thermal cycling device. The invention is
 CC useful for medical diagnosis of diseases such as AIDS, also for
 CC amplification of nucleic acids in biological samples. The invention has
 CC the advantage that it enhances operatively as the heat resisting element
 CC is directly coupled to the microscopic slide, and reduces costs as the
 CC use of a heat sink is eliminated. (Updated on 07-AUG-2003 to correct OS
 CC field.)

XX Sequence 20 BP; 2 A; 6 C; 1 G; 11 T; 0 U; 0 Other;

XX Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1875 ATCTCCTGTTTTTT 1889

Db 1 ATCCCTGTTTTTT 15

RESULT 1612
 ABK33223/c

XX ABK33223 standard; DNA; 20 BP.

XX ABK33223;

XX 23-APR-2002 (first entry)

XX Human vascular endothelial growth factor VEGF-B-associated primer #15.

XX Human; vascular endothelial growth factor B; VEGF-B; cytostatic;
 KW antidiabetic; ophthalmological; antipsoriatic; tumour; metastasis;
 KW rheumatoid arthritis; ocular; diabetic retinopathy; angiogenesis; iris;
 KW retinal vein occlusion; angiogenesis-dependent tumour; psoriasis;
 KW arthropathy; vascular tumour; haemangioma; primer; ss.

XX Unidentified.

XX US6331301-B1.

XX 18-DEC-2001.

XX 06-MAY-1997; 97US-00851896.

XX 01-MAR-1995; 95US-00397651.

XX 06-JUN-1995; 95US-00469427.

XX 06-DEC-1995; 95US-00569063.

XX 01-MAR-1996; 96US-00609443.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (UYHE-) UNIV HELSINKI LICENSING LTD OY.

XX Eriksson U, Olofsson B, Alitalo K, Pajusola K;

XX WPI; 2002-129543/17.

XX New antibody, reacting with a vascular endothelial growth factor B (VEGF-

XX B) protein, is useful in tumor diagnosis and retardation.

XX Disclosure; Col 59; 52pp; English.

XX The invention relates to an antibody (I) that reacts with a vascular
 CC endothelial growth factor B (VEGF-B) protein (II) having a characteristic
 CC formula, where (II) has the property of promoting proliferation of
 CC endothelial cells or mesodermal cells. (I), when labelled, can be used to
 CC quantitatively detect (II) in a test sample, comprising contacting the
 CC sample with (I) and detecting binding of (I). Assays for VEGF-B
 CC expression can be used as tools in tumour diagnosis, and suppression of
 CC VEGF-B expression, e.g., using (I) may be useful to retard tumour growth.
 CC (I) could be used as an indicator of metastatic risk. Labelled (I), in
 CC particular, should be useful in screening for conditions associated with
 CC abnormal levels of VEGF-B in the body. For example, an assay of VEGF-B in
 CC synovial fluids and/or joint tissue by immunofluorometric techniques may
 CC be useful as a diagnostic indicator of rheumatoid arthritis. A
 CC radioimmunoassay of VEGF-B in ocular fluid using techniques may be useful
 CC as a diagnostic indicator of diabetic retinopathy, neovascularisation of
 CC the iris or retinal vein occlusion. Immunoassays of VEGF-B levels in
 CC blood, urine or other bodily fluids may be useful also as a tumour
 CC marker. (I) may also be useful in inhibiting angiogenesis associated with
 CC high levels of VEGF-B in the body, e.g. in rapidly proliferating,
 CC angiogenesis-dependent tumours in mammals, and thereby may retard the
 CC growth of such tumours. Treatment with (I) may be useful to suppress or
 CC inhibit tumour growth in vivo. (I) also may be useful to inhibit new
 CC blood vessels in diabetic retinopathy, psoriasis, arthropathies and/or
 CC vascular tumours such as haemangiomas. ABK33190- ABK33235 represent VEGF-
 CC B coding sequences and PCR primers of the invention

XX Sequence 20 BP; 2 A; 9 C; 7 G; 2 T; 0 U; 0 Other;

XX Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1183 CCGCAGCAGCTGGG 1197
 Db 20 CCGCAGCTACCTGGG 6

RESULT 1613
 ABT13276/c
 ID ABT13276 standard; DNA; 20 BP.
 XX
 AC ABT13276;
 XX
 DT 30-JAN-2003 (first entry)
 XX
 DE Fanconi anaemia FANCD exon amplifying PCR primer SEQ ID No 179.
 XX
 KW Cytostatic; dermatological; vasotropic; anti-anaemic; FA pathway defect;
 KW Fanconi anaemia protein complex; FANCD; DNA repair; Cockayne's syndrome;
 KW cell cycle abnormality; Fanconi anaemia; ataxia telangiectasia; cancer;
 KW Bloom's syndrome; Hereditary non-polyposis colon cancer; gene therapy;
 KW Xeroderma pigmentosum; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 EN WO200236761-A2.
 XX
 PD 10-MAY-2002.
 XX
 PF 02-NOV-2001; 2001WO-US045561.
 XX
 PR 03-NOV-2000; 2000US-0245756P.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 XX
 PI D'andrea AD, Taniguchi T, Timmers C, Grompe M;
 XX
 DR WPI; 2002-519251/55.
 XX
 PT Novel isolated Fanconi anemia protein complex polypeptide, termed FANCD2,
 PT useful for treating Fanconi anemia pathway defect in cell target or for
 PT treating patient with defective FANCD2 gene.
 XX
 PS Claim 8; Page 56; 103pp; English.
 XX
 CC The invention relates to an isolated Fanconi anaemia protein complex
 CC (FANCD2) polypeptide. The FANCD2 protein comprises a sequence of 1472
 CC amino acids fully defined in the specification, its 90% identical
 CC sequence, a sequence encoded by a polynucleotide that is at least 90%
 CC identical to sequences given in specification such as a 5127 base pair
 CC sequence, or a fragment which is at least 50 amino acids in length. The
 CC FANCD2 protein is useful for treating an FA pathway defect in a cell
 CC target or for treating a patient with a defective FANCD2 gene. The FANCD2
 CC gene is useful for making a recombinant expression vector. The FANCD2
 CC protein and its gene are useful as a novel target for therapeutic
 CC development, and in diagnostic test and screening assays for diseases
 CC associated with DNA repair and cell cycle abnormalities such as Fanconi
 CC anaemia, Bloom's syndrome, Cockayne's syndrome, Hereditary non-polyposis
 CC colon cancer, ataxia telangiectasia and Xeroderma pigmentosum. The FANCD2
 CC gene is useful in producing probes and primers for screening patients in
 CC genetic based test, for diagnosing Fanconi anaemia and cancer, for
 CC preparing an experimental mouse model for use in screening new
 CC therapeutics for treating conditions involving defective DNA repair, and
 CC in gene therapy methods. A recombinant vector containing the FANCD2 gene
 CC of the invention is useful in gene therapy. This polynucleotide sequence
 CC represents a PCR primer for amplifying a FANCD2 exon relating to the
 CC invention
 XX
 SQ Sequence 20 BP; 5 A; 3 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 939 CCTGCTATGCTGAT 953
 Db 20 CCAGCCTATGCTGAT 6

RESULT 1614
 AAS98015
 ID AAS98015 standard; DNA; 20 BP.
 XX
 AC AAS98015;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Murine SAC1 gene-specific oligonucleotide PCR primer #568.
 XX
 KW Human; mouse; SAC1; carbohydrate; sweetener; ethanol; alcoholism; ss;
 KW obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
 KW blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
 KW protein replacement therapy.
 XX
 OS Mus sp.
 XX
 PN WO200183749-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 25-APR-2001; 2001WO-US013387.
 XX
 PR 28-APR-2000; 2000US-0200794P.
 XX
 PR 28-JUL-2000; 2000US-0221419P.
 PR 10-NOV-2000; 2000US-0247443P.
 XX
 PA (WARN) WARNER LAMBERT CO.
 PA (MONE-) MONELL CHEM SENSES CENT.
 XX
 PI Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PJ, Li S, Li X;
 PI Ohmen JD, Reed DR, Ross D, Tordoff MG;
 XX
 DR WPI; 2002-075162/10.
 XX
 PT Novel isolated polypeptide comprising variant form of mouse or human SAC1
 PT polypeptide, and is associated with altered preference for carbohydrates
 PT or other sweeteners, useful for preventing obesity, diabetes, alcoholism.
 XX
 PS Claim 14; Page 96; 239pp; English.
 XX
 CC The invention relates to an isolated polypeptide, comprising a variant
 CC form of mouse or human SAC1 polypeptide. The variant form is associated
 CC with altered preference for carbohydrates, other sweeteners or ethanol.
 CC The polypeptide and its associated DNA sequence can be produced by
 CC recombinant techniques and is useful for preventing obesity, diabetes or
 CC alcoholism associated with SAC1 expression. The sequences are useful in
 CC screening for drugs and sweeteners. Recombinant cell lines and transgenic
 CC embryos may be used in screening for and identifying agents that induce
 CC or repress function of SAC1. Predisposition to diabetes, obesity or
 CC alcoholism can be ascertained by testing any fluid or tissue of a human
 CC (such as blood, pancreas or tongue) for sequence variations of the SAC1
 CC gene. A sequence variation of the SAC1 locus may indicate a
 CC predisposition to diabetes, obesity and/or alcoholism and may provide a
 CC diagnostic mark. The polynucleotide can be detected in a biological
 CC sample by contacting the DNA with a probe to form a hybridisation complex
 CC which is then detected. The sequences represent cDNA encoding human and
 CC mouse SAC1 polypeptides and PCR primers specific for the SAC1 genes
 XX
 SQ Sequence 20 BP; 3 A; 10 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1516 GACCTCTCCAGCTCT 1530
 ||| |||||

Db 4 GACTTCTCCAGCTCT 18

RESULT 1615
ABK37133/c
ID ABK37133 standard; DNA; 20 BP.
XX
XX
AC ABK37133;
XX
XX 08-MAY-2002 (first entry)
DT
DT
XX
XX Human lysophospholipase I gene, antisense oligonucleotide #85.
DE
DE
XX
XX Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;
KW antilipidemic; cardiant; lysophospholipase I; inflammation; ischaemia;
KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;
KW antisense gene therapy; primer; ss.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX WO200210185-A1.
PN
XX
XX 07-FEB-2002.
PD
XX
XX 20-JUL-2001; 2001WO-US022975.
PF
XX
XX 31-JUL-2000; 2000US-00629645.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Bennett CF, Wyatt JR;
PI
XX
XX WPI; 2002-188720/24.
DR
XX
XX Novel antisense compound useful for treating inflammation,
PT hyperlipidemia, and cardiovascular disorders such as atherosclerosis and
PT myocardial ischemia, inhibits Lysophospholipase I.
XX
XX Claim 3; Page 82; 13lpp; English.
PS
XX The invention relates to an antisense compound (I) 8-30 nucleobases in
CC length targeted to a nucleic acid molecule encoding lysophospholipase I
CC (II), where (I) specifically hybridises with and inhibits the expression
CC of (II). (I) is useful for inhibiting the expression of (II) in cells or
CC tissues, and for treating a human having a disease or condition
CC associated with Lysophospholipase I e.g. inflammation, hyperlipidaemia,
CC and cardiovascular disorders such as atherosclerosis and myocardial
CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
CC useful for distinguishing functions of various members of a biological
CC pathway. (I) is useful in antisense gene therapy. ABK37028-ABK37191
CC represent lysophospholipase I coding sequences, antisense
CC oligonucleotides and related PCR primers of the invention. Note:
CC Antisense oligonucleotides are modified such that bases 1-5 and 16-20 are
CC 2'-methoxyethyl (2'-MOE) nucleotides, all bases have phosphorothioate
CC linkages, and all cytidines are 5-methyl cytidines
XX
SQ Sequence 20 BP; 7 A; 3 C; 2 G; 8 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1616 ATTAAATATAAATAT 1630
|||||||
Db 19 ATTAAATATGAATAT 5

RESULT 1616
ABS73936/c
ID ABS73936 standard; DNA; 20 BP.
XX
XX
AC ABS73936;

06-DEC-2002 (first entry)
Human cytohesin-1 3' UTR antisense oligonucleotide, ISIS#111029.
Human; antisense; cytohesin-1; guanine nucleotide exchange protein; ARF;
ADP ribosylation factor; inflammation; antiinflammatory; tumour;
cytostatic; ss.
Homo sapiens.
WO200268584-A2.
06-SEP-2002.
30-OCT-2001; 2001WO-US047583.
22-FEB-2001; 2001US-00791243.
(ISIS-) ISIS PHARM INC.
(BOEH) BOEHRINGER INGELHEIM PHARM INC.
Bennett CF, Rothlein R, Kishimoto TK, Cowsett LM;
WPI; 2002-723198/78.
New antisense oligonucleotide encoding human cytohesin-1, useful for
preventing or treating a disease or condition associated with cytohesin-1
expression e.g. tumor or inflammation.
Example 15; Page 81; 107pp; English.
The invention relates to a new antisense compound, comprising 8-30
nucleobases targeted to a nucleic acid molecule encoding human cytohesin-
1, specifically hybridises with, and inhibits the expression of, human
cytohesin-1, a guanine nucleotide exchange protein for ARF (ADP
ribosylation factor). The antisense compound may be used in a
pharmaceutical composition for inhibiting the expression of cytohesin-1
in human cells or tissues, and in treating a disease or condition
associated with cytohesin-1 by administering to the human the antisense
compound e.g. tumour or inflammation. The antisense compound is also
useful for diagnostics, therapeutics, prophylaxis and as research
reagents and kits. The present sequence is an antisense oligonucleotide
targeting human cytohesin-1
Sequence 20 BP; 6 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1798 ATCCCAAGTCCTGC 1812
|||||||
Db 15 ATCCCAAGTCCTGC 1

RESULT 1617
AAS17346/c
ID AAS17346 standard; DNA; 20 BP.
XX
XX AAS17346;
AC
XX
XX 29-AUG-2003 (revised)
DT 25-FEB-2002 (first entry)
DT
XX
XX Sequencing primer Seq3F for HIV-1 pol gene.
XX Human immunodeficiency virus; HIV-1; HIV pol gene mutation analysis;
KW AIDS; acquired immunodeficiency syndrome; sequencing primer; ss.
XX
XX Human immunodeficiency virus 1.
XX
XX WO200181624-A1.
PN


```

PF 04-APR-2001; 2001WO-US010958.
XX
PR 14-APR-2000; 2000US-0197271P.
XX
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Baranyi F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch.
XX
PS Example 5; Fig 29; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridize with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC medinesis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention
XX
SQ Sequence 20 BP; 0 A; 7 C; 4 G; 9 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 320 AGTACAGCAAGCAGA 334
DB 15 AGCACAGCAAGCAGA 1

RESULT 1622
ABI96229/C
ID ABI96229 standard; DNA; 20 BP.
XX
AC ABI96229;
XX
DT 16-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#3316 oligo #9.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
XX WO200179548-A2.
XX
XX 25-OCT-2001.
XX

PF 04-APR-2001; 2001WO-US010958.
XX
PR 14-APR-2000; 2000US-0197271P.
XX
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Baranyi F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch.
XX
PS Example 5; Fig 29; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridize with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC medinesis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention
XX
SQ Sequence 20 BP; 7 A; 6 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1528 TCTGGCTTCCTGCTG 1542
DB 15 TATGGCTTCCTGCTG 1

RESULT 1623
ABI96729/C
ID ABI96729 standard; DNA; 20 BP.
XX
AC ABI96729;
XX
DT 16-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#3816 oligo #9.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
XX WO200179548-A2.
XX
XX 25-OCT-2001.
XX

```

```

PF 04-APR-2001; 2001WO-US010958.
XX
PR 14-APR-2000; 2000US-0197271P.
XX
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch.
XX
PS Example 5; Fig 29; 300pp; English.
XX
XX The present invention describes a method (M1) for designing capture
XX oligonucleotide probes (I) for use on a support to which complementary
XX oligonucleotide probes (II) will hybridize with little mismatch, where
XX (I) have melting temperatures within a narrow range. The method is useful
XX for detecting infectious diseases caused by bacterial infectious agents
XX e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
XX infectious agents e.g. Cryptococcus neoformans, Candida albicans and
XX Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
XX Epstein-Barr virus and polio virus, and parasitic infectious agents
XX selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
XX medinensis. The method is also useful for detecting genetic diseases such
XX as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
XX CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
XX involved in DNA amplification, replication, recombination or repair, the
XX cancer is specifically associated with a gene selected from BRCA1 gene,
XX p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
XX method is also used for environmental monitoring, forensics and the food
XX and feed industry, detecting comprises scanning (using e.g. a scanning
XX electron microscope and infrared microscope) the support at the
XX particular sites and identifying if ligation of the oligonucleotide probe
XX sets occurred and correlating (using a computer) identified ligation to a
XX presence or absence of the target nucleotide sequences. AB182074 to
XX AB197546 represent oligonucleotide sequences used in the exemplification
XX of the present invention
XX
SQ Sequence 20 BP; 2 A; 7 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 60 CAAGATGGCGCAGAC 74
Db 20 CAAGATGGCGCAGGC 6
RESULT 1624
ABZ85828/C
ID ABZ85828 standard; DNA; 20 BP.
XX
XX AC ABZ85828;
XX
XX 17-OCT-2003 (first entry)
XX Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX

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XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Claim 15; SEQ ID NO 1070; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 8 A; 3 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1032 GATCCCTAATGAGCT 1046
Db 16 GATCTCTAATGAGCT 2
RESULT 1625
ABZ93174/C
ID ABZ93174 standard; DNA; 20 BP.
XX
XX AC ABZ93174;
XX
XX 17-OCT-2003 (first entry)
XX Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX

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XX PF 23-APR-2002; 2002WO-US013135.
XX PF
XX PR 24-APR-2001; 2001US-0286137P.
XX PR
XX PA (EPIG-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahabuddin S;
XX DR WPI; 2003-229219/22.
XX DR
XX PT Pharmaceutical composition for treating ailments associated with impaired
XX PT respiration, has oligo(s) antisense to specific gene(s) or its
XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX PT ubiquinone.
XX PS Disclosure; SEQ ID NO 8416; 872pp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a
XX CC first active agent comprising an oligonucleotide antisense to the
XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX CC junctions of genes encoding a polypeptide associated with lung and/or
XX CC nasal airway dysfunction and a second active agent comprising an
XX CC antiinflammatory steroid and ubiquinone. A composition of the invention
XX CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX CC immunosuppressive, and cytostatic activity. The composition may have a
XX CC use in antisense gene therapy. The composition is useful for treating or
XX CC preventing a respiratory, lung or malignant disease or condition, also
XX CC for enhancing the prophylactic or therapeutic respiratory effect of an
XX CC antiinflammatory steroid in a subject, for reducing or depleting levels
XX CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or
XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX CC lung inflammation, lung allergies, or a respiratory disease or condition.
XX CC Note: The sequence data for this patent is not represented in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 20 BP; 9 A; 3 C; 0 G; 8 T; 0 U; 0 Other;
      Query Match      0.6%; Score 13.4; DB 1; Length 20;
      Best Local Similarity 93.3%; Pred. No. 1.2e+03;
      Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 120 TCGAAATTAATTA 134
Db 15 TCGAAATTAATTA 1
      |||||
      15 TCGAAATTAATTA 1

RESULT 1626
ABZ93051
ID ABZ93051 standard; DNA; 20 BP.
XX AC ABZ93051;
XX AC
XX DT 17-OCT-2003 (first entry)
XX DE Human oligonucleotide sequence.
XX DE
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
XX KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
XX KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX KW lung inflammation; respiratory disease; ds.
XX OS Homo sapiens.
XX PN WO200285308-A2.
XX XX
XX PD 31-OCT-2002.

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XX PF 23-APR-2002; 2002WO-US013135.
XX PF
XX PR 24-APR-2001; 2001US-0286137P.
XX PR
XX PA (EPIG-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahabuddin S;
XX DR WPI; 2003-229219/22.
XX DR
XX PT Pharmaceutical composition for treating ailments associated with impaired
XX PT respiration, has oligo(s) antisense to specific gene(s) or its
XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX PT ubiquinone.
XX PS Disclosure; SEQ ID NO 8293; 872pp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a
XX CC first active agent comprising an oligonucleotide antisense to the
XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX CC junctions of genes encoding a polypeptide associated with lung and/or
XX CC nasal airway dysfunction and a second active agent comprising an
XX CC antiinflammatory steroid and ubiquinone. A composition of the invention
XX CC has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive,
XX CC immunosuppressive, and cytostatic activity. The composition may have a
XX CC use in antisense gene therapy. The composition is useful for treating or
XX CC preventing a respiratory, lung or malignant disease or condition, also
XX CC for enhancing the prophylactic or therapeutic respiratory effect of an
XX CC antiinflammatory steroid in a subject, for reducing or depleting levels
XX CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or
XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX CC lung inflammation, lung allergies, or a respiratory disease or condition.
XX CC Note: The sequence data for this patent is not represented in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 20 BP; 10 A; 0 C; 1 G; 9 T; 0 U; 0 Other;
      Query Match      0.6%; Score 13.4; DB 1; Length 20;
      Best Local Similarity 93.3%; Pred. No. 1.2e+03;
      Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1598 GTATTATATAAAA 1612
Db 6 GTATTATATAATA 20
      |||||
      6 GTATTATATAATA 20

RESULT 1627
ABZ89784
ID ABZ89784 standard; DNA; 20 BP.
XX AC ABZ89784;
XX AC
XX DT 17-OCT-2003 (first entry)
XX DE Human oligonucleotide sequence.
XX DE
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
XX KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
XX KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX KW lung inflammation; respiratory disease; ds.
XX OS Homo sapiens.
XX PN WO200285308-A2.
XX XX
XX PD 31-OCT-2002.

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XX 23-APR-2002; 2002WO-US013135.
PF
XX
XX 24-APR-2001; 2001US-0286137P.
PR
XX
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
PI
XX WPI; 2003-229219/22.
DR
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 5026; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiasthmatic, antiallergic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 5 A; 5 C; 0 G; 10 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1580 TATTTCTATTCTC 1594
Db |||||||
2 TATTTCTATTCTC 16

RESULT 1628
ABZ90246
ID ABZ90246 standard; DNA; 20 BP.
XX
XX ABZ90246;
AC
XX
XX 17-OCT-2003 (first entry)
DT
XX
XX Human oligonucleotide sequence.
DE
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200285308-A2.
PN
XX
XX 31-OCT-2002.
PD
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XX 23-APR-2002; 2002WO-US013135.
PF
XX
XX 24-APR-2001; 2001US-0286137P.
PR
XX
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
PI
XX WPI; 2003-229219/22.
DR
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 5488; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiasthmatic, antiallergic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 571 GTGCTGTACATTGAC 585
Db |||||||
3 GTGCTGTACATTGAC 17

RESULT 1629
ABZ93637
ID ABZ93637 standard; DNA; 20 BP.
XX
XX ABZ93637;
AC
XX
XX 17-OCT-2003 (first entry)
DT
XX
XX Human oligonucleotide sequence.
DE
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200285308-A2.
PN
XX
XX 31-OCT-2002.
PD
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XX 23-APR-2002; 2002WO-US013135.
 XX PF
 XX 24-APR-2001; 2001US-0286137P.
 PR XX
 XX (EPIC-) EPIGENESIS PHARM INC.
 PA XX
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 DR XX
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX PS
 XX Disclosure; SEQ ID NO 8879; 872pp; English.
 XX CC
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive, and
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX CC
 SQ Sequence 20 BP; 10 A; 2 C; 6 G; 1 T; 0 U; 1 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 87.5%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1441 ACCGAAGAGGAGAAAA 1456
 DB 1 ACCTAAGAGAGAAAA 16
 RESULT 1630
 ABZ87840
 ID ABZ87840 standard; DNA; 20 BP.
 XX AC
 XX ABZ87840;
 XX DT 17-OCT-2003 (first entry)
 XX DE
 XX Human oligonucleotide sequence.
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 OS Homo sapiens.
 XX PN WO200285308-A2.
 XX 31-OCT-2002.
 PD

XX 23-APR-2002; 2002WO-US013135.
 PF XX
 XX 24-APR-2001; 2001US-0286137P.
 PR XX
 XX (EPIC-) EPIGENESIS PHARM INC.
 PA XX
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 DR XX
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX PS
 XX Disclosure; SEQ ID NO 3082; 872pp; English.
 XX CC
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiasthmatic, hypotensive, and
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX CC
 SQ Sequence 20 BP; 9 A; 7 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 229 CCTCAGAAAGCCAAT 243
 DB 5 CCTCAGAAAGCCAAT 19
 RESULT 1631
 ABZ92577/c
 ID ABZ92577 standard; DNA; 20 BP.
 XX AC
 XX ABZ92577;
 XX DT 17-OCT-2003 (first entry)
 XX DE
 XX Human oligonucleotide sequence.
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 OS Homo sapiens.
 XX PN WO200285308-A2.
 XX 31-OCT-2002.
 PD

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XX 23-APR-2002; 2002WO-US013135.
XX
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Disclosure; SEQ ID NO 7819; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiasthmatic, antiallergic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.4; DB 1; Length 20;
XX Best Local Similarity 93.3%; Pred. No. 1.2e+03;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1138 CTGGAGAGATCAAA 1152
XX | | | | | | | | | |
XX Db 20 CTGGAGAGATCAAA 6
XX
XX RESULT 1632
XX ABZ98082/c
XX ID ABZ98082 standard; DNA; 20 BP.
XX
XX AC ABZ98082;
XX
XX XX 17-OCT-2003 (first entry)
XX
XX DE Human MCP4 oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX OS Homo sapiens.
XX
XX FN W0200285308-A2.
XX
XX PD 31-OCT-2002.

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XX 23-APR-2002; 2002WO-US013135.
XX
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Disclosure; SEQ ID NO 13324; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.4; DB 1; Length 20;
XX Best Local Similarity 93.3%; Pred. No. 1.2e+03;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1417 GACCCAGAGGAGAG 1431
XX | | | | | | | | | |
XX Db 17 GACCCAGAGGAGAG 3
XX
XX RESULT 1633
XX ABZ98130/c
XX ID ABZ98130 standard; DNA; 20 BP.
XX
XX AC ABZ98130;
XX
XX XX 17-OCT-2003 (first entry)
XX
XX DE Human MCP4 oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX OS Homo sapiens.
XX
XX FN W0200285308-A2.
XX
XX PD 31-OCT-2002.

```

XX PF 23-APR-2002; 2002WO-US013135.
 XX PR 24-APR-2001; 2001US-0286137P.
 XX PA (EPIG-) EPIGENESIS PHARM INC.
 XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 XX PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX PS Disclosure; SEQ ID NO 13372; 872pp; English.
 XX CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiasthmatic, antiallergic, hypotensive, and
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1417 GACCCAGAGGAGAAG 1431
 Db ||||| |||||
 17 GACCCAAAGGAGAAG 3
 RESULT 1634
 ABZ86895/C
 ID ABZ86895 standard; DNA; 20 BP.
 XX AC ABZ86895;
 XX DT 17-OCT-2003 (first entry)
 XX DE Human oligonucleotide sequence.
 XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX OS Homo sapiens.
 XX FN WO200285308-A2.
 XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.
 XX PR 24-APR-2001; 2001US-0286137P.
 XX PA (EPIG-) EPIGENESIS PHARM INC.
 XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 XX PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX PS Claim 15; SEQ ID NO 2137; 872pp; English.
 XX CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 20 BP; 1 A; 4 C; 9 G; 6 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1645 ACCAAGGCCCCGAGC 1659
 Db ||||| |||||
 20 ACCAAGGCCCCGATC 6
 RESULT 1635
 ADA66546
 ID ADA66546 standard; DNA; 20 BP.
 XX AC ADA66546;
 XX DT 20-NOV-2003 (first entry)
 XX DE Transforming growth factor-beta 3 antisense oligonucleotide, SEQ ID 105.
 XX KW Cytostatic; antirheumatic; antiarthritic; gynecological;
 KW antierosive; transforming Growth Factor beta-3; TGF beta-3;
 KW hyperproliferative disorder; cancers; atherosclerosis;
 KW rheumatoid arthritis; preeclampsia; fibrosis; phosphorothioate; ss.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "This oligonucleotide has a phosphorothioate

FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
FT and 3' ends, which are 5 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX
XX PN WO2003008544-A2.
XX
XX PD 30-JAN-2003.
XX
XX PF 12-JUL-2002; 2002WO-US022423.
XX
XX PR 14-JUL-2001; 2001US-00906158.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Monia BP, Freier SM;
XX
XX WPI; 2003-229569/22.
XX
XX PT Novel antisense compound which is targeted to nucleic acid encoding
PT transforming growth factor beta-3, and inhibits expression of TGF-beta 3,
PT useful for treating a condition associated with TGF-beta 3, e.g. cancer.
XX
XX PS Claim 3; Page 90; 154pp; English.
XX
XX CC The present invention relates to antisense oligonucleotides (ADA66459-
CC ADA66609), which inhibit transforming growth factor (TGF) beta-3
CC expression. The oligonucleotides are useful for inhibiting the expression
CC of TGF-beta3 in cells or tissues, and for treating an animal having a
CC disease condition associated with TGF-beta3, e.g. a hyperproliferative,
CC disorder such as cancers of lung, liver, colon, oesophagus, pancreas,
CC breast, skin or haematopoietic, atherosclerosis, rheumatoid arthritis,
CC preeclampsia and fibrosis.
XX
XX SQ Sequence 20 BP; 2 A; 4 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1670 TGTGCTGGTGAGCT 1684
||| ||||| |||||
Db 1 TGGCTGGTGAGCT 15

RESULT 1636
AAL55534
ID AAL55534 standard; DNA; 20 BP.
AC
XX AAL55534;
XX
XX DT 12-JUN-2003 (first entry)
XX
XX DE qSH-1 gene related PCR primer, SEQ ID No 11.
XX
XX KW Plant; inducing plant thresholdability; rice; mechanical harvesting; qSH-1;
XX rice; PCR; primer; ss.
XX
XX OS Unidentified.
XX
XX PN WO2003016533-A1.
XX
XX PD 27-FEB-2003.
XX
XX PF 23-JUL-2002; 2002WO-JP007430.
XX
XX PR 20-AUG-2001; 2001JP-00249651.
XX
XX PA (NAG-) NAT INST AGROBIOLOGICAL SCI.
XX
XX PI Yano M, Konishi S;
XX
XX DR WPI; 2003-256707/25.
XX

PT Gene qSH-1 inducing plant thresholdability, useful in providing improved
PT breeds particularly of rice suitably modified and controlled to enable
PT mechanical harvesting.
XX
XX PS Example 2; Page 20; 85pp; Japanese.
XX
XX CC The invention relates to a novel DNA that encodes a plant-originated
CC protein with a function of inducing plant thresholdability. The novel DNA
CC comprises: a DNA encoding a protein with an amino acid sequence of 612
CC amino acids; or a DNA containing a region coding for a base sequence of
CC 2450 or 4486 base pairs. The novel gene is useful in providing improved
CC plant breeds, particularly of rice, suitably modified and controlled to
CC enable mechanical harvesting. This sequence represents a qSH-1 related
CC PCR primer of the invention
XX
XX SQ Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1833 CCCTTATTGAACATT 1847
||| ||||| |||||
Db 3 CGCTTATTGAACATT 17

RESULT 1637
ADA00224/C
ID ADA00224 standard; DNA; 20 BP.
XX
XX AC ADA00224;
XX
XX DT 06-NOV-2003 (first entry)
XX
XX DE VEGF receptor gene PCR primer SEQ ID NO:4.
XX
XX KW substrate; ligand; signal; ligand binding; immobilisation;
XX gene engineering; genetic engineering; structure; biological activity;
XX ligand-receptor binding; PCR primer; amplification; ss.
XX
XX OS Synthetic.
XX
XX OS Homo sapiens.
XX
XX PN WO2003019199-A1.
XX
XX PD 06-MAR-2003.
XX
XX PF 22-AUG-2002; 2002WO-JP008444.
XX
XX PR 22-AUG-2001; 2001JP-00250974.
XX
XX PA (TAKA-) TAKARA BIO INC.
XX
XX PI Ohmi T, Kato I;
XX
XX DR WPI; 2003-290095/28.
XX
XX PT Substrates having number of ligands immobilized on predetermined regions
PT of its surface, applicable in gene engineering for studying relationship
PT between structures and biological activity of endocrine disruptors.
XX
XX PS Example 1; Page 26; 52pp; Japanese.
XX
XX CC The present invention describes a substrate having a number of ligands
CC which have been immobilised onto a predetermined region of its surface,
CC in which the region on the substrate has such a shape as to allow the
CC concentration of signals caused by binding of the ligands to receptors in
CC the region toward the receiver. Also described is a substrate for the
CC immobilisation of such ligands. The substrates are applicable in gene
CC engineering for studying relationship between structures and biological
CC activity e.g. effect of endocrine disruptors on various genes and also in
CC investigating the effect of hormones, drugs and other chemicals on the
CC environment. Such substrates are highly sensitive in detecting the ligand

CC -receptor binding, with affinity and reproducibility. The ligand-
 CC immobilised substrates can be produced in high density e.g. in microarray
 CC form to provide finely tuned results. ADA00221 to ADA00282 represent PCR
 CC primers used for amplifying genes in the exemplification of the present
 CC invention.

XX SQ Sequence 20 BP; 9 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 458 CTGTGAATTGGCTG 472
 DB 15 CTGTGAATTGGCTG 1

RESULT 1638
 ABT13589
 ID ABT13589 standard; DNA; 20 BP.

XX AC ABT13589;
 XX DT 07-FEB-2003 (first entry)
 XX DE Liver regeneration-related gene panel PCR primer #117.

XX KW PCR; primer; ss; liver regeneration; gene panel; expression profile;
 XX KW drug screening; drug development; hepatitis; liver transplantation.
 XX OS Unidentified.

XX PN WO200277222-A1.
 XX PD 03-OCT-2002.

XX PF 13-MAR-2002; 2002WO-JP002372.
 XX PR 13-MAR-2001; 2001JP-00070940.

XX PA (AJTN) AJTNOMOTO CO INC.
 XX PI Yokoya F, Okutsu T, Mori M, Takahara Y, Fukuda H, Aburatani H;

XX PI Sonaka I;
 XX DR WPI; 2003-018922/01.

XX PT Gene panel participating in liver regeneration, applicable in providing
 PT expression data, diagnosis and development of drugs for promoting liver
 PT regeneration e.g. after transplantation or removal of liver during
 PT cancer.

XX PS Claim 19; Page 77; 101pp; Japanese.

XX CC The invention comprises a gene panel constructed from the expression
 CC profile of known genes which show a change in expression level between
 CC normal liver cells and liver cells under regeneration. The gene panel is
 CC useful for providing expression data and screening/development of drugs
 CC for liver regeneration (e.g. when treating hepatitis, after
 CC transplantation or removal of the liver during cancer or hepatitis
 CC therapy). The present DNA sequence represents a PCR primer used in the
 CC invention

XX SQ Sequence 20 BP; 7 A; 4 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1722 TTAACTTTGAACCAT 1736
 DB 3 TTCACTTTGAACCAT 17

RESULT 1639
 ABZ76301/c
 ID ABZ76301 standard; DNA; 20 BP.

XX AC ABZ76301;
 XX DT 12-JUN-2003 (first entry)
 XX DE Tubulin-beta-2 specific RT-PCR forward primer.

XX KW Transcriptomic; osteopathic; nephrotropic; gene therapy; osteoarthritis;
 KW RT-PCR; primer; tubulin-beta-2; ss.
 XX OS Homo sapiens.

XX PN WO2003018839-A1.
 XX PD 06-MAR-2003.

XX PF 23-AUG-2001; 2001WO-IE000108.
 XX PR 23-AUG-2001; 2001WO-IE000108.

XX PA (UYDU-) UNIV COLLEGE DUBLIN.
 XX PI Brady HR, Doran PP, McCarthy GM;

XX DR WPI; 2003-278674/27.

XX PT Identifying a cohort of genes for diagnosing or treating e.g.
 PT osteoarthritis or diabetic nephropathy by identifying in the genes a
 PT common promoter module, which governs the transcriptomic response to
 PT disease-associated stimuli.

XX PS Example 3; Page 29; 64pp; English.

XX CC The invention relates to identifying a cohort of genes and involves
 CC identifying in the genes a common promoter module, which governs the
 CC transcriptomic response to disease-associated stimuli. The expression of
 CC the genes is altered in a disease state and their expression products are
 CC involved in the pathogenesis of the disease. The method is useful for
 CC identifying targets for the rational diagnosis of disease or rational
 CC design of therapeutic agents for treating an associated disease e.g.
 CC osteoarthritis or diabetic nephropathy. Sequences ABZ76293-306 represent
 CC primers used in RT-PCR analysis of the expression of various gene
 CC transcripts in osteoarthritis

XX SQ Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1670 TGTGCTGGGTGAGCT 1684
 DB 15 TGTGCTGGGTGAGCT 1

RESULT 1640
 ABT43413
 ID ABT43413 standard; DNA; 20 BP.

XX AC ABT43413;

XX DT 22-SEP-2003 (first entry)
 XX DE Neuroblastoma-related DNA sequence #328.

XX KW Neuroblastoma; prognosis; ds; oligonucleotide.
 XX OS Unidentified.


```

QY      1648 AAGGCCCGAGCTCA 1662
DB      ||||| ||||| |||||
        4 AAGGTCGAGCTCA 18

RESULT 1643
AAL60306
ID      AAL60306 standard; DNA; 20 BP.
XX
AC      AAL60306;
XX
DT      27-AUG-2003 (first entry)
XX
DE      Human HNF-3 alpha specific reverse RT-PCR primer.
XX
KW      Human embryonic stem cells; HES; human; reverse transcription PCR; HNF;
KW      RT-PCR; primer; hepatocyte nuclear factor-3 alpha; ss.
XX
OS      Homo sapiens.
XX
PN      WO2003040355-A1.
XX
PD      15-MAY-2003.
XX
PF      11-NOV-2002; 2002WO-AU001534.
XX
PR      09-NOV-2001; 2001AU-00008781.
PR      15-MAR-2002; 2002AU-00001129.
XX
PA      (ESCE-) ES CELL INT PTE LTD.
XX
PI      Pera MF, Laslett A, Hawes S, Gion T;
XX      WPI; 2003-449455/42.
DR
PT      Identifying a viable subpopulation of human embryonic stem (HES) cells by
PT      obtaining a source of HES cells and identifying the subpopulation of HES
PT      cells that are at least GCTW-2 positive.
XX
PS      Example 2; Page 38; 83pp; English.
XX
CC      The invention relates to a method for identifying a viable subpopulation
CC      of human embryonic stem (HES) cells. The method involves obtaining a
CC      source of HES cells and identifying the subpopulation of HES cells that
CC      are at least GCTW-2 positive. The present sequence is human hepatocyte
CC      nuclear factor (HNF)-3 alpha specific reverse transcription PCR (RT-PCR)
CC      primer, used to illustrate the method of the invention
XX
SQ      Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match      0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1209 GCGGATTCCTGAGGA 1223
DB      ||||| ||||| |||||
        4 GCGAATTCCTGAGGA 18

RESULT 1644
ACD67183/c
ID      ACD67183 standard; DNA; 20 BP.
XX
AC      ACD67183;
XX
DT      17-SEP-2003 (first entry)
XX
DE      Derivatized oligonucleotide oligomer 42.
XX
KW      ICAM-1; intracellular cell adhesion molecule-1; antisense; ss;
KW      improved transfer; improved uptake; steroid/reporter molecule; porphyrin;
KW      non-aromatic lipophilic molecule; reporter enzyme; metal chelator;
XX

QY      1332 TGAAGAGGGGAGA 1346
DB      ||||| ||||| |||||
        18 TGAAGAGGATGGAGA 4

RESULT 1645
ACD67160/c
ID      ACD67160 standard; DNA; 20 BP.
XX
AC      ACD67160;
XX
DT      17-SEP-2003 (first entry)
XX
DE      Derivatized oligonucleotide oligomer 12.
XX
KW      ICAM-1; intracellular cell adhesion molecule-1; antisense; ss;
KW      improved transfer; improved uptake; steroid/reporter molecule; porphyrin;
KW      non-aromatic lipophilic molecule; reporter enzyme; metal chelator;
KW      water/lipid soluble vitamin; RNA cleaving complex; alkylator;
KW      hybrid photo-nuclease/intercalator; aryl azide photo-crosslinking agent.
XX
OS      Synthetic.

```

water/lipid soluble vitamin; RNA cleaving complex; alkylator;
hybrid photo-nuclease/intercalator; aryl azide photo-crosslinking agent.
Synthetic.

US2002177150-A1.
28-NOV-2002.
11-FEB-2002; 2002US-00073718.
23-OCT-1992; 92WO-US009196.
15-DEC-1998; 98US-00211882.
07-AUG-2000; 2000US-00633659.
(ISIS-) ISIS PHARM INC.
Manoharan M, Cook PD, Bennett CF;
WPI; 2003-521529/49.
New derivatized oligonucleotide, useful for effecting cellular uptake,
comprises several linked nucleosides bearing a substituent such as
steroid/reporter molecule, reporter enzyme or peptide.
Example 13; Page 13; 23pp; English.

The invention relates to a derivatized oligonucleotide comprising several
linked nucleosides having a functionalized nucleoside bearing a
substituent such as steroid/reporter molecule, non-aromatic lipophilic
molecule, reporter enzyme, peptide, protein, water/lipid soluble vitamin,
RNA cleaving complex, metal chelator, porphyrin, alkylator, hybrid photo-
nuclease/intercalator or aryl azide photo-crosslinking agent. The
oligonucleotide is useful for effecting cellular uptake of the
oligonucleotide by contacting an organism with the oligonucleotide. The
oligonucleotide is useful in research and diagnostic methods, for
assaying bodily states in animals, especially disease states, or for
treatment of diseases through modulation of the activity of DNA or RNA.
The oligonucleotide has improved transfer across cellular membranes and
uptake properties. The effect of conjugation of an oligonucleotide with
folic acid was determined by the inhibition of intercellular cell
adhesion molecule-I (ICAM-I). The present sequence represents a
derivatized oligonucleotide oligomer

Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1332 TGAAGAGGGGAGA 1346
18 TGAAGAGGATGGAGA 4

RESULT 1645
ACD67160/c
ID ACD67160 standard; DNA; 20 BP.
XX
AC ACD67160;
XX
DT 17-SEP-2003 (first entry)
XX
DE Derivatized oligonucleotide oligomer 12.
XX
KW ICAM-1; intracellular cell adhesion molecule-1; antisense; ss;
KW improved transfer; improved uptake; steroid/reporter molecule; porphyrin;
KW non-aromatic lipophilic molecule; reporter enzyme; metal chelator;
KW water/lipid soluble vitamin; RNA cleaving complex; alkylator;
KW hybrid photo-nuclease/intercalator; aryl azide photo-crosslinking agent.
XX
OS Synthetic.


```

PA (ISIS-) ISIS PHARM INC.
XX
PI Manoharan M, Cook PD, Bennett CF;
XX
DR WPI; 2003-521529/49.
XX
PT New derivatized oligonucleotide, useful for effecting cellular uptake,
PT comprises several linked nucleosides bearing a substituent such as
PT steroid/reporter molecule, reporter enzyme or peptide.
XX
PS Example 9; Page 11; 23pp; English.
XX
CC The invention relates to a derivatised oligonucleotide comprising several
CC linked nucleosides having a functionalised nucleoside bearing a
CC substituent such as steroid/reporter molecule, non-aromatic lipophilic
CC molecule, reporter enzyme, peptide, protein, water/lipid soluble vitamin,
CC RNA cleaving complex, metal chelator, porphyrin, alkylator, hybrid photo-
CC nuclease/intercalator or aryl azide photo-crosslinking agent. The
CC oligonucleotide is useful for effecting cellular uptake of the
CC oligonucleotide by contacting an organism with the oligonucleotide. The
CC oligonucleotide is useful in research and diagnostic methods, for
CC assaying bodily states in animals, especially disease states, or for
CC treatment of diseases through modulation of the activity of DNA or RNA.
CC The oligonucleotide has improved transfer across cellular membranes and
CC uptake properties. The effect of conjugation of an oligonucleotide with
CC folic acid was determined by the inhibition of intercellular cell
CC adhesion molecule-I (ICAM-I). The present sequence represents a
CC derivatised oligonucleotide oligomer
XX
SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1332 TGAAGAGGAGGGAGA 1346
DB 18 TGAAGAGGATGGAGA 4

RESULT 1648
ACD67196/c
ID ACD67196 standard; DNA; 20 BP.
XX
AC ACD67196;
XX
DT 17-SEP-2003 (first entry)
XX
DE Derivatized oligonucleotide oligomer 55 #1.
XX
KW ICAM-1; intracellular cell adhesion molecule-1; antisense; ss;
KW improved transfer; improved uptake; steroid/reporter molecule; porphyrin;
KW non-aromatic lipophilic molecule; reporter enzyme; metal chelator;
KW water/lipid soluble vitamin; RNA cleaving complex; alkylator;
KW hybrid photo-nuclease/intercalator; aryl azide photo-crosslinking agent.
XX
OS Synthetic.
XX
PN US2002177150-A1.
XX
PD 28-NOV-2002.
XX
PF 11-FEB-2002; 2002US-00073718.
XX
PR 23-OCT-1992; 92WO-US0009196.
XX
PR 15-DEC-1998; 98US-00211882.
XX
PR 07-AUG-2000; 2000US-00633659.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Manoharan M, Cook PD, Bennett CF;
XX
DR WPI; 2003-521529/49.
XX

New derivatized oligonucleotide, useful for effecting cellular uptake,
comprises several linked nucleosides bearing a substituent such as
steroid/reporter molecule, reporter enzyme or peptide.

Example 28; Page 18; 23pp; English.

The invention relates to a derivatised oligonucleotide comprising several
linked nucleosides having a functionalised nucleoside bearing a
substituent such as steroid/reporter molecule, non-aromatic lipophilic
molecule, reporter enzyme, peptide, protein, water/lipid soluble vitamin,
RNA cleaving complex, metal chelator, porphyrin, alkylator, hybrid photo-
nuclease/intercalator or aryl azide photo-crosslinking agent. The
oligonucleotide is useful for effecting cellular uptake of the
oligonucleotide by contacting an organism with the oligonucleotide. The
oligonucleotide is useful in research and diagnostic methods, for
assaying bodily states in animals, especially disease states, or for
treatment of diseases through modulation of the activity of DNA or RNA.
The oligonucleotide has improved transfer across cellular membranes and
uptake properties. The effect of conjugation of an oligonucleotide with
folic acid was determined by the inhibition of intercellular cell
adhesion molecule-I (ICAM-I). The present sequence represents a
derivatised oligonucleotide oligomer

Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1332 TGAAGAGGAGGGAGA 1346
DB 18 TGAAGAGGATGGAGA 4

RESULT 1649
ACD67170/c
ID ACD67170 standard; DNA; 20 BP.
XX
AC ACD67170;
XX
DT 17-SEP-2003 (first entry)
XX
DE Derivatized oligonucleotide oligomer 23.
XX
KW ICAM-1; intracellular cell adhesion molecule-1; antisense; ss;
KW improved transfer; improved uptake; steroid/reporter molecule; porphyrin;
KW non-aromatic lipophilic molecule; reporter enzyme; metal chelator;
KW water/lipid soluble vitamin; RNA cleaving complex; alkylator;
KW hybrid photo-nuclease/intercalator; aryl azide photo-crosslinking agent.
XX
OS Synthetic.
XX
PN US2002177150-A1.
XX
PD 28-NOV-2002.
XX
PF 11-FEB-2002; 2002US-00073718.
XX
PR 23-OCT-1992; 92WO-US0009196.
XX
PR 15-DEC-1998; 98US-00211882.
XX
PR 07-AUG-2000; 2000US-00633659.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Manoharan M, Cook PD, Bennett CF;
XX
DR WPI; 2003-521529/49.
XX

New derivatized oligonucleotide, useful for effecting cellular uptake,
comprises several linked nucleosides bearing a substituent such as
steroid/reporter molecule, reporter enzyme or peptide.

```

PS Example 8; Page 9; 23pp; English.

XX The invention relates to a derivatised oligonucleotide comprising several
 CC linked nucleosides having a functionalised nucleoside bearing a
 CC substituent such as steroid/reporter molecule, non-aromatic lipophilic
 CC molecule, reporter enzyme, peptide, protein, water/lipid soluble vitamin,
 CC RNA cleaving complex, metal chelator, porphyrin, alkylator, hybrid photo-
 CC nuclease/intercalator or aryl azide photo-crosslinking agent. The
 CC oligonucleotide is useful for effecting cellular uptake of the
 CC oligonucleotide by contacting an organism with the oligonucleotide. The
 CC oligonucleotide is useful in research and diagnostic methods, for
 CC assaying bodily states in animals, especially disease states, or for
 CC treatment of diseases through modulation of the activity of DNA or RNA.
 CC The oligonucleotide has improved transfer across cellular membranes and
 CC uptake properties. The effect of conjugation of an oligonucleotide with
 CC folic acid was determined by the inhibition of intercellular cell
 CC adhesion molecule-1 (ICAM-1). The present sequence represents a
 CC derivatised oligonucleotide oligomer

XX SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1332 TGAAGAGGAGGGAGA 1346
 |||||
 Db 18 TGAAGAGGATGGAGA 4

RESULT 1650
 ACD67166/c
 ID ACD67166 standard; DNA; 20 BP.
 XX
 AC ACD67166;
 XX
 DT 17-SEP-2003 (first entry)
 XX
 DE Derivatised oligonucleotide oligomer 19.
 XX
 KW ICAM-1; intracellular cell adhesion molecule-1; antisense; ss;
 KW improved transfer; improved uptake; steroid/reporter molecule; porphyrin;
 KW non-aromatic lipophilic molecule; reporter enzyme; metal chelator;
 KW water/lipid soluble vitamin; RNA cleaving complex; alkylator;
 KW hybrid photo-nuclease/intercalator; aryl azide photo-crosslinking agent.
 XX
 OS Synthetic.
 XX
 PN US2002177150-A1.
 XX
 PD 28-NOV-2002.
 XX
 PF 11-FEB-2002; 2002US-00073718.
 XX
 PR 23-OCT-1992; 92WO-US0009196.
 PR 15-DEC-1998; 98US-00211882.
 PR 07-AUG-2000; 2000US-00633659.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Manoharan M, Cook PD, Bennett CF;
 XX
 DR WPI; 2003-521529/49.
 XX
 PT New derivatised oligonucleotide, useful for effecting cellular uptake,
 PT comprises several linked nucleosides bearing a substituent such as
 PT steroid/reporter molecule, reporter enzyme or peptide.
 XX
 PS Example 8; Page 9; 23pp; English.
 XX
 CC The invention relates to a derivatised oligonucleotide comprising several
 CC linked nucleosides having a functionalised nucleoside bearing a
 CC substituent such as steroid/reporter molecule, non-aromatic lipophilic

CC molecule, reporter enzyme, peptide, protein, water/lipid soluble vitamin,
 CC RNA cleaving complex, metal chelator, porphyrin, alkylator, hybrid photo-
 CC nuclease/intercalator or aryl azide photo-crosslinking agent. The
 CC oligonucleotide is useful for effecting cellular uptake of the
 CC oligonucleotide by contacting an organism with the oligonucleotide. The
 CC oligonucleotide is useful in research and diagnostic methods, for
 CC assaying bodily states in animals, especially disease states, or for
 CC treatment of diseases through modulation of the activity of DNA or RNA.
 CC The oligonucleotide has improved transfer across cellular membranes and
 CC uptake properties. The effect of conjugation of an oligonucleotide with
 CC folic acid was determined by the inhibition of intercellular cell
 CC adhesion molecule-1 (ICAM-1). The present sequence represents a
 CC derivatised oligonucleotide oligomer

XX SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1332 TGAAGAGGAGGGAGA 1346
 |||||
 Db 18 TGAAGAGGATGGAGA 4

RESULT 1651
 ACD67167/c
 ID ACD67167 standard; DNA; 20 BP.
 XX
 AC ACD67167;
 XX
 DT 17-SEP-2003 (first entry)
 XX
 DE Derivatised oligonucleotide oligomer 20.
 XX
 KW ICAM-1; intracellular cell adhesion molecule-1; antisense; ss;
 KW improved transfer; improved uptake; steroid/reporter molecule; porphyrin;
 KW non-aromatic lipophilic molecule; reporter enzyme; metal chelator;
 KW water/lipid soluble vitamin; RNA cleaving complex; alkylator;
 KW hybrid photo-nuclease/intercalator; aryl azide photo-crosslinking agent.
 XX
 OS Synthetic.
 XX
 PN US2002177150-A1.
 XX
 PD 28-NOV-2002.
 XX
 PF 11-FEB-2002; 2002US-00073718.
 XX
 PR 23-OCT-1992; 92WO-US0009196.
 PR 15-DEC-1998; 98US-00211882.
 PR 07-AUG-2000; 2000US-00633659.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Manoharan M, Cook PD, Bennett CF;
 XX
 DR WPI; 2003-521529/49.
 XX
 PT New derivatised oligonucleotide, useful for effecting cellular uptake,
 PT comprises several linked nucleosides bearing a substituent such as
 PT steroid/reporter molecule, reporter enzyme or peptide.
 XX
 PS Example 8; Page 9; 23pp; English.
 XX
 CC The invention relates to a derivatised oligonucleotide comprising several
 CC linked nucleosides having a functionalised nucleoside bearing a
 CC substituent such as steroid/reporter molecule, non-aromatic lipophilic
 CC molecule, reporter enzyme, peptide, protein, water/lipid soluble vitamin,
 CC RNA cleaving complex, metal chelator, porphyrin, alkylator, hybrid photo-
 CC nuclease/intercalator or aryl azide photo-crosslinking agent. The
 CC oligonucleotide is useful for effecting cellular uptake of the
 CC oligonucleotide by contacting an organism with the oligonucleotide. The

CC oligonucleotide is useful in research and diagnostic methods, for
 CC assaying bodily states in animals, especially disease states, or for
 CC treatment of diseases through modulation of the activity of DNA or RNA.
 CC The oligonucleotide has improved transfer across cellular membranes and
 CC uptake properties. The effect of conjugation of an oligonucleotide with
 CC folic acid was determined by the inhibition of intercellular cell
 CC adhesion molecule-I (ICAM-I). The present sequence represents a
 CC derivatised oligonucleotide oligomer

XX Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
 SQ

Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1332 TGAAGAGGAGGAGGA 1346
 DB 18 TGAAGAGGAGGAGGA 4
 |||||

RESULT 1652
 ACD67174/c
 ID ACD67174 standard; DNA; 20 BP.
 XX
 AC ACD67174;
 DT 17-SEP-2003 (first entry)
 XX
 DE Derivatised oligonucleotide oligomer 27.
 XX
 XX ICAM-1; intracellular cell adhesion molecule-1; antisense; ss;
 KW improved transfer; improved uptake; steroid/reporter molecule; porphyrin;
 KW non-aromatic lipophilic molecule; reporter enzyme; metal chelator;
 KW water/lipid soluble vitamin; RNA cleaving complex; alkylator;
 KW hybrid photo-nuclease/intercalator; aryl azide photo-crosslinking agent.
 OS Synthetic.
 XX
 XX US2002177150-A1.
 PN 28-NOV-2002.
 XX
 XX 11-FEB-2002; 2002US-00073718.
 PF
 XX 23-OCT-1992; 92WO-US009196.
 PR 15-DEC-1998; 98US-00211882.
 PR 07-AUG-2000; 2000US-00633659.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA Manoharan M, Cook PD, Bennett CF;
 PI WPI; 2003-521529/49.
 DR
 XX New derivatised oligonucleotide, useful for effecting cellular uptake,
 PT comprises several linked nucleosides bearing a substituent such as
 PT steroid/reporter molecule, reporter enzyme or peptide.
 XX
 PS Example 9; Page 10; 23pp; English.

CC The invention relates to a derivatised oligonucleotide comprising several
 CC linked nucleosides having a functionalised nucleoside bearing a
 CC substituent such as steroid/reporter molecule, non-aromatic lipophilic
 CC molecule, reporter enzyme, peptide, protein, water/lipid soluble vitamin,
 CC RNA cleaving complex, metal chelator, porphyrin, alkylator, hybrid photo-
 CC nuclease/intercalator or aryl azide photo-crosslinking agent. The
 CC oligonucleotide is useful for effecting cellular uptake of the
 CC oligonucleotide by contacting an organism with the oligonucleotide. The
 CC oligonucleotide is useful in research and diagnostic methods, for
 CC assaying bodily states in animals, especially disease states, or for
 CC treatment of diseases through modulation of the activity of DNA or RNA.
 CC The oligonucleotide has improved transfer across cellular membranes and
 CC uptake properties. The effect of conjugation of an oligonucleotide with

CC folic acid was determined by the inhibition of intercellular cell
 CC adhesion molecule-I (ICAM-I). The present sequence represents a
 CC derivatised oligonucleotide oligomer

XX Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
 SQ

Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1332 TGAAGAGGAGGAGGA 1346
 DB 18 TGAAGAGGAGGAGGA 4
 |||||

RESULT 1653
 ACD67171/c
 ID ACD67171 standard; DNA; 20 BP.
 XX
 AC ACD67171;
 DT 17-SEP-2003 (first entry)
 XX
 DE Derivatised oligonucleotide oligomer 24.
 XX
 XX ICAM-1; intracellular cell adhesion molecule-1; antisense; ss;
 KW improved transfer; improved uptake; steroid/reporter molecule; porphyrin;
 KW non-aromatic lipophilic molecule; reporter enzyme; metal chelator;
 KW water/lipid soluble vitamin; RNA cleaving complex; alkylator;
 KW hybrid photo-nuclease/intercalator; aryl azide photo-crosslinking agent.
 OS Synthetic.
 XX
 XX US2002177150-A1.
 PN 28-NOV-2002.
 XX
 XX 11-FEB-2002; 2002US-00073718.
 PF
 XX 23-OCT-1992; 92WO-US009196.
 PR 15-DEC-1998; 98US-00211882.
 PR 07-AUG-2000; 2000US-00633659.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA Manoharan M, Cook PD, Bennett CF;
 PI WPI; 2003-521529/49.
 DR
 XX New derivatised oligonucleotide, useful for effecting cellular uptake,
 PT comprises several linked nucleosides bearing a substituent such as
 PT steroid/reporter molecule, reporter enzyme or peptide.
 XX
 PS Example 8; Page 9; 23pp; English.

CC The invention relates to a derivatised oligonucleotide comprising several
 CC linked nucleosides having a functionalised nucleoside bearing a
 CC substituent such as steroid/reporter molecule, non-aromatic lipophilic
 CC molecule, reporter enzyme, peptide, protein, water/lipid soluble vitamin,
 CC RNA cleaving complex, metal chelator, porphyrin, alkylator, hybrid photo-
 CC nuclease/intercalator or aryl azide photo-crosslinking agent. The
 CC oligonucleotide is useful for effecting cellular uptake of the
 CC oligonucleotide by contacting an organism with the oligonucleotide. The
 CC oligonucleotide is useful in research and diagnostic methods, for
 CC assaying bodily states in animals, especially disease states, or for
 CC treatment of diseases through modulation of the activity of DNA or RNA.
 CC The oligonucleotide has improved transfer across cellular membranes and
 CC uptake properties. The effect of conjugation of an oligonucleotide with
 CC folic acid was determined by the inhibition of intercellular cell
 CC adhesion molecule-I (ICAM-I). The present sequence represents a
 CC derivatised oligonucleotide oligomer

XX Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Oy 1332 TGAAGAGGAGGAGA 1346
Db 18 TGAAGAGGATGGAGA 4
|||||
RESULT 1654
ACD67154/C
ID ACD67154 standard; DNA; 20 BP.
XX AC ACD67154;
XX XX
XX XX
XX 17-SEP-2003 (first entry)
XX XX
DE Derivatised oligonucleotide oligomer 3.
XX ICAM-1; intracellular cell adhesion molecule-1; antisense; ss;
KW improved transfer; improved uptake; steroid/reporter molecule; porphyrin;
KW non-aromatic lipophilic molecule; reporter enzyme; metal chelator;
KW water/lipid soluble vitamin; RNA cleaving complex; alkylator;
KW hybrid photo-nuclease/intercalator; aryl azide photo-crosslinking agent.
XX
OS Synthetic.
XX US2002177150-A1.
XX 28-NOV-2002.
XX 11-FEB-2002; 2002US-00073718.
XX 23-OCT-1992; 92WO-US0009196.
XX 15-DEC-1998; 98US-00211882.
XX 07-AUG-2000; 2000US-00633659.
XX (ISIS-) ISIS PHARM INC.
XX Manoharan M, Cook PD, Bennett CF;
XX WPI; 2003-521529/49.
XX
PT New derivatized oligonucleotide, useful for effecting cellular uptake,
PT comprises several linked nucleosides bearing a substituent such as
PT steroid/reporter molecule, reporter enzyme or peptide.
XX
PS Example 4; Page 6; 23pp; English.
XX
CC The invention relates to a derivatised oligonucleotide comprising several
CC linked nucleosides having a functionalised nucleoside bearing a
CC substituent such as steroid/reporter molecule, non-aromatic lipophilic
CC molecule, reporter enzyme, peptide, protein, water/lipid soluble vitamin,
CC RNA cleaving complex, metal chelator, porphyrin, alkylator, hybrid photo-
CC nuclease/intercalator or aryl azide photo-crosslinking agent. The
CC oligonucleotide is useful for effecting cellular uptake of the
CC oligonucleotide by contacting an organism with the oligonucleotide. The
CC oligonucleotide is useful in research and diagnostic methods, for
CC assaying bodily states in animals, especially disease states, or for
CC treatment of diseases through modulation of the activity of DNA or RNA.
CC The oligonucleotide has improved transfer across cellular membranes and
CC uptake properties. The effect of conjugation of an oligonucleotide with
CC folic acid was determined by the inhibition of intercellular cell
CC adhesion molecule-1 (ICAM-I). The present sequence represents a
CC derivatised oligonucleotide oligomer
XX
SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
```

Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Oy 1332 TGAAGAGGAGGAGA 1346
Db 18 TGAAGAGGATGGAGA 4
|||||
RESULT 1655
ACD67172/C
ID ACD67172 standard; DNA; 20 BP.
XX AC ACD67172;
XX XX
XX XX
XX 17-SEP-2003 (first entry)
XX XX
DE Derivatised oligonucleotide oligomer 25.
XX ICAM-1; intracellular cell adhesion molecule-1; antisense; ss;
KW improved transfer; improved uptake; steroid/reporter molecule; porphyrin;
KW non-aromatic lipophilic molecule; reporter enzyme; metal chelator;
KW water/lipid soluble vitamin; RNA cleaving complex; alkylator;
KW hybrid photo-nuclease/intercalator; aryl azide photo-crosslinking agent.
XX
OS Synthetic.
XX US2002177150-A1.
XX 28-NOV-2002.
XX 11-FEB-2002; 2002US-00073718.
XX 23-OCT-1992; 92WO-US0009196.
XX 15-DEC-1998; 98US-00211882.
XX 07-AUG-2000; 2000US-00633659.
XX (ISIS-) ISIS PHARM INC.
XX Manoharan M, Cook PD, Bennett CF;
XX WPI; 2003-521529/49.
XX
PT New derivatized oligonucleotide, useful for effecting cellular uptake,
PT comprises several linked nucleosides bearing a substituent such as
PT steroid/reporter molecule, reporter enzyme or peptide.
XX
PS Example 8; Page 9; 23pp; English.
XX
CC The invention relates to a derivatised oligonucleotide comprising several
CC linked nucleosides having a functionalised nucleoside bearing a
CC substituent such as steroid/reporter molecule, non-aromatic lipophilic
CC molecule, reporter enzyme, peptide, protein, water/lipid soluble vitamin,
CC RNA cleaving complex, metal chelator, porphyrin, alkylator, hybrid photo-
CC nuclease/intercalator or aryl azide photo-crosslinking agent. The
CC oligonucleotide is useful for effecting cellular uptake of the
CC oligonucleotide by contacting an organism with the oligonucleotide. The
CC oligonucleotide is useful in research and diagnostic methods, for
CC assaying bodily states in animals, especially disease states, or for
CC treatment of diseases through modulation of the activity of DNA or RNA.
CC The oligonucleotide has improved transfer across cellular membranes and
CC uptake properties. The effect of conjugation of an oligonucleotide with
CC folic acid was determined by the inhibition of intercellular cell
CC adhesion molecule-1 (ICAM-I). The present sequence represents a
CC derivatised oligonucleotide oligomer
XX
SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
```

Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Oy 1332 TGAAGAGGAGGAGA 1346
Db 18 TGAAGAGGATGGAGA 4
|||||
```

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RESULT 1656
ACD67173/c
ID ACD67173 standard; DNA; 20 BP.
XX
AC ACD67173;
XX
DT 17-SEP-2003 (first entry)
XX
DE Derivatized oligonucleotide oligomer 26.
XX
KW ICAM-1; intracellular cell adhesion molecule-1; antisense; ss;
KW improved transfer; improved uptake; steroid/reporter molecule; porphyrin;
KW non-aromatic lipophilic molecule; reporter enzyme; metal chelator;
KW water/lipid soluble vitamin; RNA cleaving complex; alkylator;
KW hybrid photo-nuclease/intercalator; aryl azide photo-crosslinking agent.
XX
OS Synthetic.
XX
PN US2002177150-A1.
XX
PD 28-NOV-2002.
XX
PF 11-FEB-2002; 2002US-00073718.
XX
PR 23-OCT-1992; 92WO-US009196.
PR 15-DEC-1998; 98US-00211882.
PR 07-AUG-2000; 2000US-00633659.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Manoharan M, Cook PD, Bennett CF;
XX
DR WPI; 2003-521529/49.
XX
PT New derivatized oligonucleotide, useful for effecting cellular uptake,
PT comprises several linked nucleosides bearing a substituent such as
PT steroid/reporter molecule, reporter enzyme or peptide.
XX
PS Example 8; Page 10; 23pp; English.
XX
CC The invention relates to a derivatized oligonucleotide comprising several
CC linked nucleosides having a functionalised nucleoside bearing a
CC substituent such as steroid/reporter molecule, non-aromatic lipophilic
CC molecule, reporter enzyme, peptide, protein, water/lipid soluble vitamin,
CC RNA cleaving complex, metal chelator, porphyrin, alkylator, hybrid photo-
CC nuclease/intercalator or aryl azide photo-crosslinking agent. The
CC oligonucleotide is useful for effecting cellular uptake of the
CC oligonucleotide by contacting an organism with the oligonucleotide. The
CC assaying bodily states in animals, especially disease states, or for
CC treatment of diseases through modulation of the activity of DNA or RNA.
CC The oligonucleotide has improved transfer across cellular membranes and
CC uptake properties. The effect of conjugation of an oligonucleotide with
CC folic acid was determined by the inhibition of intercellular cell
CC adhesion molecule-I (ICAM-I). The present sequence represents a
CC derivatized oligonucleotide oligomer
XX
SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1332 TGAAGAGGAGGAGGA 1346
Db ||||| |||||
18 TGAAGAGGAGGAGGA 4

RESULT 1657
ACD67169/c
ID ACD67169 standard; DNA; 20 BP.
XX
AC ACD67169;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human connective tissue growth factor antisense oligo DNA (SeqID 70).
XX

```

KW antisense; human; ss; connective tissue growth factor; CTGF;
 KW chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;
 KW fisp-12; NOV2;
 KW insulin-like growth factor binding protein-related protein 2; IGFBP-rP2;
 KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
 KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
 KW scleroderma; atherosclerosis; cytostatic; dermatological;
 KW antiarteriosclerotic.
 XX Homo sapiens.
 OS
 XX
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 FT 5-methylcytidines"
 XX
 PN W02003053340-A2.
 XX
 XX
 PD 03-JUL-2003.
 XX
 XX
 PF 09-DEC-2002; 2002WO-US038618.
 XX
 XX
 PR 10-DEC-2001; 2001US-00006191.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 XX Gaarde WA, Watt AT;
 XX WPI; 2003-559091/52.
 DR
 XX
 XX New antisense oligonucleotides for modulating connective tissue growth
 FT factor expression, particularly useful for treating cancers (e.g. breast
 FT or prostate cancer), pulmonary or renal fibrosis, scleroderma or
 FT atherosclerosis.
 XX
 PS Claim 3; Page 86; 139pp; English.
 XX
 CC This invention relates to novel methods for modulating the expression of
 CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
 CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
 CC as ctgofact, fibroblast inducible secreted protein, fisp-12, NOV2,
 CC insulin-like growth factor binding protein-related protein 2, IGFBP-rP2,
 CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
 CC promote chemotaxis of fibroblasts, however, it is also upregulated in
 CC acute lymphoblastic leukaemia and in tumour or endothelial cells
 CC associated with the vasculature. Accordingly, antisense oligonucleotides
 CC that inhibit the expression of CTGF in cells or tissues can be used in
 CC gene therapy to treat various conditions including hyperproliferative
 CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),
 CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
 CC such, the present invention describes these antisense oligos as having
 CC cytostatic, dermatological and antiarteriosclerotic activities. This
 CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
 CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
 CC human CTGF of the invention.
 XX
 SQ Sequence 20 BP; 8 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1435 GAAGTCACCAAGAG 1449
 |||||
 Db 6 GAAGTCACCAAGAG 20

RESULT 1659
 ADB81402/c
 ID ADB81402 standard; DNA; 20 BP.

XX
 AC ADB81402;
 XX
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human oestrogen receptor alpha antisense oligonucleotide DNA (SeqID 22).
 XX
 KW antisense; human; ss; oestrogen receptor alpha; ESR-alpha;
 KW oestrogen receptor 1; ESR1; NR3A1; bone maintenance;
 KW cardiovascular system; cancer; gene therapy; hyperproliferative disease;
 KW inflammation; tumour formation; infection; cytostatic; antiinflammatory;
 KW antimicrobial.
 KW
 XX Homo sapiens.
 OS
 XX
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 FT 5-methylcytidines"
 XX
 PN W02003052072-A2.
 XX
 XX
 PD 26-JUN-2003.
 XX
 XX
 PF 13-DEC-2002; 2002WO-US040083.
 XX
 XX
 PR 18-DEC-2001; 2001US-00027983.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Dobie KW, Roach MP;
 XX WPI; 2003-577322/54.
 DR
 XX
 XX New antisense compound targeted to nucleic acid encoding estrogen
 FT receptor alpha and inhibiting expression of estrogen receptor alpha,
 FT useful for treating a disease or condition e.g. a hyperproliferative
 FT disease.
 XX
 PS Example 15; Page 77; 232pp; English.
 XX
 CC This invention relates to human oestrogen receptor alpha (ESR-alpha), and
 CC the novel antisense oligonucleotides that modulate its expression. The
 CC oestrogen receptor alpha protein is also known as oestrogen receptor 1,
 CC ESR1, and NR3A1. Oestrogen, the steroid hormone ligand of ESR-alpha, is
 CC important for bone maintenance and plays a protective role in the
 CC cardiovascular system, as well as being required for normal sexual
 CC maturation through promoting growth and differentiation. Splice variants
 CC of ESR-alpha, however, have been associated with various cancers
 CC including the breast and pituitary. Accordingly, antisense
 CC oligonucleotides that inhibit the expression of ESR-alpha in cells or
 CC tissues can be used in gene therapy to treat conditions such as
 CC hyperproliferative disease, inflammation, tumour formation and to prevent
 CC or delay infection. As such, the present invention describes these
 CC antisense oligos as having cytostatic, antiinflammatory and antimicrobial
 CC activities. This oligonucleotide sequence is an antisense oligo used to
 CC inhibit expression of human oestrogen receptor alpha of the invention.
 XX
 SQ Sequence 20 BP; 5 A; 3 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1724 AACTTTGACCATAA 1738
 |||||
 Db 19 AACTTTGACCATCA 5

RESULT 1660

19-JUN-2003.

10-DEC-2002; 2002WO-EP013995.

10-DEC-2001; 2001DE-01060563.

(OGHA-) OGHAM GMBH.

Cullen P, Seedorf U;

WPI, 2003-505402/47.

Investigating male genetic infertility, useful for diagnosis e.g. for assessing suitability for in vitro fertilization, based on multifactorial analysis of infertility-related mutations.

Claim 13; SEQ ID NO 172; 110pp; German.

This invention describes a novel method for investigating genetic infertility or predisposition in males. The method involves selecting at least two infertility-associated mutations which are recessive or intermediate that are associated with infertility in the heterozygous state and/or only in the homozygous state. Preferably at least one azoospermia factor is detected which may be lost by microdeletions in intervals 5 or 6 of the Y-chromosome. Also any of several hundred mutations, listed, present in the cystic fibrosis transmembrane conductance regulator (CFTR), Kallmann syndrome (KAL1), androgen resistance (AR) or steroid 21-hydroxylase (CYP21) genes may be detected. Probes for the mutated genes and/or native nucleic acid, or their complementary strands, are fixed to a carrier, particularly as a microarray, then tested for hybridization with oligonucleotides from or synthesized from, a patient sample and hybridization detected.

Multifactorial analysis is by standard hybridization methods, particularly the quantitative trait locus method. The method is used to diagnose inherited male infertility or predisposition to its, especially in conjunction with in vitro fertilization programs, e.g. for assessing subjects with oligospermia for possible application of the intracytoplasmic sperm injection method. Analysis of many mutations improves diagnosis of the genetic basis of male infertility, including polygenic origins (complex interactions between different heterozygotic mutations). A chip for analyzing genetic infertility in males comprises oligonucleotides that represent known mutations (nonsense or missense, insertions, allelic variants deletions or rearrangements) in the cystic fibrosis transmembrane conductance regulator, Kallmann syndrome, androgen resistance and steroid 21-hydroxylase genes. ADD42140-ADD42633 represent oligonucleotides used in the microarray described in the method of the invention. NOTE: there are no SEQ ID's 133, 472 or 473 represented in the SEQ ID list of the specification.

Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0

1498 GTCAAGTTGGCTGA 1512
18 GTCAAGTTGGCTGA 4

RESULT 1663
ADE43551/c

ID ADE43551 standard; DNA; 20 BP.

AC ADE43551;

29-JAN-2004 (first entry)

Human IDE PCR primer, SEQ ID 156.

Neurodegenerative disease; uPA; SMC; IDB; KNS1; LIPA; TNFRSF6;
Alzheimer's disease; neuroprotective; nootropic; gene therapy;

KW poliomyelitis-like syndrome; PCR primer; ss.
 XX Human enterovirus 71.
 OS WO200134848-A2.
 XX 17-MAY-2001.
 PD 20-OCT-2000; 2000WO-US029021.
 XX 10-NOV-1999; 99US-0164520P.
 PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Brown BA, Kilpatrick DR, Pallansch MA, Oberste MS;
 PI WPI; 2001-329101/34.
 XX Novel nucleic acids, useful as primers in amplification and sequencing
 PT reactions to rapidly amplify and sequence target enterovirus 71 nucleic
 PT acids.
 XX Claim 1; Page 11; 75pp; English.
 PS The present sequence is a degenerate RT (reverse transcription)-PCR
 CC primer, 163S which is used in the amplification and sequencing of
 CC enterovirus 71 (EV71). The present invention relates to a method of
 CC serotype-specific identification of EV71 by RT-PCR. The invention also
 CC provides nucleic acids which are used as primers in amplification or
 CC sequencing reactions to rapidly amplify or sequence EV71 DNA. EV71 is
 CC responsible for hand-foot-and-mouth disease (HFMD) and neurologic
 CC diseases such as encephalitis, meningitis, cranial nerve palsies, Guillan
 CC -Barre syndrome and poliomyelitis-like syndrome. The DNAs of the present
 CC invention are useful for detecting the presence or absence of EV71. They
 CC are also useful for determining the nucleotide sequence of EV71 DNA.
 CC (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 22 BP; 10 A; 3 C; 6 G; 0 T; 0 U; 3 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 22;
 Best Local Similarity 66.7%; Pred. No. 1.3e+03;
 Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 OY 930 GAGCTTTACCTGCCTATGCT 950
 Db |: ||||| ||||| : |||||
 22 GRTCTTCTCCTGTYTGTCT 2
 RESULT 1665
 ADD56535/c
 ID ADD56535 standard; DNA; 24 BP.
 XX
 AC ADD56535;
 XX
 DT 15-JAN-2004 (first entry)
 DE Human gene expression analysis multiplex Start-PCR primer #55.
 XX
 KW Gene expression; multiplex standardised reverse transcriptase-PCR;
 KW Start-PCR; high density oligonucleotide array; cDNA array;
 KW small biological sample; fine needle aspirate biopsy;
 KW laser captured microdissected material; human; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003186246-A1.
 XX
 PD 02-OCT-2003.
 XX
 PF 28-MAR-2002; 2002US-00109349.
 XX
 PR 28-MAR-2002; 2002US-00109349.
 XX

PA (WILL/) WILLEY J C.
 PA (CRAW/) CRAWFORD E L.
 XX Willey JC, Crawford EL;
 PI WPI; 2003-811730/76.
 XX
 DR Direct comparison of numerical gene expression values between samples of
 PT genes comprises using multiplex standardized reverse transcription-
 PT polymerase chain reaction.
 XX
 PS Example 1; SEQ ID NO 55; 59pp; English.
 XX
 CC The present invention relates to a method for the direct comparison of
 CC numerical gene expression values between samples of genes. The method
 CC comprises amplifying cDNA in the presence of a competitive template
 CC mixture and primer pairs for several genes and then amplifying aliquots
 CC of the PCR products using a primer pair specific for each gene. The
 CC method of amplification is by multiplex standardised reverse
 CC transcriptase-polymerase chain reaction (Start-PCR). High density
 CC oligonucleotide or cDNA arrays are used to measure PCR products following
 CC quantitative Start-PCR. The method is useful for the assessment of gene
 CC expression in small biological samples such as fine needle aspirate
 CC biopsies, and laser captured microdissected materials. The method allows
 CC for the standardised measurement of hundreds of genes from the same
 CC sample, which in prior art, could only be assessed for one gene. The
 CC present sequence represents a multiplex Start-PCR primer which can be
 CC used in the method of the present invention.
 XX
 SQ Sequence 24 BP; 11 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.4; DB 1; Length 24;
 Best Local Similarity 73.9%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 525 TGATATCGCTTGGCCATCTG 547
 Db ||||| ||||| |||||
 23 TGATATCTCTGCTCTTGG 1
 RESULT 1666
 AAQ50403/c
 ID AAQ50403 standard; DNA; 18 BP.
 XX
 AC AAQ50403;
 XX
 DT 11-APR-1994 (first entry)
 DE Terminator used in a recombinant avipox virus genome.
 XX
 KW APV; proliferation; genome; infectious bursal disease; IBD; vaccine; ss.
 XX
 OS Synthetic.
 XX
 PN JP0524940-A.
 XX
 PD 24-SEP-1993.
 XX
 PF 04-MAR-1992; 92JP-00082800.
 XX
 PR 09-AUG-1991; 91JP-00224868.
 XX
 PA (JAPG) NIPPON ZEON KK.
 XX
 DR WPI; 1993-347471/44.
 XX
 PT Recombinant avipox virus used for vaccine for domestic animals - consists
 PT of genome region and CDNA to encode polypeptide having identical
 PT antigenicity for large segment.
 XX
 PS Disclosure; Page 11; 18pp; Japanese.
 XX
 CC The sequence is that of a synthetic terminator sequence used as part of a

```

CC recombinant APV capable of expressing antigens in large amounts and
CC containing the DNA sequences required for viral proliferation. The DNA
CC also comprises cDNA encoding the polypeptide having identical
CC antigenicity for RNA large subunit from infectious bursal disease. The
CC recombinant DNA is useful for a live vaccine for domestic animals. See
CC also AAQ50398-402
XX
SQ Sequence 18 BP; 8 A; 1 C; 1 G; 8 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1596 GTGATTATTATATAAAAT 1613
Db 18 GTACATTTTATATAAAAT 1

RESULT 1667
AAQ86233/C
ID AAQ86233 standard; DNA; 18 BP.
XX
AC AAQ86233;
XX
11-JAN-1996 (first entry)
XX
DNA used in construction of recombinant poxvirus promoter.
XX
promoter; pox virus; combined promoter; recombinant; vaccine; poultry;
XX live; ds.
XX
Synthetic.
XX
JP07067655-A.
PN
14-MAR-1995.
PD
30-AUG-1993; 93JP-00238953.
PF
30-AUG-1993; 93JP-00238953.
PR
(JAPG ) NIPPON ZEON KK.
PA (SHIO ) SHIONOGI & CO LTD.
PA
WPI; 1995-143849/19.
DR
Combined pox-virus promoters contain at least four promoter fragments -
XX and pox-virus containing the combined promoters and a foreign gene.
XX
Example 1; Fig 3; 12pp; Japanese.
XX
The DNA shown is a DNA fragment contg. a MluI site used in the
XX construction of a combined promoter for recombinant poxvirus. Combined
XX promoters for poxvirus comprise at least four DNA fragments having a
XX promoter activity, pref. these fragments have early and late activity,
XX and the promoter has at least one, pref. more than two promoters. The
XX combined promoter has a strong activity and hence is useful in an
XX effective vaccine, esp. against poxvirus in poultry
XX
SQ Sequence 18 BP; 8 A; 1 C; 1 G; 8 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1596 GTGATTATTATATAAAAT 1613
Db 18 GTACATTTTATATAAAAT 1

RESULT 1668
AAQ20109
ID AAQ20109 standard; DNA; 18 BP.

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XX AAQ20109;
AC
XX 01-APR-1992 (first entry)
DT
XX Cross-linking oligomer 943 to target human TNF Receptor mRNA.
DE
XX deoxyribonucleic acid; major groove; ethanoino group;
KW tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;
KW cross-linking group; ss.
XX
OS Synthetic.
XX
Key Location/Qualifiers
FH modified_base 5 /*tag= a
FT /mod_base= OTHER
FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT modified_base 18 /*tag= b
FT /mod_base= OTHER
FT /note= "N4N4-ethanocytosine"
XX
WO9118997-A.
PN
12-DEC-1991.
PD
25-MAY-1990; 90US-00529346.
PF
25-MAY-1990; 90US-00529346.
PR 14-JAN-1991; 91US-00640654.
PR
XX (GILE-) GILEAD SCIE INC.
PA
XX Matteucci MD, Krawczyk S;
XX
WPI; 1992-007480/01.
XX
New sequence-specific non-photo-activated crosslinking agents - bind to
XX the major groove of duplex DNA and are esp. useful for treating latent
XX infections e.g. HIV.
XX
Example 4; Page 27; 42pp; English.
XX
The oligomer was designed to target human TNF receptor mRNA beginning at
XX nucleotide 2354 and to covalently cross-link to the target via the N4N4-
XX ethanocytosine group. See also AAQ20108
XX
SQ Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1575 TTTTATATTTTCTATTTC 1592
Db 1 TTTTATATTTTCTATTTC 18

RESULT 1669
AAQ25495
ID AAQ25495 standard; DNA; 18 BP.
XX
AC AAQ25495;
XX
25-MAR-2003 (revised)
DT 07-DEC-1992 (first entry)
DT
DE Purine rich HUMIL6B target duplex sequence.
XX
Target; human interleukin-6 gene; AIDS; triplex; HIV; hepatitis;
XX malignancy; inflammation; ds.
XX

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OS Synthetic.
XX WO9209705-A1.
XX PD 11-JUN-1992.
XX PF 25-NOV-1991; 91WO-US008811.
XX PR 23-NOV-1990; 90US-00617907.
XX PR 18-JAN-1991; 91US-00643382.
XX PR 08-APR-1991; 91US-00683420.
XX PR 17-APR-1991; 91US-00686544.
XX PR 17-APR-1991; 91US-00686546.
XX PR 17-APR-1991; 91US-00686547.
XX PR 27-SEP-1991; 91US-00766733.
XX PA (GILE-) GILEAD SCI INC.
XX PI Froehler B, Krawczyk S, Matteucci MD, Milligan J;
XX WPI; 1992-217083/26.
XX PS Claim 11; Page 64; 77pp; English.
XX CC The sequence depicts a HUMIL6B (interleukin-6) sequence beginning at
CC nucleotide 18. The sequence is a viral duplex sequence contg. a purine-
CC rich region concentrated on one chain of the duplex. The sequence may be
CC prep'd. by standard DNA synthesis. The HUMIL6B duplex sequence is used as
CC a target for novel oligomers which are capable of forming a triplex at
CC physiological pH by coupling into the major groove of the DNA duplex. Two
CC such oligomers 16 801-2 are capable of forming a triplex with this
CC sequence. The oligomers are used in the treatment of inflammation.
CC Similar oligomers may be used to target viral DNA duplexes specific for
CC HIV, herpes and other viruses. The triple helices form under mild
CC conditions thus assays may be carried out without subjecting the test
CC specimen to harsh conditions. The oligomer is able to inhibit gene
CC expression, as verified by in vitro systems. See also AAQ25452-25501 and
CC AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 18 BP; 4 A; 2 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 608 GCGTGAAGAGGCTTCT 625
Db 1 GAGGGAGAGAGGCTTCT 18
RESULT 1670
AAQ30448
ID AAQ30448 standard; DNA; 18 BP.
XX AC AAQ30448;
XX DT 25-MAR-2003 (revised)
XX DT 07-DEC-1992 (first entry)
XX DE Oligomer TFR943 for forming triplex with HUMNFR target duplex.
XX KW Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;
XX KW HPV; malignancy; hepatitis; inflammation; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 5
FT /*tag= a

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FT /mod_base= OTHER
FT /note= "N6 methyl-8-oxo-2' deoxyadenine"
FT modified_base 18
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= N4 N4 ethanocytosine"
XX PN WO9209705-A1.
XX PD 11-JUN-1992.
XX PF 25-NOV-1991; 91WO-US008811.
XX PR 23-NOV-1990; 90US-00617907.
XX PR 18-JAN-1991; 91US-00643382.
XX PR 08-APR-1991; 91US-00683420.
XX PR 17-APR-1991; 91US-00686544.
XX PR 17-APR-1991; 91US-00686546.
XX PR 17-APR-1991; 91US-00686547.
XX PR 27-SEP-1991; 91US-00766733.
XX PA (GILE-) GILEAD SCI INC.
XX PI Froehler B, Krawczyk S, Matteucci MD, Milligan J;
XX WPI; 1992-217083/26.
XX PS Claim 12; Page 72; 77pp; English.
XX CC The synthetic oligomer is capable of forming a triplex at physiological
CC pH with a purine rich target sequence by coupling into the major groove
CC of the duplex. The specific target sequence of this oligomer is the human
CC tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
CC a purine rich sequence concd. on one strand of the duplex. The oligomer,
CC and others like it are useful in diagnosis and therapy of diseases
CC characterised by specific DNA duplex targets, e.g. HPV, HBV, HIV,
CC hepatitis B, herpes, malignant tumours and inflammation. The triple
CC helices form under mild conditions thus assays may be carried out without
CC subjecting the test specimen to harsh conditions. See also AAQ25452-25501
CC and AAQ30226-447. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 25-MAR-2003 to correct PD field.)
XX SQ Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1575 TTTTATATTTCTATTTTC 1592
Db 1 TTTTATATTTTTTTC 18
RESULT 1671
AAQ34456/c
ID AAQ34456 standard; DNA; 18 BP.
XX AC AAQ34456;
XX DT 17-DEC-2001 (revised)
XX DT 12-MAY-1993 (first entry)
XX DE DQA1 probe AG2.3, for allele 0103.
XX KW Amplification; conformation polymorphism; SSCP; DQ-alpha; DQ-beta;
XX KW cystic fibrosis; neurofibromatosis; ss.
XX OS Synthetic.

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PN USN7751892-N.
 XX
 PD 01-DEC-1992.
 XX
 XX 29-AUG-1991; 91US-00751892.
 PF
 XX 29-AUG-1991; 91US-00751892.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICE.
 PA Mann D, Dean M, Carrington M, White MB;
 XX
 PI WPI; 1993-017809/02.
 XX
 DR Distinguishing multiple alleles and identifying new alleles - by single-
 XX strand conformation polymorphism technique using specific gel
 PT electrophoresis conditions.
 XX
 XX Disclosure; Page 19; 36pp; English.
 PS
 XX The oligomer AG2.3 represents a specific probe for DQA1 allele 0103 and
 CC is used to distinguish multiple alleles of a gene of the immunoglobulin
 CC supergene family. The DNA encoding the gene of interest in a sample is
 CC amplified and then denatured. The amplified DNA is then separated on a
 CC non-denaturing polyacrylamide gel consisting of 5 percent bis-acrylamide
 CC with 0-10 percent glycerol, and the presence or absence of DNA bands
 CC showing hybridisation is detected. Before amplification of the gene, the
 CC alleles may be divided into subsets by oligonucleotide hybridisation.
 CC Using single stranded conformation polymorphism (SSCP) multiple alleles
 CC in complex genetic systems can be distinguished e.g. DQ-alpha and DQ-beta
 CC and new alleles identified. The method may be used in studying genetic
 CC associations with disease, in forensic analyses and typing tissues for
 CC transplantation. The SSCP method has been used for detection of mutant
 CC alleles which correlate with the presence of disorders such as cystic
 CC fibrosis and neurofibromatosis. See also AAQ34443-73. (Note: Revised
 CC entry submitted to correct the patent number format of US Government-
 CC owned NTIS applications to prevent clashes with ongoing US granted patent
 CC numbers. For further information please visit the Derwent web site at
 CC www.derwent.com/dwpi/updates/ntis_us.html.
 XX
 SQ Sequence 18 BP; 8 A; 2 C; 7 G; 1 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1994 TCTCCTAATTCGACGT 2011
 Db 18 TCTCCTTCTTCTCCAGT 1
 RESULT 1672
 AAQ67133
 ID AAQ67133 standard; DNA; 18 BP.
 AC AAQ67133;
 XX
 XX 25-MAR-2003 (revised)
 DT 22-MAR-1995 (first entry)
 XX
 XX DNA primer P2 specific for an Adh1 promoter sequence.
 DE
 XX DNA primer; Adh1 promoter; maize; Zea mays; cereal; grass; protoplast;
 KW ss.
 XX
 XX Synthetic.
 OS
 XX WO9417176-A1.
 PN
 XX 04-AUG-1994.
 PD
 XX 27-JAN-1994; 94WO-US000927.
 PF
 XX

PR 29-JAN-1993; 93US-00010997.
 XX
 PA (PURD) PURDUE RES FOUND.
 XX
 XX Hodges TK, Lyznik LA;
 PI
 XX WPI; 1994-264090/32.
 DR
 XX DNA constructs - for creating transgenic eukaryotic cells.
 XX
 XX Disclosure; Page 49; 79pp; English.
 PS
 XX This primer is used in DNA analysis, specifically for the detection of an
 CC Adh1 promoter coding sequence in the protoplasts of maize (Zea mays).
 CC A188XBMS suspension cell culture, during the construction of transgenic
 CC eukaryotic cells. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 18 BP; 3 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1264 CCTGACAGGCGCATCTCG 1281
 Db 1 CCTCACAGGCTCATCTCG 18
 RESULT 1673
 AAQ91358
 ID AAQ91358 standard; DNA; 18 BP.
 AC AAQ91358;
 XX
 XX 25-MAR-2003 (revised)
 DT 14-SEP-1995 (first entry)
 XX
 XX Chromosome 11 (locus D11S1007) STS primer ZNF6-Z.
 DE
 XX sequence sampled mapping; genomic analysis; complex genome mapping;
 KW cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
 XX
 XX Synthetic.
 OS
 XX WO9429486-A1.
 PN
 XX 22-DEC-1994.
 PD
 XX 15-JUN-1994; 94WO-US006810.
 PF
 XX 15-JUN-1993; 93US-00078471.
 PR 07-SEP-1993; 93US-00117952.
 XX
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 PA
 XX Evans GA, Smith MW;
 PI
 XX WPI; 1995-036508/05.
 DR
 XX Sequencing complex genomes, present as fragments in a cosmid library - by
 PT sequencing end-specific nucleotides of each clone then correlating with
 PT spatial relationship of cosmid, esp. for mammalian chromosomes.
 XX
 XX Example 4; Page 96; 128pp; English.
 PS
 XX Sequences were determined from the ends of chromosome 11-specific cosmids
 CC by automated sequencing without intermediate subcloning. A sample of 371
 CC DNA sequence fragments were determined and of these, 277 were suitable
 CC for STS primer prediction by computer analysis (using the "Primer"
 CC program available from E.Lander, MIT). The STSs and cosmids were mapped
 CC by in situ hybridisation, somatic cell hybrid analysis or both. Using
 CC this method, 370 STSs specific for human chromosome 11 were generated and
 CC most of them were regionally mapped. This procedure illustrates a novel

CC method for sequencing complex genomes, designated "sequence sampled
 CC mapping". The sequence sampled mapping method is useful for the
 CC completion of high density sequence-based maps, and ultimately, for the
 CC complete sequencing of genomic DNA directly from cosmid clones. See
 CC AAQ2001-Q82706 and AAQ91325-Q91358 for STS primers. (Updated on 25-MAR-
 CC 2003 to correct PN field.)

XX Sequence 18 BP; 2 A; 11 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1549 TCACGTTTCTTCCCAAC 1566
 DB 1 TCCCTCTCTTCCCAAC 18

RESULT 1674
 AAX32947
 ID AAX32947 standard; DNA; 18 BP.

XX AAX32947;
 AC
 DT 30-JUN-1999 (first entry)

XX Duplex target sequence Seq ID No: 14.

XX OCH2O linkage; analogue; 2,6-diethylpyridine; DEP; molecular sieve;
 KW tetrabutylammonium fluoride; TBAF; tetrahydrofuran; chemical synthesis;
 KW THF; thioformacetal linkage; diagnostic agent; ss.

XX Synthetic.

XX US5495009-A.

XX 27-FEB-1996.

XX 24-APR-1992; 92US-00874334.

XX 24-OCT-1989; 89US-00426286.

PR 11-DEC-1989; 89US-00448941.

PR 30-JUL-1990; 90US-00559957.

PR 24-APR-1991; 91US-00690786.

XX (GILE-) GILEAD SCI INC.

XX Lin K, Jones B, Matteucci M;

XX WPI; 1996-178794/18.

XX Prodn. of nucleoside dimers with methylenedioxy linkage - by reacting 5'-
 PT protected nucleoside 3'-methylthio:methyl ether and 3'-protected
 PT nucleoside with bromine.

XX Example 2; Col 25; 27pp; English.

XX The invention relates to a method for linking a first nucleoside or
 CC oligonucleotide to a second nucleoside or nucleotide through an OCH2O
 CC linkage, starting with a 5'-protected nucleoside or nucleotide which is
 CC derivatised in the 3' position with an OCH2SMe group. The method
 CC comprises (a) treating the derivatised nucleoside or nucleotide and a 3'-
 CC protected nucleoside or nucleotide with bromine in the presence of 2,6-
 CC diethylpyridine (DEP) and molecular sieves; and (b) treating the product
 CC with tetrabutylammonium fluoride (TBAF) in tetrahydrofuran (THF). The
 CC OCH2O-linked dimers can be used in the synthesis of oligonucleotide
 CC analogues (containing thioformacetal linkages) e.g. useful as diagnostic
 CC agents (see WO9106629)

XX Sequence 18 BP; 13 A; 0 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1393 AAAACAGAGGATGAAAA 1410
 DB 1 AAAAGAAAGGAGGAAAA 18

RESULT 1675

AAT73428
 ID AAT73428 standard; DNA; 18 BP.

XX AAT73428;

XX 14-JAN-1998 (first entry)

XX S182 gene mutation detection wild type exon 8/exon 9.

XX S182 gene; Alzheimer's disease; polymorphism; mismatch; mutation;
 KW intronic sequence; polymerase chain reaction; primer; ss.

XX Synthetic.

XX Key Location/Qualifiers
 FH exon 1..10
 FT exon /tag= a
 FT /number= 8
 FT /note= "End of exon 8"

FT exon 11..18
 FT /tag= b
 FT /number= 9
 FT /note= "Start of exon 9"

XX WO9715689-A1.

XX 01-MAY-1997.

XX 25-OCT-1996; 96WO-US017132.

XX 25-OCT-1995; 95US-0007048P.

XX (UNIW) UNIV WASHINGTON SCHOOL MED.
 PA (UYSF-) UNIV SOUTH FLORIDA.

XX Hardy JA, Goate AM;

XX WPI; 1997-259039/23.

XX P-PSDB; AAW22378.

XX Diagnosing Alzheimer's disease by detecting polymorphism in the S182 gene
 DR - using mismatch polymerase chain reaction primers derived from intronic
 DR sequences.

XX Disclosure; Fig 2C; 30pp; English.

XX A method has been developed for the detection of polymorphism (mutations)
 CC in the S182 gene. The mutations are detected using selected mismatch
 CC polymerase chain reaction (PCR) primers derived from intronic sequences
 CC of the gene. The present sequence represents the spliced exon 8/exon 9
 CC boundary. Mutations in the S182 gene indicate that a subject is
 CC susceptible to late onset Alzheimer's disease. The method allows rapid
 CC analysis of many samples by PCR, restriction enzyme digestion and gel
 CC electrophoresis. Use of intronic sequences allows mutations to be
 CC detected in splice donor and acceptor sites (this would be almost
 CC impossible without intronic primers)

XX Sequence 18 BP; 6 A; 5 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 182 ATTTGCTGCTCAACTATG 199
 ||||| || ||||| |||||

Db 1 ATTACTCTCAACAATG 18

RESULT 1676
AAT93487/C
ID AAT93487 standard; DNA; 18 BP.
XX
AC AAT93487;
XX
DT 11-FEB-1998 (first entry)
XX
DE DQA1 allele determining DNA DQA4102 strand A.
XX
KW DQA1; DQA4102; histocompatibility locus; allele; resequencing analysis;
KW flow cytometry; Differentially fluorescent microsphere; DFM; human;
KW multiplex assay; bead-set; fluorophore; epitope mapping; screening;
KW therapeutic drug; multiple analyte; gene mutation; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9714028-A2.
XX
PD 17-APR-1997.
XX
PF 10-OCT-1996; 96WO-US016198.
XX
PR 11-OCT-1995; 95US-00540814.
PR 11-OCT-1995; 95US-00542401.
XX
PA (LUMI-) LUMINEX CORP.
XX
PI Chandler VS, Fulton RJ, Chandler MB;
XX
DR WPI; 1997-236023/21.
XX
PT Bead-sets for simultaneous assay of multiple analytes by cytometric
PT analysis - comprise many subsets carrying specific reagent and
PT identifiable from all other subsets by fluorescence parameters,
PT especially for clinical assays, and detecting gene mutation.
XX
PS Disclosure; Page 102; 293pp; English.
XX
CC This DNA sequence DQA4102 determines DQA1 allele. The allele specific for
CC this DNA is 0103. The 8 major alleles of the DQA1 gene are determined by
CC fourteen unique DNA sequences contained within a 227 bp PCR product. This
CC is used in flow cytometry to perform resequencing analysis of the PCR
CC products where the presence or absence of all fourteen DNA sequences can
CC be determined simultaneously in a single reaction tube containing the
CC mixed bead-set. The system is based on competitive hybridisation between
CC the PCR product and complementary oligonucleotide pairs representing the
CC unique DNA sequences. This strand is labelled with a green emitting
CC fluorophore and the complementary strand of this oligonucleotide pair is
CC coupled to a unique subset of microspheres. This fluorescent
CC oligonucleotide and the PCR product are added to the bead-set containing
CC the microsphere subset and the mixture is hybridised and analysed by flow
CC cytometry. The other DNA pairs of sequences are labelled and coupled
CC similarly. The ability of the PCR product to inhibit the hybridisation of
CC the fluorescent oligonucleotides to their respective microsphere subset
CC is used to determine the DNA sequence and the corresponding alleles
CC present in the PCR product. The flow cytometry method using the novel
CC bead-sets can also be used in quantitative and qualitative assay of
CC illicit or therapeutic drugs, antigens, auto antibodies, analytes
CC commonly elevated during pregnancy or nucleic acids, epitope screening of
CC a monoclonal antibody and for detecting specific gene mutations
XX
SQ Sequence 18 BP; 8 A; 2 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. NO. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1994 TCTCCTAAATCTCGAGT 2011

Db 18 TCTCCTTCTTCTCGAGT 1

RESULT 1677
AAT93488
ID AAT93488 standard; DNA; 18 BP.
XX
AC AAT93488;
XX
DT 11-FEB-1998 (first entry)
XX
DE DQA1 allele determining DNA DQA4102 strand B.
XX
KW DQA1; DQA4102; histocompatibility locus; allele; resequencing analysis;
KW flow cytometry; Differentially fluorescent microsphere; DFM; human;
KW multiplex assay; bead-set; fluorophore; epitope mapping; screening;
KW therapeutic drug; multiple analyte; gene mutation; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9714028-A2.
XX
PD 17-APR-1997.
XX
PF 10-OCT-1996; 96WO-US016198.
XX
PR 11-OCT-1995; 95US-00540814.
PR 11-OCT-1995; 95US-00542401.
XX
PA (LUMI-) LUMINEX CORP.
XX
PI Chandler VS, Fulton RJ, Chandler MB;
XX
DR WPI; 1997-236023/21.
XX
PT Bead-sets for simultaneous assay of multiple analytes by cytometric
PT analysis - comprise many subsets carrying specific reagent and
PT identifiable from all other subsets by fluorescence parameters,
PT especially for clinical assays, and detecting gene mutation.
XX
PS Disclosure; Page 102; 293pp; English.
XX
CC This DNA sequence DQA4102 determines DQA1 allele. The allele specific for
CC this DNA is 0103. The 8 major alleles of the DQA1 gene are determined by
CC fourteen unique DNA sequences contained within a 227 bp PCR product. This
CC is used in flow cytometry to perform resequencing analysis of the PCR
CC products where the presence or absence of all fourteen DNA sequences can
CC be determined simultaneously in a single reaction tube containing the
CC mixed bead-set. The system is based on competitive hybridisation between
CC the PCR product and complementary oligonucleotide pairs representing the
CC unique DNA sequences. This strand is coupled to a unique subset of
CC microspheres and the complementary strand of this oligonucleotide pair is
CC labelled with a green emitting fluorophore. The fluorescent
CC oligonucleotide and the PCR product are added to the bead-set containing
CC the microsphere subset and the mixture is hybridised and analysed by flow
CC cytometry. The other DNA pairs of sequences are labelled and coupled
CC similarly. The ability of the PCR product to inhibit the hybridisation of
CC the fluorescent oligonucleotides to their respective microsphere subset
CC is used to determine the DNA sequence and the corresponding alleles
CC present in the PCR product. The flow cytometry method using the novel
CC bead-sets can also be used in quantitative and qualitative assay of
CC illicit or therapeutic drugs, antigens, auto antibodies, analytes
CC commonly elevated during pregnancy or nucleic acids, epitope screening of
CC a monoclonal antibody and for detecting specific gene mutations
XX
SQ Sequence 18 BP; 1 A; 7 C; 2 G; 8 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. NO. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;


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QY      1994  TCTCCTAATTCTGCAGGT 2011
          ||||| ||||| |||||
Db      1  TCTCCTTCTTCTCAGGT 18

RESULT 1678
AA70303
ID  AAX70303 standard; RNA; 18 BP.
XX
AC  AAX70303;
XX
DT      28-JUL-1999 (first entry)
XX
DE  Human flt1 VEGF receptor hairpin ribozyme substrate #71.
XX
KW  Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW  KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW  tumor angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW  fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW  foetal liver kinase 1; ss.
XX
OS  Homo sapiens.
XX
PN  WO9715662-A2.
XX
PD  01-MAY-1997.
XX
PF  25-OCT-1996; 96WO-US017480.
XX
PR  26-OCT-1995; 95US-0005974P.
XX  11-JAN-1996; 96US-00584040.
XX
PA  (RIBO-) RIBOZYME PHARM INC.
PA  (CHIR ) CHIRON CORP.
XX
PI  Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
PI  WPI; 1997-259017/23.
XX
DR
XX
PT  Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT  stability - useful for treating e.g. tumor angiogenesis, psoriasis,
PT  rheumatoid arthritis, etc., in a human patient.
XX
PS  Claim 4; Page 94; 21pp; English.
XX
CC  The present invention describes nucleic acid molecules which modulate the
CC  synthesis, expression and/or stability of a mRNA encoding 1 or more
CC  receptors of vascular endothelial growth factor (VEGF). A patient
CC  (preferably human) having a condition associated with the level of the
CC  fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC  receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC  angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC  treated by administering the nucleic acid molecule or the expression
CC  vector to the patient. AAX67275 to AAX75752 represent specific examples
CC  of nucleic acid molecules from the present invention
XX
SQ  Sequence 18 BP; 6 A; 3 C; 8 G; 0 T; 1 U; 0 Other;

Query Match      0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      440  AGCAGCAGCGACGATCG 457
          ||||| ||||| |||||
Db      1  AGGAGCAGAGGACGCG 18

RESULT 1679
AA76262
ID  AAT76262 standard; DNA; 18 BP.
XX
AC  AAT76262;
XX

15-SEP-1997 (first entry)
Human IL6 receptor antisense oligonucleotide.
Asthma; airway epithelium; adenosine free; cystic fibrosis;
chronic obstructive pulmonary disease; bronchitis; interleukin; ss.
Synthetic.
WO9640162-A1.
19-DEC-1996.
06-JUN-1996; 96WO-US009306.
07-JUN-1995; 95US-00474497.
(UYEC-) UNIV EAST CAROLINA.
Nyce JW, Metzger WJ;
WPI; 1997-051871/05.
Treatment of airway diseases such as asthma - by topically applying
adenosine-free antisense oligonucleotide to airway epithelium of
subject.
Example 5; Page 32; 71pp; English.
A method for treating airway disease in a subject has been produced,
which involves the topical administration of an essentially adenosine
free antisense oligonucleotide (ON) to the airway epithelium of the
subject. The present sequence is an antisense oligonucleotide specific
for the human IL6 receptor. The method can be used to treat airway
diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary
disease, bronchitis and other airway diseases characterised by an
inflammatory response. By eliminating adenosine from the antisense ON,
its liberation upon antisense degradation is prevented, thereby
preventing adenosine-induced bronchoconstriction in patients with hyper-
reactive airways
SQ  Sequence 18 BP; 0 A; 4 C; 5 G; 9 T; 0 U; 0 Other;

Query Match      0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      377  GCCTGTTTGAGTCTGTC 394
          ||||| ||||| |||||
Db      1  GCCCGTTTGTTTGTC 18

RESULT 1680
AAV30371/c
ID  AAV30371 standard; DNA; 18 BP.
XX
AC  AAV30371;
XX
DT      29-SEP-1998 (first entry)
XX
DE  Oligomer p18g9 used in construction of recombinant HBsAg/ayw.
XX
KW  Hepatitis B virus; surface antigen; yeast; PHO5; promoter; vaccine; ss.
XX
OS  Synthetic.
OS  Hepatitis B virus.
XX
PN  RU2088664-Cl.
XX
PD  27-AUG-1997.
XX
PF  26-JAN-1996; 96RU-00101565.
XX

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PR 26-JAN-1996; 96RU-00101565.
XX
PA (KOMB-) KOMBIOTEKH STOCK CO.
XX
PI Druitsa VL, Budanov MV, Borisova VN;
XX
DR WPI; 1998-191876/17.
XX
XX New recombinant plasmid DNA pDES 20 coding for HBsAg-ayw - and new
PT Saccharomyces cerevisiae yeast strain containing it, for producing non-
PT toxic, highly immunogenic hepatitis B vaccines.
XX
XX Disclosure; Col 8; 11pp; Russian.
XX
XX The oligonucleotides AAV30347-V30394 were used in the construction of a
CC recombinant hepatitis B virus surface antigen ayw coding sequence
CC (AAV23279). The recombinant sequence was cloned into the plasmid pDES20
CC under control of a modified yeast PHO5 gene promoter (AAV23280) and the
CC PHO5 terminator sequence (AAV23281). The recombinant plasmid also
CC contains a ColEI bacterial replication origin; a bacterial beta-lactamase
CC gene; the natural yeast 2-micron plasmid fragment allowing autonomous
CC replication of pDES20 in yeast; a yeast Leu2 gene and the recombinant
CC HBsAg/ayw gene. The plasmid is used to generate the yeast strain DAN-
CC 041/pDES20 for expressing the antigen. The antigen can then be used to
CC generate an anti-hepatitis virus vaccine
XX
XX Sequence 18 BP; 1 A; 4 C; 4 G; 9 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1432 AAGAGAGTCCCGAAGAG 1449
DB 18 AAGAGAGTCCCGAAGAG 1
||||||| | |||||

RESULT 1681
AAV02565/c
ID AAV02565 standard; DNA; 18 BP.
XX
AC AAV02565;
XX
XX 04-AUG-1998 (first entry)
XX
DE Transcriptional activator fragment LS130.
XX
KW Activating sequence; Gal4; transcriptional activator; RNA polymerase;
KW Protein-protein interaction; gene therapy; therapeutic; holoenzyme;
KW Gal1; DNA binding domain; ss.
XX
OS Synthetic.
XX
XX WO9744447-A2.
XX
XX 27-NOV-1997.
XX
XX 02-MAY-1997; 97WO-US007338.
XX
XX 03-MAY-1996; 96US-0017016P.
XX
XX 01-MAY-1997; 97US-00017016.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Ptashne M, Lu X, Wu Y;
XX
XX WPI; 1998-018502/02.
XX
XX P-PSDB; AAW31467.
XX
XX New transcriptional activator containing DNA binding domain bound to
PT peptide - useful for controlling gene expression, especially in gene
PT therapy, and in protein-protein interaction assays, does not inhibit
PT other transcription activators.
PT

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XX
PS
XX
XX AAV02501-V02522, AAV02524-V02584, AAV02586-V02592 and AAV02594-V02616 are
CC DNA fragments used in an assay to determine novel transcriptional
CC activators. The method involves the production of transcriptional
CC activators comprising of a DNA-binding group and a 6-25 amino acid
CC peptide that is covalently bonded to the DNA binding group and does not
CC represent a fragment of a natural transcription activator. Protein-
CC protein interactions are identified in the assay by fusing a DNA-binding
CC domain to a library of DNA fragments and introducing this and a fusion of
CC target protein and a polypeptide containing a region of Gal4 which
CC interacts with Gal1p into a cell containing Gal1p and identifying
CC members of the library that interact with the target from activation of
CC transcription. Such constructs are used to activate transcription in a
CC cell, e.g. for controlling gene activity, particularly in gene therapy
CC (e.g. recognizing a site close to a selected therapeutic gene).
CC Transcription can be activated without blocking other transcriptional
CC activators. They probably act by interacting with a component of the RNA
CC polymerase II holoenzyme, Gal1, the strongest known yeast activator,
CC which provides a more sensitive assay allowing detection of even weak
CC protein-protein interactions. Such activators do not create toxicity
XX
XX problems even when overexpressed
XX
XX Sequence 18 BP; 2 A; 6 C; 3 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 442 CACGACAGCGACATCGCT 459
DB 18 CACGACAGCGAATCGGT 1
||||||| | |||||

RESULT 1682
AAV02552/c
ID AAV02552 standard; DNA; 18 BP.
XX
AC AAV02552;
XX
XX 04-AUG-1998 (first entry)
XX
DE Transcriptional activator fragment LS108.
XX
KW Activating sequence; Gal4; transcriptional activator; RNA polymerase;
KW Protein-protein interaction; gene therapy; therapeutic; holoenzyme;
KW Gal1; DNA binding domain; ss.
XX
OS Synthetic.
XX
XX WO9744447-A2.
XX
XX 27-NOV-1997.
XX
XX 02-MAY-1997; 97WO-US007338.
XX
XX 03-MAY-1996; 96US-0017016P.
XX
XX 01-MAY-1997; 97US-00017016.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Ptashne M, Lu X, Wu Y;
XX
XX WPI; 1998-018502/02.
XX
XX P-PSDB; AAW31455.
XX
XX New transcriptional activator containing DNA binding domain bound to
PT peptide - useful for controlling gene expression, especially in gene
PT therapy, and in protein-protein interaction assays, does not inhibit
PT other transcription activators.
XX
XX Example 1; Page 25; 55pp; English.
PS

```


CC sequences to detect the presence of pathogenic nucleic acid sequences
 CC indicative of an infection, the presence of variants or alleles of
 CC mammalian genes associated with disease and cancers, and the
 CC identification of the source of nucleic acids found in forensic samples,
 CC as well as in paternity determinations. The methods allow simultaneous
 CC analysis of both strands (e.g. the sense and antisense strands) and are
 CC ideal for high-level multiplexing. The products produced are amenable to
 CC qualitative, quantitative and positional analysis. The methods may be
 CC performed in solution or in the solid phase (e.g. on a solid support).
 CC The methods are powerful in that they allow for analysis of longer
 CC fragments of nucleic acid than current methodologies. The present
 CC sequence represents a bridging primer that can hybridize to a HCV
 CC amplicon

XX
 SQ Sequence 18 BP; 2 A; 8 C; 3 G; 5 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1846 TTCTAGAGGGTGGCTG 1863
 | | | | | | | | | |
 DB 18 TCCAGAGGGGAGGCTG 1

RESULT 1685
 AAX82245
 ID AAX82245 standard; DNA; 18 BP.
 XX AC AAX82245;
 XX DT 18-AUG-1999 (first entry)
 XX DE Influenza virus PB2 gene specific primer.
 XX KW Cold-adapted influenza virus; passage culture; PB2 protein; PB1 protein;
 KW PA protein; NP protein; M protein; NS protein; temperature sensitivity;
 KW vaccine; flu; influenza; PCR primer; ss.
 XX OS Synthetic.
 OS Influenza virus.
 XX WO9928445-A1.
 XX PN 10-JUN-1999.
 XX PD 30-NOV-1998; 98WO-KR000384.
 XX PF 29-NOV-1997; 97KR-00064854.
 XX PR (CHEI-) CHEIL JEDANG CORP.
 XX PA Seong BL, Lee KH, Yoon JW, Kim SU, Cheoun KH, Kim J, Kim HG;
 XX PI WPI; 1999-385377/32.
 XX DR Cold-adapted influenza viruses useful for the production of protective
 XX PT vaccines against flu.
 XX PS Example 4; Page 15; 62pp; English.
 XX CC The invention relates to cold-adapted influenza viruses prepared by
 CC passage culture of A/X-31, B/Yamagata/16/98 or B/Lee/40 viruses at low
 CC temperatures. A cDNA gene of cold-adapted influenza virus HTCA-A101 can
 CC be selected from a group consisting of PB2 protein gene, PB1 protein
 CC gene, PA protein gene, NP protein gene, M protein gene and NS protein
 CC gene (AAX82192-X82197). The method is useful for the production of cold-
 CC adapted influenza virus that exhibit temperature sensitivity and can be
 CC actively grown in fertilized eggs. The virus is useful for vaccines for
 CC protection against flu. Live vaccines containing cold-adapted viruses
 CC have several advantages over killed vaccines. It can prevent reduction of
 CC immunogenicity, which may occur in the killed vaccine where antigenic
 CC proteins would be denatured at its inactivation. It can also avoid
 CC hyper-sensitivity due to the prolonged administration of heterologous
 CC proteins. It promotes the immunity by inducing IgA and it can be
 CC administered into a spray formulation via nasal cavity and thus its
 CC application is convenient for children. It is able to inhibit the growth
 CC of the wild-type virus and thus its therapeutic effect can be expected.
 CC Sequences AAX82222-X82257 represent PCR primers specific for the various

CC hypersensitivity due to the prolonged administration of heterologous
 CC proteins. It promotes the immunity by inducing IgA and it can be
 CC administered into a spray formulation via nasal cavity and thus its
 CC application is convenient for children. It is able to inhibit the growth
 CC of the wild-type virus and thus its therapeutic effect can be expected.
 CC Sequences AAX82222-X82257 represent PCR primers specific for the various
 CC genes of influenza virus

XX
 SQ Sequence 18 BP; 2 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1521 CTCACGCTGTGGCTTCT 1538
 | | | | | | | | | |
 DB 1 CTCACGCTGTGGCTTCT 18

RESULT 1686
 AAX82246/c
 ID AAX82246 standard; DNA; 18 BP.
 XX AC AAX82246;
 XX DT 18-AUG-1999 (first entry)
 XX DE Influenza virus PB2 gene specific primer.
 XX KW Cold-adapted influenza virus; passage culture; PB2 protein; PB1 protein;
 KW PA protein; NP protein; M protein; NS protein; temperature sensitivity;
 KW vaccine; flu; influenza; PCR primer; ss.
 XX OS Synthetic.
 OS Influenza virus.
 XX WO9928445-A1.
 XX PN 10-JUN-1999.
 XX PD 30-NOV-1998; 98WO-KR000384.
 XX PF 29-NOV-1997; 97KR-00064854.
 XX PR (CHEI-) CHEIL JEDANG CORP.
 XX PA Seong BL, Lee KH, Yoon JW, Kim SU, Cheoun KH, Kim J, Kim HG;
 XX PI WPI; 1999-385377/32.
 XX DR Cold-adapted influenza viruses useful for the production of protective
 XX PT vaccines against flu.
 XX PS Example 4; Page 15; 62pp; English.
 XX CC The invention relates to cold-adapted influenza viruses prepared by
 CC passage culture of A/X-31, B/Yamagata/16/98 or B/Lee/40 viruses at low
 CC temperatures. A cDNA gene of cold-adapted influenza virus HTCA-A101 can
 CC be selected from a group consisting of PB2 protein gene, PB1 protein
 CC gene, PA protein gene, NP protein gene, M protein gene and NS protein
 CC gene (AAX82192-X82197). The method is useful for the production of cold-
 CC adapted influenza virus that exhibit temperature sensitivity and can be
 CC actively grown in fertilized eggs. The virus is useful for vaccines for
 CC protection against flu. Live vaccines containing cold-adapted viruses
 CC have several advantages over killed vaccines. It can prevent reduction of
 CC immunogenicity, which may occur in the killed vaccine where antigenic
 CC proteins would be denatured at its inactivation. It can also avoid
 CC hyper-sensitivity due to the prolonged administration of heterologous
 CC proteins. It promotes the immunity by inducing IgA and it can be
 CC administered into a spray formulation via nasal cavity and thus its
 CC application is convenient for children. It is able to inhibit the growth
 CC of the wild-type virus and thus its therapeutic effect can be expected.
 CC Sequences AAX82222-X82257 represent PCR primers specific for the various

```

CC genes of influenza virus
XX
SQ Sequence 18 BP; 6 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

Query Match      0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1521 CTCCAGCTCTGGCTTCCT 1538
Db 18 CTCCAGCTGTGCTTCAT 1

RESULT 1687
AAX54052
ID AAX54052 standard; DNA; 18 BP.
XX
AC AAX54052;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human IL-6 receptor antisense oligonucleotide fragment.
XX
KW Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
OS Synthetic.
XX
PN WO9913886-A1.
XX
PD 25-MAR-1999.
XX
PF 17-SEP-1998; 98WO-US019419.
XX
PR 17-SEP-1997; 97US-0059160P.
PR 09-JUN-1998; 98US-00093972.
XX
PA (UYSC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 1999-229400/19.
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction.
XX
PS Disclosure; Page 50; 120pp; English.
XX
CC The specification describes antisense oligonucleotides (AAX52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene initiation
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
CC end and the juxta-section between coding and non-coding regions and all
CC segments of RNAs encoding proteins associated with one or more diseases,
CC conditions or mixtures. The antisense oligonucleotides may be derived
CC from sequences AAX5272-74. These multiple target oligonucleotides
CC (specifically AAX55180-271) can be used for the antisense treatment of
CC diseases and conditions. Typical diseases and conditions are those
CC associated with impaired respiration and inflammation, including lung
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC acute asthma, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,

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CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC well as all types of cancers which may metastasize or have metastasized
CC to the lungs, including breast and prostate cancer
XX
SQ Sequence 18 BP; 0 A; 4 C; 5 G; 9 T; 0 U; 0 Other;

Query Match      0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 377 GCGTGTTCAGTCTGTC 394
Db 1 GCCCGTTGTGTTGTC 18

RESULT 1688
AAX90266/c
ID AAX90266 standard; DNA; 18 BP.
XX
AC AAX90266;
XX
DT 27-SEP-1999 (first entry)
XX
DE DQA1 gene PCR primer DQA4102 A strand.
XX
KW Monoclonal antibody; epitope; multiplexed analysis; diagnosis;
KW genetic analysis; flow cytometry; human myelin basic protein; MBP;
KW microbial antigen; viral antigen; pathological condition; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9936564-A1.
XX
PD 22-JUL-1999.
XX
PF 15-JAN-1999; 99WO-US000918.
XX
PR 16-JAN-1998; 98US-00008387.
XX
PA (LUMI-) LUMINEX CORP.
XX
PI Chandler VS, Fulton JR, Chandler MB;
XX
DR WPI; 1999-444409/37.
XX
PT Beadset for simultaneous detection of many analytes by flow cytometry,
PT e.g. for detecting antigens, antibodies, or nucleic acid mutations.
XX
PS Example; Page 102; 301pp; English.
XX
CC The present invention describes a beadset (A), able to detect many
CC analytes (I) in a single sample by flow cytometry (FC). (A) is produced
CC by: (i) providing many subsets of beads which, within each subset, are
CC homogeneous as regards at least 3 selected class parameters (C) but
CC sufficiently different in at least one C from beads in other subsets to
CC provide a profile of C values unique for each subset in FC; (ii) coupling
CC the beads in each subset with a reactant (R), specific for a given (I)
CC and (iii) mixing the subsets to form an (A) in which subsets (and thus
CC bound R) are identifiable in FC from the unique profile of C. A method of
CC flow cytometry analysis using (A) is used to detect a very wide range of
CC (I), e.g. microbial or viral antigens (particularly from pathogens that
CC cause venereal, pulmonary or gastrointestinal disease); therapeutic or
CC illicit drugs; antigens or antibodies associated with particular
CC pathological conditions (malignancy, allergy, autoimmune disease, blood-
CC borne viruses or cardiovascular disease); hormones, including those
CC indicative of pregnancy; enzymes; immunoglobulins (Ig), particularly of
CC different (sub)classes; Ig that form part of a particular epitope
CC (specifically an epitope of human immune deficiency virus) or nucleic
CC acids (particularly for detecting a wide variety of mutations, e.g. those
CC present in the ret proto-oncogene, the low density lipoprotein receptor,
CC the Duchenne muscular dystrophy, angiotensin p3, and Rb genes. The
CC process is particularly used for diagnosis of disease and for genetic
CC analysis. The present sequence represents a DQA gene PCR primer used in

```

CC the exemplification of the present invention

XX

SQ Sequence 18 BP; 8 A; 2 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1994 TCTCCTAATTCGAGGT 2011

Db 18 TCTCCTTCTTCAGGT 1

RESULT 1689

AA33496

ID AAA33496 standard; DNA; 18 BP.

XX AC AAX90267;

XX DT 27-SEP-1999 (first entry)

XX DE DOA1 gene PCR primer DOA4102 B strand.

XX KW Monoclonal antibody; epitope; multiplexed analysis; diagnosis;

XX KW genetic analysis; flow cytometry; human myelin basic protein; MBP;

XX KW microbial antigen; viral antigen; pathological condition; PCR primer; ss.

XX OS Synthetic.

XX PN WO9936564-A1.

XX PD 22-JUL-1999.

XX PF 15-JAN-1999; 99WO-US000918.

XX PR 16-JAN-1998; 98US-00008387.

XX PA (LUMI-) LUMINEX CORP.

XX PI Chandler VS, Fulton JR, Chandler MB;

XX DR WPI; 1999-444409/37.

XX PT Beadset for simultaneous detection of many analytes by flow cytometry,

XX PT e.g. for detecting antigens, antibodies, or nucleic acid mutations.

XX PS Example; Page 102; 301pp; English.

CC The present invention describes a beadset (A), able to detect many

CC analytes (I) in a single sample by flow cytometry (FC). (A) is produced

CC by: (i) providing many subsets of beads which, within each subset, are

CC homogeneous as regards at least 3 selected class parameters (C) but

CC sufficiently different in at least one C from beads in other subsets to

CC provide a profile of C values unique for each subset in FC; (ii) coupling

CC the beads in each subset with a reactant (R), specific for a given (I)

CC and (iii) mixing the subsets to form an (A) in which subsets (and thus

CC bound R) are identifiable in FC from the unique profile of C. A method of

CC flow cytometry analysis using (A) is used to detect a very wide range of

CC (I), e.g. microbial or viral antigens (particularly from pathogens that

CC cause venereal, pulmonary or gastrointestinal disease); therapeutic or

CC illicit drugs; antigens or antibodies associated with particular

CC pathological conditions (malignancy, allergy, autoimmune disease, blood-

CC borne viruses or cardiovascular disease); hormones, including those

CC indicative of pregnancy; enzymes; immunoglobulins (Ig), particularly of

CC different (sub)classes; Ig that form part of a particular epitope

CC (specifically an epitope of human immune deficiency virus) or nucleic

CC acids (particularly for detecting a wide variety of mutations, e.g. those

CC present in the ret proto-oncogene, the low density lipoprotein receptor,

CC the Duchenne muscular dystrophy, angiotensin p53, and RB genes. The

CC process is particularly used for diagnosis of disease and for genetic

CC analysis. The present sequence represents a DOA gene PCR primer used in

CC the exemplification of the present invention

SQ Sequence 18 BP; 1 A; 7 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1994 TCTCCTAATTCGAGGT 2011

Db 1 TCTCCTTCTTCAGGT 18

RESULT 1690

AA33496

ID AAA33496 standard; DNA; 18 BP.

XX AC AAA33496;

XX DT 28-JUL-2000 (first entry)

XX DE Low adenosine antisense oligonucleotide SEQ ID NO:1185.

XX KW Human; adenosine receptor; low adenosine antisense oligonucleotide;

XX KW phosphorothioate; impaired respiration; inflammation; allergy;

XX KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;

XX KW antiallergic; antiasthmatic; cytosstatic; analgesic; impaired airway;

XX KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;

XX KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;

XX KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;

XX KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX OS Homo sapiens.

XX PN WO200009525-A2.

XX PD 24-FEB-2000.

XX PF 03-AUG-1999; 99WO-US017712.

XX PR 03-AUG-1998; 98US-0095212P.

XX PA (UYEC-) UNIV EAST CAROLINA.

XX PI Nyce JW;

XX DR WPI; 2000-205971/18.

XX PT New antisense oligonucleotides useful for treating e.g. pulmonary

XX PT vasoconstriction, inflammation, allergies, asthma, hypertension,

XX PT bronchitis, emphysema, respiratory distress syndrome, ischemia or

XX PT cancers.

XX PS Claim 18; Page 413; 1343pp; English.

CC The present invention describes a new composition comprising an antisense

CC oligonucleotide (ON) with low adenosine (up to 15%), which targets

CC nucleic acids involved in bronchoconstriction, allergies, and/or

CC inflammation. The ON can have antiinflammatory, antiallergic,

CC antiasthmatic, cytosstatic and analgesic activities. The compositions are

CC useful for the treatment of diseases associated with inflammation,

CC impaired airways, including lung disease and diseases whose secondary

CC effects afflict the lungs of a subject. They can be used for treating

CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,

CC impaired respiration, respiratory distress syndrome, pain, cystic

CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive

CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,

CC carcinomas, and cancers which may metastasise to the lungs, including

CC breast and prostate cancer. The reduction of the adenosine content of the

CC ONs reduces side effects. The A-containing ONs break down with the

CC release of deoxyadenosine which activates adenosine receptors causing

CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the

CC nucleotide sequences given in the sequence listing from the present

CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185

CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ

CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing

XX
 SQ Sequence 18 BP; 0 A; 4 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 377 GCCTGTTTGAGTCTGTC 394
 ||| ||||| ||| |||||
 Db 1 GCCCGTTTGCTTTGTC 18

RESULT 1691
 AAA35485
 ID AAA35485 standard; DNA; 18 BP.
 XX
 AC AAA35485;
 XX
 DT 06-AUG-2003 (revised)
 DT 25-JUL-2000 (first entry)
 XX
 DE Myrtaceae microsatellite scul09TT detection PCR primer.
 XX
 KW Myrtaceae; microsatellite; isolation; genotyping; plant; tea tree;
 KW breeding; Melaleuca alternifolia; broad-spectrum germicidal oil;
 KW pharmaceutical; cosmetic; identification; detection; PCR primer; ss.
 XX
 OS Myrtaceae.
 XX
 PN WO200017341-A1.
 XX
 PD 30-MAR-2000.
 XX
 PF 23-SEP-1999; 99WO-AU000820.
 XX
 PR 23-SEP-1998; 98AU-00006099.
 PR 16-FEB-1999; 99AU-00008718.
 XX
 PA (BUSI-) BUSINESS & RES MANAGEMENT PTY LTD.
 XX
 PI Rossetto M, McLauchlan A, Harriss FCL, Henry RJ, Baverstock PR;
 PI Lee LS, Maguire TL, Edwards KJ;
 XX
 DR WPI; 2000-292840/25.
 XX
 PT Isolating microsatellites from Myrtaceae, useful for genotyping,
 PT particularly in breeding programs for tea tree, by reacting plant nucleic
 PT acid with immobilized oligonucleotides.
 XX
 PS Claim 10; Page 38; 100pp; English.

CC A method has been developed of isolating a microsatellite (MS) from
 CC nucleic acid extract of a plant of Myrtaceae family. The method
 CC comprises: (i) treating the extract with one or more immobilised, single-
 CC stranded oligonucleotides (ON) having a consensus MS repeat sequence
 CC (MSRS) or its complement; (ii) washing under specified stringent
 CC conditions; (iii) eluting nucleic acid bound to ON; and (iv) sequencing
 CC the eluted nucleic acids to identify those containing an MSRS.
 CC Microsatellites (MS) isolated by the method, specifically from Melaleuca
 CC alternifolia (the tea tree, a source of a broad-spectrum germicidal oil,
 CC useful in pharmaceuticals and cosmetics), are useful as genotyping
 CC markers, particularly for breeding plants that produce the oil in higher
 CC yield or of better quality. Primers based on MS are useful for both inter
 CC - and intra-species genotyping. The selected washing conditions improve
 CC efficiency of recovery of microsatellites (MS) and reduce the number of
 CC washing stages required. Particularly about 86% of recovered sequence
 CC contain an MS repeat sequence, compared with 50-70% when the conventional
 CC washing procedure is followed. AAA35313 to AAA35357, and AAA35562 to

CC AAA35575 represent nucleotide sequences from the present invention which
 CC contain microsatellite sequences. AAA35358 to AAA35561 represent
 CC oligonucleotide PCR primers used for identifying Myrtaceae microsatellite
 CC sequences. (Updated on 06-AUG-2003 to correct OS field.)

XX
 SQ Sequence 18 BP; 3 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1548 CTCACGTTTCTTCCCA 1565
 ||| ||||| |||||
 Db 1 CCCATGTTTCTGCCCA 18

RESULT 1692
 AAZ6505/C
 ID AAZ6505 standard; DNA; 18 BP.
 XX
 AC AAZ6505;
 XX
 DT 30-MAR-2000 (first entry)
 DT
 XX
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-98-8.
 XX
 KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.
 XX
 OS Unidentified.
 XX
 PN WO963975-A2.
 XX
 PD 16-DEC-1999.
 XX
 PF 10-JUN-1999; 99WO-BP004013.
 XX
 PR 10-JUN-1998; 98EP-00110709.
 PR 25-JUL-1998; 98EP-00113974.
 XX
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX
 PI Schlingensiepen K, Schlingensiepen R, Brysch W;
 XX
 DR WPI; 2000-097470/08.
 XX
 PT Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.
 XX
 PS Claim 10; Fig 1; 30pp; English.

CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
 CC inflammatories for treating e.g. asthma, Crohn's disease, ulcerative

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CC colitis, diabetes, glomerulonephritis, acute respiratory distress
CC syndrome and the formation of atherosclerotic plaque
XX
SQ Sequence 18 BP; 0 A; 10 C; 6 G; 2 T; 0 U; 0 Other;
    Query Match          0.6%; Score 13.2; DB 1; Length 18;
    Best Local Similarity 83.3%; Pred. No. 1.1e+03;
    Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 12 CGGCGGGAGGGCGGACG 29
Db 18 CGAGCCGAGGGCGGCG 1

RESULT 1693
AAZ46809
ID AAZ46809 standard; DNA; 18 BP.
XX
AC AAZ46809;
XX
DT 31-MAR-2000 (first entry)
XX
DE Interleukin-10 (IL-10) mRNA inhibiting antisense oligo #4.
XX
KW Interleukin-10; IL-10; atopic dermatitis; allergic dermatitis; SLE;
KW EB viral infection; lymphoma; antisense; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9967388-A1.
XX
PD 29-DEC-1999.
XX
PF 22-JUN-1999; 99WO-JP003315.
XX
PR 24-JUN-1998; 98JP-00177188.
XX
PA (HISM) HISAMITSU PHARM CO LTD.
XX
PI Arima H, Tsuchiya S, Hirata T, Akiyama K, Goto T;
XX WPI; 2000-106294/09.
XX
DR Antisense oligonucleotide for inhibiting expression of IL-10 protein,
PT useful as active ingredient in remedies for atopic dermatitis.
XX
PS Claim 1; Page 17; 22pp; Japanese.
XX
CC Sequences AAZ46806-812 represent antisense oligonucleotides for
CC inhibiting expression of interleukin-10 (IL-10) protein. A composition
CC which is formulated with the antisense oligonucleotide or its derivatives
CC as active ingredient can be used for treating atopic dermatitis, allergic
CC dermatitis, SLE, EB viral infection or lymphoma
XX
SQ Sequence 18 BP; 3 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
    Query Match          0.6%; Score 13.2; DB 1; Length 18;
    Best Local Similarity 83.3%; Pred. No. 1.1e+03;
    Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1674 CTGGGTGAGCTCTTCCAG 1691
Db 1 CTGGGTGAGCTATCCCG 18

RESULT 1694
AAZ70756/C
ID AAZ70756 standard; DNA; 18 BP.
XX
AC AAZ70756;
XX
DT 10-SEP-2001 (first entry)
XX

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XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:5112.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
XX
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 8; Page 1321; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 18 BP; 6 A; 6 C; 2 G; 4 T; 0 U; 0 Other;
    Query Match          0.6%; Score 13.2; DB 1; Length 18;
    Best Local Similarity 83.3%; Pred. No. 1.1e+03;
    Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 832 GTGGTCTTACAGTGTGGC 849
Db 18 GAGGTTTACAGTATGGC 1

RESULT 1695
AAZ69768
ID AAZ69768 standard; DNA; 18 BP.
XX
AC AAZ69768;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:4124.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX

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PS Example 1; Fig 15; 19pp; Chinese.

XX The present invention describes a method which comprises making a high-density gene chip, specifically for making high-density micro-array of oligonucleotide probes. An oligonucleotide probe selecting process to seek preferentially length variable and coverage variable probes is provided to ensure identical cross melting temperature of probes to the maximum limit, and this can make the cross control of gene chip relatively simple and raise the reliability of the gene chip detecting results. The process proposes a specific probe selection method for detecting target sequence directly, detecting mutation in both specific and non-specific sites and a probe overall arrangement scheme. AA79738 CC to AA80201 represent oligonucleotide probe sequences which are used in CC examples from the present invention

XX SQ Sequence 18 BP; 7 A; 4 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 484 CATGCAAGAGTCCGAG 501

Db 1 CAGGCAAGAGGACCGAG 18
|| ||||| | |||||

RESULT 1698

AAFI9618
ID AAF19618 standard; DNA; 18 BP.

XX
AC AAF19618;

XX 14-MAR-2001 (first entry)

XX Human IL6 receptor polynucleotide fragment #1185.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; antiaspasmic; bronchodilator; antiinflammatory;
KW immunosuppressive; antiallergic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.

XX Homo sapiens.

XX WO200062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008020.

XX 06-APR-1999; 99US-0127958P.

XX (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

XX Nyce JW;

XX WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.

XX Claim 14; Page 209; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.

CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiallergic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention

XX SQ Sequence 18 BP; 0 A; 4 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 377 GCTGTGTTGAGTCTGTC 394

Db 1 GCCCGTTGTTGTTGTC 18
|| ||||| | |||||

RESULT 1699

AAZ87163

ID AAZ87163 standard; RNA; 18 BP.

XX AAZ87163;

XX 08-MAY-2000 (first entry)

XX Oligoarabinonucleotide SEQ ID NO:4.

XX Beta-D-arabinose; antisense; inhibition; transcription; expression;
KW reverse transcription; viral replication; RNase H cleavage;
KW triple helix formation; ss.

XX Synthetic.

PH Key Location/Qualifiers

FT modified_base 1..18

FT /*tag= a

FT /note= "Ribose moiety replaced by beta-D-arabinose"

XX WO9967378-A1.

XX 29-DEC-1999.

XX 17-JUN-1999; 99WO-CA000571.

XX 19-JUN-1998; 98CA-02241361.

XX (UYMC-) UNIV MCGILL.

XX Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;

XX WPI; 2000-160584/14.

PT -phosphoinositide dependent protein kinase-1, useful e.g. for treating
 PT inflammation, tumors and infections.

PS Claim 3; Col 39; 41pp; English.

XX The present sequence is one of a large number of antisense
 CC oligonucleotides which are targeted to a nucleic acid molecule encoding
 CC human 3-phosphoinositide dependent protein kinase-1 (PDK-1). The
 CC antisense compounds may be oligodeoxynucleotides or chimeric
 CC oligonucleotides containing a central gap region, consisting of ten 2'-
 CC deoxynucleotides, which is flanked on both sides by 2'-methoxyethyl (2'-
 CC MOE) wings. The oligonucleotides have a phosphorothioate backbone. The
 CC antisense oligonucleotides are useful for inhibiting the expression of
 CC human PDK-1 in human cells or tissues. They are also useful for
 CC preventing or delaying infection, inflammation or tumours and are useful
 CC for research and diagnostics

XX Sequence 18 BP; 6 A; 1 C; 10 G; 1 T; 0 U; 0 Other;

SQ Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1241 GTGCGATGAGGAGGAG 1258

Db |||||
 1 GTGAGGAGGAGGAGGAG 18

RESULT 1702

AAC84044
 ID AAC84044 standard; DNA; 18 BP.

XX AAC84044;

XX 02-MAR-2001 (first entry)

XX Human pro-insulin fusion protein primer #7.

XX Antidiabetic; fusion protein; linker; insulin; diabetes; PCR primer; ss.

XX Homo sapiens.

XX W0200066738-Al.

XX 09-NOV-2000.

XX 26-APR-2000; 2000WO-JP002736.

XX 30-APR-1999; 99JP-00124877.

XX (ITOH-) ITOHAM FOODS INC.

XX Oka S, Sato S, Higashikuni N, Kondo M, Kudo T, Watanabe S;

PI Waki Y, Yuki H;

XX WPI; 2000-679760/66.

XX Efficient and highly-productive preparation of genes encoding recombinant
 PT insulin fusion proteins, having biological activity comparable with
 PT natural product, for use in treating diabetes.

XX Example 1; Page 15; 54pp; Japanese.

XX The invention relates to a DNA molecule encoding a fused protein of
 CC formula (I): (V)-(X1)-(B-chain)-(X2)-(Linker)-(X3)-(A-chain) (I) where
 CC (V) = a leader peptide sequence of at least 1 amino acid (aa) for the
 CC expression and secretion of the protein; (X1) (X2) and (X3) = enzymatic
 CC or chemical cleavage peptide motifs, and motif (X3) especially comprises
 CC the aa sequence Pro-Arg; and (B-chain) and (A-chain) = insulin B and A
 CC chains respectively. PCR primers AAC84038-C84048 were used to amplify the
 CC sequence encoding the human pro-insulin gene and insert thrombin cleavage
 CC motifs for generating the insulin fusion construct. The insulin is used
 CC in therapy e.g. to treat insulin-dependent diabetes

XX Sequence 18 BP; 3 A; 8 C; 5 G; 2 T; 0 U; 0 Other;

SQ Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1509 CTGAATGGACCTCTCCAG 1526

Db |||||
 1 CTGCAGGAGCCCTCCAG 18

RESULT 1703

AAC87924
 ID AAC87924 standard; DNA; 18 BP.

XX AAC87924;

XX 06-MAR-2001 (first entry)

XX PCR-restriction fragment length polymorphism primer SEQ ID NO:2.

XX PCR-RFLP; polymerase chain reaction; primer; optimisation; separation;
 KW restriction fragment length polymorphism; bacteria; fungi; yeast;
 KW identification; microbe; analysis; ss.

XX Synthetic.

XX JP2000270875-A.

XX 03-OCT-2000.

XX 26-MAR-1999; 99JP-00083691.

XX 26-MAR-1999; 99JP-00083691.

XX (OSAG) OSAKA GAS CO LTD.

XX WPI; 2001-011050/02.

XX Optimization of a separation medium for separating and analyzing microbes
 PT present in the environment using polymerase chain reaction-restriction
 PT fragment linked polymorphism.

XX Disclosure; Page 3; 9pp; Japanese.

XX The present invention describes a method for the optimisation of a
 CC separation medium for separating bacteria, fungi or yeasts from the
 CC environment by simply identifying microbes in the environment by using a
 CC polymerase chain reaction-restriction fragment length polymorphism (PCR-
 CC RFLP) method. The method can be used for completely separating and
 CC analysing microbes present in environment. AAC87923 to AAC87926 represent
 CC PCR-RFLP primers which are used in the exemplification of the present
 CC invention

XX Sequence 18 BP; 6 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

SQ Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 807 AATGGAGATGTTCCAGCC 824

Db |||||
 1 AAAGGAGGTGATCCAGCC 18

RESULT 1704

AAH40502/C
 ID AAH40502 standard; DNA; 18 BP.

XX AAH40502;

XX 14-AUG-2001 (first entry)

XX SNP specific lower PCR primer SEQ ID 3298.
 DE Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 XX SNPs; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
 KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
 OS Homo sapiens.
 XX WO200129262-A2.
 PN 26-APR-2001.
 XX 13-OCT-2000; 2000WO-US028436.
 PF 15-OCT-1999; 99US-0160096P.
 PR (ORCH-) ORCHID BIOSCIENCES INC.
 XX Picourt-Newburg L, Pohl M;
 PI WPI; 2001-290930/30.
 DR New genotyping oligonucleotide, useful for detecting the presence,
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample.
 XX Claim 1; Page 66; 83pp; English.
 PS Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a PCR primer specific
 CC for a human SNP containing DNA sequence
 XX Sequence 18 BP; 2 A; 9 C; 3 G; 4 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 950 TGAATGCTGGAGCGGTG 967
 DB 18 TGAACCTGGAGCGGAG 1
 RESULT 1705
 AA166638
 ID AA166638 standard; DNA; 18 BP.
 XX AA166638;
 AC AA166638;
 XX

DT 07-JAN-2002 (first entry)
 XX Nucleotide sequence of a PCR primer seq Id No. 10.
 DE Protein disulfide isomerase; cell wall protein; isomerase; insulin;
 XX glucagon; interferon; calcitonin; growth hormone; PCR primer; ss.
 KW Synthetic.
 OS WO200168884-A1.
 PN 20-SEP-2001.
 XX 13-MAR-2001; 2001WO-JP001987.
 PF 14-MAR-2000; 2000JP-00070753.
 PR (ITOH-) ITOHAM FOODS INC.
 XX (UDAK/) UDAKA S.
 PA Udaoka S, Sato S, Kudo T, Oka S, Higashikuni N, Kondo M;
 PI WPI; 2001-611394/70.
 DR Production of recombinant polypeptides having correctly positioned
 XX disulfide bonds for preparation of insulin and other active substances
 PT with full natural activity.
 PT Example 1; Page 13; 61pp; Japanese.
 PS The invention provides a DNA for co-expression of a peptide containing
 CC disulfide bonds together with a protein disulfide isomerase. It has the
 CC structure 5'-(Promoter)-(SD)-(CWPsp)-(X1)-(Promoter)n-(SD)-(CWPsp)-(X2)
 CC -3', where X1 = sequence encoding a polypeptide containing disulfide
 CC bonds; X2 = sequence encoding a protein disulfide isomerase; SD = a SD
 CC sequence; CWPsp = signal peptide sequence from a cell wall protein
 CC originating in a Bacillus strain; and n = 0 or 1. Alternatively, X1 is
 CC the isomerase gene and X2 is the polypeptide gene. The DNA is used for
 CC the production of recombinant polypeptides containing disulfide bonds,
 CC such as insulin, glucagon, interferon, calcitonin and growth hormone,
 CC having full natural activity. The method produces polypeptides having
 CC accurately positioned disulfide bonds. Sequences AA166629-651 represent
 CC PCR primers used during the course of the invention
 XX Sequence 18 BP; 3 A; 8 C; 5 G; 2 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1509 CTGAATGGACCTCTCCAG 1526
 DB 1 CTGCAGGCGACCTCCAG 18
 RESULT 1706
 AA166638
 ID AA166638 standard; DNA; 18 BP.
 XX AA166638;
 AC AA166638;
 XX 05-JUN-2001 (first entry)
 DT Cycloclasticus pugetii 16S rRNA gene PCR primer, SEQ ID NO:9.
 XX 16S rRNA gene; ribosomal RNA gene; petroleum degrading bacterium;
 KW hydrocarbon; detection; quantitation; identification; oil spill;
 KW polluted environment; environmental decontamination; PCR primer; ss.
 XX Cycloclasticus pugetii.
 OS WO200114587-A1.
 PN WO200114587-A1.
 XX

PD 01-MAR-2001.
 XX
 PF 24-AUG-2000; 2000WO-JP005711.
 XX
 PF 25-AUG-1999; 99JP-00237818.
 XX
 PR (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 PA (NISH-) NISHIMATSU CONSTRUCTION CO LTD.
 PA (NYKL-) NYK LOGISTICS TECHNOLOGY INST CO LTD.
 XX
 XX Maruyama A, Higashihara T, Ishiwata H, Fujita T;
 PI WPI; 2001-218458/22.
 DR
 XX
 XX Detection and quantitation of microorganism having specific function and
 PT its gene from natural environment, with identification of petroleum-
 PT digesting bacterium cycloclasticus for treating oil spillage.
 XX
 XX Example 1; Page 25; 54pp; Japanese.
 PS
 XX The invention relates to a method for detecting, identifying and
 CC quantitating a microorganism which has a specific function, or DNA
 CC therefrom, from the environment. The method comprises broadly classifying
 CC the microorganism after serial dilution; amplifying and cloning specific
 CC gene domains using extracted DNA as a template; examining the differences
 CC between the gene domains cloned and determining their base sequences; and
 CC positively identifying the microorganism from the base sequence data. The
 CC invention also relates to a method to evaluate the function of such an
 CC organism in various of environments, especially polluted environments
 CC (particularly those contaminated with oil or harmful chemicals) using
 CC migratory analysis. The methods enable the detection and quantitation of
 CC a microorganism obtained from a polluted site in order to identify
 CC strains capable of degrading petroleum and harmful chemicals. Such
 CC organisms are particularly used for environmental decontamination. The
 CC invention is particularly concerned with the detection and quantitation
 CC of petroleum-degrading bacteria of the genus Cycloclasticus.
 CC Cycloclasticus puetii 16S rRNA gene sequences (AAF76234-AAF76237) are
 CC specifically claimed, as are probes (AAF76238- AAF76240) which hybridise
 CC to these sequences. Sequences AAF76241-AAF76242 represent Cycloclasticus
 CC puetii 16S rRNA (ribosomal RNA) gene PCR primers used in an
 CC exemplification of the invention
 XX
 SQ Sequence 18 BP; 6 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 807 AATGGAGATGTTCAGCC 824
 Db 1 AAAGGAGGTATCCAGCC 18
 RESULT 1707
 ABK24068/c
 ID ABK24068 standard; DNA; 18 BP.
 XX
 AC ABK24068;
 XX
 XX 09-APR-2002 (first entry)
 DT
 DE B7-related protein, BSL3, PCR primer #1.
 XX
 KW Human; immunosuppressive; antirheumatic; antiarthritic; antiulcer;
 KW antianemic; antiporiatic; B7-related polypeptide; BSL1; BSL2; BSL3;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
 KW Hashimoto's thyroiditis; Graves' disease; Crohn's disease; psoriasis;
 KW ulcerative colitis; pernicious anaemia; bone marrow transplantation;
 KW graft versus host disease; organ transplantation; PCR primer; ss.
 XX
 OS Homo sapiens.
 OS
 XX
 XX
 XX W0200194413-A2.
 PN

XX 13-DEC-2001.
 PD
 XX 06-JUN-2001; 2001WO-US018257.
 PF
 XX 06-JUN-2000; 2000US-0209811P.
 PR
 XX 28-FEB-2001; 2001US-0272107P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA
 XX Mikesell GE, Chang H, Finger JN, Yang G, Lu P, Zhou X, Peach R;
 PI WPI; 2002-090141/12.
 DR
 XX
 XX Nucleic acids encoding B7-related polypeptides, i.e. BSL1, BSL2, or BSL3
 PT polypeptides, useful for treating autoimmune diseases (e.g. rheumatoid
 PT arthritis, multiple sclerosis, and psoriasis), and graft versus host
 PT disease.
 XX
 XX Example 5; Page 114; 179pp; English.
 PS
 XX The invention relates to novel nucleic acids encoding B7-related
 CC polypeptides. The B7-related polypeptides include the BSL1, BSL2, or BSL3
 CC polypeptides, or their soluble fragments. The nucleic acid, polypeptide,
 CC and antibodies are useful for treating autoimmune diseases (e.g.
 CC rheumatoid arthritis, multiple sclerosis, Hashimoto's thyroiditis,
 CC Graves' disease, Crohn's disease, ulcerative colitis, pernicious anaemia
 CC and psoriasis. They may also be used to treat tissue, bone marrow, and
 CC organ transplantation, and graft versus host disease. ABK24010-ABK24093
 CC represent B7-related proteins, BSL1, BSL2 and BSL3 coding sequences and
 CC PCR primers of the invention
 XX
 SQ Sequence 18 BP; 4 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 607 GCGGTGGAGAGGCGCTTC 624
 Db 18 GACCTGGTAGAGCGCTTC 1
 RESULT 1708
 ABK51670
 ID ABK51670 standard; DNA; 18 BP.
 XX
 AC ABK51670;
 XX
 XX 30-JUL-2002 (first entry)
 DT
 DE Human ABCG5 gene PCR primer #16.
 XX
 KW Human; ABCG5; ATP-binding cassette gene 5; sitosterolemia; cholesterol;
 KW arteriosclerosis; heart disease; hypersterolemia; Alzheimer's disease;
 KW PCR; primer; ss.
 XX
 OS Homo sapiens.
 OS
 XX
 XX W0200227016-A2.
 PN
 XX 04-APR-2002.
 PD
 XX 25-SEP-2001; 2001WO-US029859.
 PF
 XX 25-SEP-2000; 2000US-0235268P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (FATE/) FATEL S B.
 PA (DEAN/) DEAN M.
 XX
 XX Patel SB, Dean M;
 PI
 XX

DR WPI; 2002-416483/44.
 XX Novel mammalian ATP-binding cassette gene 5 polypeptide, and the nucleic
 PT acid encoding the polypeptide, useful for treating sitosterolemia,
 PT arteriosclerosis and heart diseases.
 XX
 PS Example 2; Page 31; 66pp; English.
 XX
 CC The present invention relates to a new mammalian ATP-binding cassette
 CC gene 5 (ABCG5) polypeptide. The invention is useful for identifying a
 CC predisposition for developing sitosterolemia, arteriosclerosis or heart
 CC disease. The molecules of the invention are also useful for identifying a
 CC compound which alters ABCG5 activity level comprising contacting a cell
 CC culture or mammal which have ABCG5 polypeptide with a compound and
 CC measuring ABCG5 biological activity in the cell culture or in mammal,
 CC where an increase or decrease in ABCG5 biological activity compared to
 CC ABCG5 biological activity in a control cell culture or mammal not
 CC contacted with the compound, identifies a compound that increases or
 CC decreases ABCG5 activity respectively. The cell culture or mammal
 CC comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The
 CC ABCG5 biological activity, or level of ABCG5 mRNA, or level of the
 CC polypeptide in a cell culture or mammal is also compared with that of a
 CC second cell culture or mammal comprising a wild type ABCG5 polypeptide.
 CC Stimulation of ABCG5 activity is useful for treating or preventing
 CC hypersterolemia, arteriosclerosis, heart disease and/or Alzheimer's
 CC disease. The method of the invention is useful for increasing cholesterol
 CC excretion and/or decreasing cholesterol adsorption. The present nucleic
 CC acid sequence represents one of a collection (ABK51655-ABK51680) of human
 CC ABCG5 gene PCR primers
 XX
 SQ Sequence 18 BP; 3 A; 5 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 2049 TTTTCATTTTGTGAGCCT 2066
 Db 1 TTTTCATTTTGTGAGCCT 18
 RESULT 1709
 ID ABK81848
 XX ABK81848 standard; DNA; 18 BP.
 AC ABK81848;
 XX
 DT 13-AUG-2002 (first entry)
 DE Lung specific gene PCR primer #10.
 DE
 KW Lung specific gene; gene therapy; vaccine; lung cancer; cancer staging;
 KW cancer monitoring; cancer diagnosis; imaging lung cancer; metastases;
 KW PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 XX WO200218576-A2.
 PN
 PD 07-MAR-2002.
 XX
 PF 27-AUG-2001; 2001WO-US026684.
 XX
 PR 28-AUG-2000; 2000US-0228378P.
 XX
 PA (DIAD-) DIADEXUS INC.
 PA
 XX Chen S, Macina RA, Sun Y, Recipon H;
 PI WPI; 2002-434904/46.
 DR
 XX New lung specific genes and their encoded proteins, useful in gene
 PT therapy or as a vaccine for treating lung cancer, as well as for

PT measuring metastases of lung cancer, or staging, monitoring, diagnosing
 PT or imaging lung cancer.
 XX
 PS Example 5; Page 111; 206pp; English.
 XX
 CC The invention describes a new lung specific gene and it's variants. The
 CC lung specific gene proteins and genes are useful in gene therapy or as a
 CC vaccine for treating lung cancer. Lung specific genes are also useful for
 CC staging, monitoring, diagnosing or imaging lung cancer, as well as for
 CC measuring metastases of lung cancer. This sequence represents a PCR
 CC primer used in microarray analysis to isolate a lung specific gene
 CC thought to be involved in development of lung cancer
 XX
 SQ Sequence 18 BP; 3 A; 8 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1942 TTCCCACTGGCCTCAAGT 1959
 Db 1 TTCCCACTGGCCTCAAGT 18
 RESULT 1710
 ID ABS61000
 XX ABS61000 standard; DNA; 18 BP.
 AC ABS61000;
 XX
 DT 05-NOV-2002 (first entry)
 DE Human genotyping PCR primer #153.
 DE
 KW Human; ss; aminopeptidase P; XPNEP2; bradykinin receptor B1; primer;
 KW BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;
 KW kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
 KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;
 KW myocardial infarction; ventricular hypertrophy; vascular disease;
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
 KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
 KW viral infection; bacterial infection; fungal infection; COPD;
 KW Chronic obstructive pulmonary disease; enterocolitis.
 XX
 OS Homo sapiens.
 XX
 PN WO200261131-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 03-DEC-2001; 2001WO-US047235.
 XX
 PR 04-DEC-2000; 2000US-0251015P.
 PR 23-JAN-2001; 2001US-0263678P.
 PR 02-MAR-2001; 2001US-0273037P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (HUI/) HUI L.
 XX
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
 PI Swanson BN, Powell JR;
 XX WPI; 2002-619265/66.
 DR
 XX New isolated nucleic acid with at least one polymorphic position, useful
 PT for detecting, diagnosing and treating disorders such as angioedema,
 PT cancer, viral, bacterial or fungal infection, cardiovascular and
 PT autoimmune diseases.

```

PS Example 3; Page 913; 977pp; English.
XX
CC The invention relates to an isolated nucleic acid from a human gene
CC encoding aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDRB1),
CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
CC 1 (KLK1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme
CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
CC polymorphic position. Also included are (1) a probe that hybridises to a
CC polymorphic position as provided in the detailed summary of single
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
CC obtaining the sample from one or more individuals and determining the
CC nucleic acid sequence at one or more polymorphic positions in a gene
CC encoding a protein selected from the group above; (3) constructing (M2)
CC haplotypes using the genes comprising grouping at least two nucleic acids
CC ; (4) identifying (M3) an individual at risk of developing a disorder
CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
CC using the polymorphic data; (5) a library of nucleic acids, each of which
CC comprises one or more polymorphic positions within a gene encoding a
CC human protein selected from the group above; and (6) genotyping (M4) an
CC individual comprising obtaining a nucleic acid sample, determining the
CC nucleotide present in at least one polymorphic position, and comparing at
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
CC and compositions are useful for detecting, diagnosing, treating,
CC preventing various disorders such as angioedema and diseases which
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
CC disease, trachomas, and cardiovascular diseases like angina pectoris,
CC hypertension, heart failure, myocardial infarction, ventricular
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
CC artery disease, arteriosclerosis and/or atherosclerosis, and
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
CC obstructive pulmonary disease (COPD) and enterocolitis (many other
CC diseases and disorders are listed in the specification). The
CC polynucleotides are also useful for chromosome identification. Antibodies
CC against the proteins may be utilised for immunophenotyping of cell lines
CC and biological samples. The present sequence is a genotyping PCR primer
CC for the gene encoding one of the proteins listed above
XX
SQ Sequence 18 BP; 5 A; 6 C; 7 G; 0 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1457 CCAAGGAGGAGAGCCAG 1474
Dd 1 CCCACGAGGAGGAGCCAG 18
RESULT 1711
ABS60906/c
ID ABS60906 standard; DNA; 18 BP.
XX
AC ABS60906;
XX
XX 05-NOV-2002 (first entry)
DE Human genotyping PCR primer #59.
XX
XX Human; ss; aminopeptidase P; XPNEP2; bradykinin receptor B1; primer;
XX BDRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;
XX kallikrein 1; KLK1; bradykinin receptor B2; BDRB2; gene therapy;
XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
XX polycystic; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
XX cardiovascular disease; angina pectoris; hypertension; heart failure;
XX myocardial infarction; ventricular hypertrophy; vascular disease;
XX aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
XX autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
XX viral infection; bacterial infection; fungal infection; COPD;
XX Chronic obstructive pulmonary disease; enterocolitis.
XX
OS Homo sapiens.
XX
PN WO200261131-A2.
XX
PD 08-AUG-2002.
XX
PF 03-DEC-2001; 2001WO-US047235.
XX
PR 04-DEC-2000; 2000US-0251015P.
PR 23-JAN-2001; 2001US-0263678P.
PR 02-MAR-2001; 2001US-0273037P.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX (TSUC/) TSUCHIHASHI Z.
XX (HUIL/) HUI L.
XX
XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
XX Swanson BN, Powell JR;
XX WPI; 2002-619265/66.
XX
XX New isolated nucleic acid with at least one polymorphic position, useful
XX for detecting, diagnosing and treating disorders such as angioedema,
XX cancer, viral, bacterial or fungal infection, cardiovascular and
XX autoimmune diseases.
XX
XX Example 3; Page 898; 977pp; English.
XX
XX The invention relates to an isolated nucleic acid from a human gene
XX encoding aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDRB1),
XX tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
XX 1 (KLK1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme
XX 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
XX polymorphic position. Also included are (1) a probe that hybridises to a
XX polymorphic position as provided in the detailed summary of single
XX nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
XX sequence; (2) analysing (M1) at least one nucleic acid sample comprising
XX obtaining the sample from one or more individuals and determining the
XX nucleic acid sequence at one or more polymorphic positions in a gene
XX encoding a protein selected from the group above; (3) constructing (M2)
XX haplotypes using the genes comprising grouping at least two nucleic acids
XX ; (4) identifying (M3) an individual at risk of developing a disorder
XX upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
XX using the polymorphic data; (5) a library of nucleic acids, each of which
XX comprises one or more polymorphic positions within a gene encoding a
XX human protein selected from the group above; and (6) genotyping (M4) an
XX individual comprising obtaining a nucleic acid sample, determining the
XX nucleotide present in at least one polymorphic position, and comparing at
XX least one position with a known data set. The genes, (M1, M2, M3 and M4)
XX and compositions are useful for detecting, diagnosing, treating,
XX preventing various disorders such as angioedema and diseases which
XX involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
XX disease, trachomas, and cardiovascular diseases like angina pectoris,
XX hypertension, heart failure, myocardial infarction, ventricular
XX hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
XX artery disease, arteriosclerosis and/or atherosclerosis, and
XX hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
XX arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
XX obstructive pulmonary disease (COPD) and enterocolitis (many other
XX diseases and disorders are listed in the specification). The
XX polynucleotides are also useful for chromosome identification. Antibodies
XX against the proteins may be utilised for immunophenotyping of cell lines
XX and biological samples. The present sequence is a genotyping PCR primer
XX for the gene encoding one of the proteins listed above
XX
SQ Sequence 18 BP; 6 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1010 CAGCTGTGCGCCCTGGATA 1027
Dd 1 CAGCTGTGCGCCCTGGATA 1027

```



```
Db      18 CGCGTGTGGCCTTGATA 1
RESULT 1712
ABL46097/c
ID      ABL46097 standard; DNA; 18 BP.
XX
AC      ABL46097;
XX
XX
DT      26-APR-2002 (first entry)
XX
DE      Bridging oligonucleotide capture probe SEQ ID NO:64.
XX
KW      Nucleic acid accessible hybridisation site; detection; hybridisation;
KW      characterisation; identification; nucleic acid structure; diagnosis;
KW      PCR primer; probe; ss.
XX
OS      Synthetic.
XX
PN      WO200198537-A2.
XX
PD      27-DEC-2001.
XX
PF      15-JUN-2001; 2001WO-US019401.
XX
PR      17-JUN-2000; 2000US-0212308P.
XX
PR      15-JUN-2001; 2001US-00212308.
XX
PA      (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI      Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;
XX
DR      WPI; 2002-049698/06.
XX
PT      Identifying oligonucleotides hybridizing to nucleic acids containing
PT      secondary structure, useful in clinical diagnosis, comprises identifying
PT      primers that interact with the target to form an extension product under
PT      amplification conditions.
XX
PS      Example 8; Fig 17C; 409pp; English.
XX
CC      The present invention describes a method for identifying oligonucleotides
CC      with desired hybridisation properties to nucleic acid targets containing
CC      secondary structure. The method comprises amplifying a target nucleic
CC      acid having at least one accessible and one inaccessible site. Primers
CC      that form an extension product are identified as the oligonucleotides
CC      which can interact with the folded target nucleic acid. Oligonucleotides
CC      from the present invention can be used in novel detection methods for
CC      clinical diagnostic purposes, including the detection and identification
CC      of pathogenic organisms (e.g. HIV). The method allows the ability to
CC      rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
CC      sequences used in the exemplification of the present invention
XX
SQ      Sequence 18 BP; 2 A; 8 C; 3 G; 5 T; 0 U; 0 Other;
Query Match      0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1846 TTCTAGAGGGGFGGCTG 1863
Db      18 TCCAGAGGGGAGGCTG 1
RESULT 1713
AAL44982
ID      AAL44982 standard; DNA; 18 BP.
XX
AC      AAL44982;
XX
XX
DT      14-MAY-2002 (first entry)
XX
DE      Enterobacter 16S rRNA gene PCR primer #2.
XX
```

```
XX
KW      16S rRNA; bacteria cellulose; oil recovery; PCR; primer; ss.
XX
OS      Enterobacter sp.
XX
PN      JP2001321164-A.
XX
XX
PD      20-NOV-2001.
XX
PF      12-MAY-2000; 2000JP-00140767.
XX
PR      12-MAY-2000; 2000JP-00140767.
XX
PA      (SEKI-) SEKIYU KODAN.
XX
PA      (CHPE-) CHINA PETROLEUM GAS CO LTD.
XX
DR      WPI; 2002-151504/20.
XX
XX
PT      A new microbe producing bacteria-cellulose and enhanced oil recovery by
PT      using it.
XX
PS      Example 3; Page 9; 20pp; Japanese.
XX
CC      The present invention relates to a microbe of the Enterobacter genus
CC      producing bacteria-cellulose and having a 16S-rRNA gene containing the
CC      sequence shown in AAL44980. The microbe is useful for oil recovery. The
CC      present sequence is a PCR primer for the gene of the invention
XX
SQ      Sequence 18 BP; 6 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
Query Match      0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      807 AATGGAGATGTTCCAGCC 824
Db      1 AAAGGAGGTGATCCAGCC 18
RESULT 1714
ABS98357/c
ID      ABS98357 standard; DNA; 18 BP.
XX
AC      ABS98357;
XX
XX
DT      23-DEC-2002 (first entry)
XX
DE      Human multidrug resistance associated protein 3 PCR primer #23.
XX
KW      Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; PCR;
KW      cytochrome P450 A2; CYP4501A2; cytochrome P450 O2E; CYP45002E1; LTF;
KW      adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW      aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW      cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW      epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW      glucathione-S-transferase 12; GSTI2; histamine-N-methyl transferase;
KW      HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW      NADPH quinone oxidoreductase 2; NQO2; sulfoxotransferase thermolabile; STM;
KW      UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW      UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW      multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW      multidrug resistance associated protein 3; cancer; prostate;
KW      acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW      altered drug metabolism; cardiovascular function; colorectal tumour;
KW      central nervous system; pulmonary; immunological.
XX
OS      Homo sapiens.
XX
PN      WO200257410-A2.
XX
XX
PD      25-JUL-2002.
XX
XX
PD      28-NOV-2001; 2001WO-US044838.
```

XX PR 28-NOV-2000; 2000US-00724389.
 XX PA (DNAS-) DNA SCI LAB INC.
 XX PI Guida M, Hall J;
 XX XX WPI; 2002-698522/75.
 DR Isolated nucleic acid molecules having polymorphisms in known human genes
 XX e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
 PT for locating, identifying and characterizing the genes responsible for
 PT disorder-related traits.
 XX Example 24; Page 151; 714pp; English.
 XX This invention relates to the sequence of an isolated nucleic acid
 CC molecule comprising at least one base variation from that of a known
 CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),
 CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
 CC (ARNT), cathepsin S (CNSS), cyclooxygenase 2 (COX2), diazepam binding
 CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
 CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
 CC transferase (HNMT), kallikrein 2 (KLK2), nicotinamide-N-methyl
 CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
 CC sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
 CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
 CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
 CC (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
 CC The polymorphisms in the human genes cited in the invention are useful as
 CC genetic linkage markers for locating and characterizing the genes that
 CC are responsible for specific traits within the genome and eventually
 CC identifying the genes responsible for a variety of disorder-related
 CC traits as a result of their e.g., overexpression, constitutive
 CC expression, mutation or underexpression, which may be used in diagnosing
 CC and/or treating the disorders. The nucleic acid molecules comprising the
 CC polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502B1,
 CC ARNT, EPHX2, GST12, NNMT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
 CC metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
 CC used to screen for altered cardiovascular function, in COX2 for altered
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
 CC nervous system function, in FLAP and HNMT for altered pulmonary,
 CC immunological or haematological function, in KLK2 for altered serine
 CC protease activity in the prostate, in LTF for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
 CC peripheral nervous system function. The present sequence represents a PCR
 CC primer used to amplify the sequences of the invention
 XX SQ Sequence 18 BP; 7 A; 2 C; 7 G; 2 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1990 GTCTTCCTCCATTTCTGC 2007
 DB 18 GACTTCCTCCATTTCTGC 1
 RESULT 1715
 ABN88153
 ID ABN88153 standard; DNA; 18 BP.
 XX AC ABN88153;
 XX 13-AUG-2002 (first entry)
 DT Human; human leukocyte antigen; HLA; genotype; polymorphism;
 KW Human; human leukocyte antigen; HLA; genotype; polymorphism;

DE Rabbit beta-globin related oligonucleotide sequence #1.
 XX RNA analysis; identification; RNA molecule; antibacterial; virucide;
 KW fungicide; cytostatic; antisense therapy; cancer; infection; rabbit;
 KW beta-globin; ss.
 XX Oryctolagus cuniculus.
 OS Synthetic.
 XX WO200224950-A2.
 XX 28-MAR-2002.
 PD 25-SEP-2001; 2001WO-SE002054.
 PF 25-SEP-2000; 2000US-0235029P.
 XX (NEUR-) NEUROMICS INC.
 XX Liang Z, Zhang H, Wahlestedt C;
 XX WPI; 2002-404959/43.
 DR Identifying accessible region (AR) of native RNA, involves selecting from
 PT oligonucleotide population, an oligonucleotide binding to AR, sequencing
 PT randomized portion of oligonucleotide, and identifying sequence of AR.
 XX Example; Fig 6; 41pp; English.
 PS The present invention describes a method (M1) for the single-cycle
 CC identification of an accessible region (AR) of native RNA (I). The method
 CC comprises providing an in vitro reaction mixture comprising (I) and a
 CC population of oligonucleotides (II), each having a randomised portion
 CC that can bind to a complementary AR of (I), if present, selecting a (II)
 CC that binds to an AR, sequencing the randomised portion of (II), and
 CC identifying the nucleotide sequence of the AR. An AR can have virucide,
 CC antibacterial, fungicide and cytostatic activities, and can be used in
 CC antisense therapy. The method of the invention is used for identifying an
 CC AR of a native RNA preferably mRNA. Identifying an AR of mRNA is useful
 CC for manufacturing an antisense oligonucleotide for the downregulation of
 CC expression of an mRNA molecule which involves identifying an AR on an
 CC mRNA using the method and synthesising an oligonucleotide complementary
 CC to AR. (M1) is useful for making an antisense oligonucleotide which
 CC involves identifying an AR of a native RNA by (M1) and synthesising the
 CC antisense oligonucleotide that is complementary to the AR. The antisense
 CC oligonucleotides are useful for treating disorders associated with
 CC aberrant gene expression, such as cancer and disorders associated with
 CC expression of foreign genes such as infection with bacterial, viral or
 CC fungal pathogen. The present sequence represents an oligonucleotide which
 CC is used in the exemplification of the present invention
 XX SQ Sequence 18 BP; 3 A; 4 C; 2 G; 9 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1985 TGCTGTCTTCTCTCTAAT 2002
 DB 1 TGCTGTCTTCTCTAAT 18
 RESULT 1716
 ABL30682
 ID ABL30682 standard; DNA; 18 BP.
 XX AC ABL30682;
 XX 21-MAR-2002 (first entry)
 DT Human HLA genotyping oligonucleotide SEQ ID NO 171.
 DE Human; human leukocyte antigen; HLA; genotype; polymorphism;
 XX Human; human leukocyte antigen; HLA; genotype; polymorphism;

```

KW immunogenetic; transplantation; genetic disease; ss.
XX Homo sapiens.
XX WO200192572-A1.
XX 06-DEC-2001.
XX 01-JUN-2001; 2001WO-JP004662.
XX 01-JUN-2000; 2000JP-00164798.
XX (NISN ) NISSHINBO IND INC.
XX (SYST-) SYSTEM RES INC.
XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
XX WPI; 2002-122074/16.
XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
XX individuals e.g. by determining immunogenetic differences when
XX transplanting between them.
XX Claim 10; Page 125; 345pp; Japanese.
XX The invention relates to a typing kit for judging human leukocyte antigen
XX (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
XX oligonucleotides (ABL30512-ABL31809) originating in the sequences of
XX genes e.g. belonging to HLA class I antigens on human genome and
XX containing gene polymorphisms as alloantigens have been immobilised as
XX primers for amplification of cleaved nucleic acids relating to gene
XX polymorphisms. The method is useful for judging HLA genotypes of
XX individuals by determining immunogenetic differences before transplanting
XX between them, providing genetic information to decide compatibility of
XX organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
XX pancreas, Langerhans islet in pancreas and cornea, susceptibility
XX diagnosis of genetic diseases and identifying individuals
XX Sequence 18 BP; 3 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 569 GGGTGCTGTACATTGACA 586
Db 1 GGGTGGCGTACCTGGACA 18
||||| ||||| |||||

RESULT 1717
ABL30856
ID ABL30856 standard; DNA; 18 BP.
XX ABL30856;
XX ABL30856;
XX 21-MAR-2002 (first entry)
XX Human HLA genotyping oligonucleotide SEQ ID NO 345.
XX Human; human leukocyte antigen; HLA; genotype; polymorphism;
XX immunogenetic; transplantation; genetic disease; ss.
XX Homo sapiens.
XX WO200192572-A1.
XX 06-DEC-2001.
XX 01-JUN-2001; 2001WO-JP004662.
XX 01-JUN-2000; 2000JP-00164798.
XX (NISN ) NISSHINBO IND INC.

immunogenetic; transplantation; genetic disease; ss.
XX Homo sapiens.
XX WO200192572-A1.
XX 06-DEC-2001.
XX 01-JUN-2001; 2001WO-JP004662.
XX 01-JUN-2000; 2000JP-00164798.
XX (NISN ) NISSHINBO IND INC.

(SYST-) SYSTEM RES INC.
XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
XX WPI; 2002-122074/16.
XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
XX individuals e.g. by determining immunogenetic differences when
XX transplanting between them.
XX Claim 10; Page 158; 345pp; Japanese.
XX The invention relates to a typing kit for judging human leukocyte antigen
XX (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
XX oligonucleotides (ABL30512-ABL31809) originating in the sequences of
XX genes e.g. belonging to HLA class I antigens on human genome and
XX containing gene polymorphisms as alloantigens have been immobilised as
XX primers for amplification of cleaved nucleic acids relating to gene
XX polymorphisms. The method is useful for judging HLA genotypes of
XX individuals by determining immunogenetic differences before transplanting
XX between them, providing genetic information to decide compatibility of
XX organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
XX pancreas, Langerhans islet in pancreas and cornea, susceptibility
XX diagnosis of genetic diseases and identifying individuals
XX Sequence 18 BP; 5 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1064 TTGAATACCTTGACACAG 1081
Db 1 TTGAATACCTTGATCCAG 18
||||| ||||| |||||

RESULT 1718
ABK98126
ID ABK98126 standard; DNA; 18 BP.
XX ABK98126;
XX ABK98126;
XX 07-OCT-2002 (first entry)
XX Triple helix forming associated oligonucleotide #15.
XX Triple-helix formation; purine-rich target sequence; double-helix DNA;
XX gene expression; regulatory sequence; pathogenic double-stranded DNA;
XX pathogenic bacteria; virus; replication; virulence; cancer;
XX oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX Synthetic.
XX US6403302-B1.
XX 11-JUN-2002.
XX 16-DEC-1993; 93US-00168920.
XX 17-SEP-1992; 92US-00946976.
XX (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX Dervan PB, Beal PA;
XX WPI; 2002-536030/57.
XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
XX oligonucleotide which binds in parallel and antiparallel orientation,
XX respectively, for targeting sequences on alternate strands of DHNA to
XX control gene expression.
XX Example 7; Col 41; 108pp; English.

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XX The present invention relates to methods and oligonucleotides for forming
 CC a triple-helix comprising a double helical nucleic acid comprising first
 CC and second substantially complementary strands, and an oligonucleotide
 CC bound to a purine-rich target sequence within the double helical nucleic
 CC acid, where the oligonucleotide binds in a parallel and antiparallel
 CC orientation, respectively, to target sequences on alternate strands of
 CC the double helical nucleic acid. The method has therapeutic applications,
 CC where gene expression is controlled by selective triple-helix formation
 CC within expression regulatory sequences of a target gene. The
 CC oligonucleotides can be used to form triple-helices, and are useful to
 CC detect the presence or absence of specific sequences within genomic DNA
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be
 CC selected to specifically bind to pathogenic double-stranded DNA including
 CC specific sequences required by pathogenic bacteria or viruses for
 CC replication or virulence, reducing their pathogenicity. Alternatively,
 CC the oligonucleotide can be chosen to target a unique sequence of the
 CC pathogen which is not found in the genome of pathogen's host. The
 CC oligonucleotides can be used in cancer treatment by way of triple-helix
 CC suppression of specific oncogenes including those of endogenous or viral
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-
 CC helices with such sequences in cancerous cells containing the activated
 CC oncogene, so preferentially killing or repressing the cancer causing
 CC cell. The present sequence represents an oligonucleotide used in the
 CC methods of the present invention

XX SQ Sequence 18 BP; 0 A; 2 C; 0 G; 14 T; 0 U; 2 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 77.8%; Pred. No. 1.1e+03;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1578 TATATTTCTATTCTCT 1595
 ||:|||||:|||||
 Db 1 TTTDTTTCTTTTCT 18

RESULT 1719
 ABT08399/C
 ID ABT08399 standard; DNA; 18 BP.
 XX AC ABT08399;
 XX DT 27-NOV-2002 (first entry)
 XX DE Human integrin beta-3 promoter PCR primer SEQ ID NO: 34.
 XX KW Human; cyclin-dependent kinase; CDK; cyclin-dependent kinase inhibitor;
 KW inhibitor; cancer; age-related disease; promoter; atherosclerosis;
 KW cyrostatic; antiarteriosclerotic; nootropic; neuroprotective;
 KW nephrotropic; antiarthritic; arthritis; renal disease;
 KW Alzheimer's disease; amyloidosis; PCR; primer; ss.
 XX OS Homo sapiens.
 XX PN WO200266681-A2.
 XX DT 29-AUG-2002.
 XX PF 01-FEB-2002; 2002WO-US002784.
 XX PR 01-FEB-2001; 2001US-0265840P.
 XX PR 21-MAY-2001; 2001US-00861925.
 XX PA (UNII) UNIV ILLINOIS FOUND.
 XX PI Poole J, Roninson IB, Chang B;
 XX WFPI; 2002-674960/72.
 XX New recombinant expression construct, useful for identifying compounds
 PT that inhibit the induction of genes induced by cyclin-dependent kinase
 PT inhibitors for preventing or treating cancer, renal failure or

PT Alzheimer's disease.
 XX Example 8; Page 126; 137pp; English.
 XX The present invention relates to a recombinant expression construct
 CC encoding a reporter gene operably linked to a promoter from a mammalian
 CC gene induced by a cyclin-dependent kinase (CDK) inhibitor. The construct
 CC is useful for identifying compounds that inhibit the induction of genes
 CC induced by CDK inhibitors. The compounds are useful for preventing or
 CC treating a disease caused by CDK inhibitor induced gene expression, e.g.
 CC cancer other than colon cancer, renal failure, Alzheimer's disease,
 CC amyloidosis, age-related diseases, atherosclerosis or arthritis. The
 CC present sequence is a PCR primer used to amplify a human promoter
 CC suitable for use in the construct of the invention

XX SQ Sequence 18 BP; 5 A; 8 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1660 TCAGGCGAGCTGTCTGG 1677
 ||:|||||:|||||
 Db 18 TCTGGCGGACTGTCTGG 1

RESULT 1720
 ABZ95312
 ID ABZ95312 standard; DNA; 18 BP.
 XX AC ABZ95312;
 XX DT 17-OCT-2003 (first entry)
 XX DE Human IL-6 receptor fragment no.1176.
 XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX OS Homo sapiens.
 XX PN WO200285308-A2.
 XX DT 31-OCT-2002.
 XX PF 23-APR-2002; 2002WO-US013135.
 XX PR 24-APR-2001; 2001US-0286137P.
 XX PA (EPIG-) EPIGENESIS PHARM INC.
 XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 XX PI Miller S, Tang L, Shahabuddin S;
 XX WFPI; 2003-229219/22.
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiqunone.
 XX Disclosure; SEQ ID NO 10554; 872pp; English.
 XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an

CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 18 BP; 0 A; 4 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 377 GCGTGTTCGATCTGTC 394
 ||| ||||| |||||
 Db 1 GCCCGTTGTTGTTGTC 18

RESULT 1721
 ABZ68641/C
 ID ABZ68641 standard; DNA; 18 BP.

XX AC ABZ68641;

XX DT 16-MAY-2003 (first entry)

XX DE Primer for extension of K121 antibody light chain variable region.

XX KW K121 antibody; K121-like antibody; kappa-type myeloma cell;

KW kappa-type multiple myeloma; haematopoietic cell transplantation;

KW apoptosis; kappa myeloma antigen; PCR; primer; ss.

XX OS Mus musculus.

XX PN WO2003004056-A1.

XX PD 16-JAN-2003.

XX PF 05-JUL-2002; 2002WO-A0000896.

XX PR 06-JUL-2001; 2001AU-00006179.

XX PA (PACM-) PACMAB PTY LTD.

XX PI Raison RL, Dunn RD, Choo BHA;

XX DR WPI; 2003-210317/20.

XX PT Treating kappa-type multiple myeloma in a subject by administering a K121
 XX -like antibody not conjugated to a toxin or a cytolytic agent.

XX PS Example 8; Fig 9e; 65pp; English.

XX CC PCR primers ABZ68638-42 were used for extension of the murine K121
 CC antibody light chain variable region. The primers were used to construct
 CC a K121-like antibody by oligonucleotide assembly using PCR. The K121-like
 CC antibody competes with K121 for binding to kappa-type myeloma cells. The
 CC K121-like antibody is used in the method of the invention. The
 CC specification describes a method for treating kappa-type multiple myeloma
 CC in a subject, comprising administering a K121-like antibody which is not
 CC conjugated to a toxin or a cytolytic agent. The method is useful for
 CC treating kappa-type multiple myeloma, autologous haematopoietic cell
 CC transplantation, killing kappa-type myeloma cells in a mixed population
 CC of cells and inducing apoptosis in kappa myeloma antigen (KMA) bearing
 CC cells

XX SQ Sequence 18 BP; 5 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 636 CCGGGTCATGACTGTGTC 653
 ||| ||||| |||||
 Db 18 CTGGGTCAACAGATGTC 1

RESULT 1722

ABZ11084

ID ABZ11084 standard; DNA; 18 BP.

XX AC ABZ11084;

XX DT 16-JAN-2003 (first entry)

XX DE Haematopoietic cell proliferation disorder related oligonucleotide #1224.

XX KW Human; haematopoietic cell proliferation disorder; cytostatic;

KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;

KW cytosine methylation state; probe; primer; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200277272-A2.

XX PD 03-OCT-2002.

XX PF 26-MAR-2002; 2002WO-EP003401.

XX PR 26-MAR-2001; 2001US-0278333P.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;

PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;

PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;

PI Schwöpe I, Ziebarth H;

XX DR WPI; 2003-018942/01.

XX PT Detecting and differentiating between hematopoietic cell proliferative
 XX disorders, comprises contacting a target nucleic acid with a reagent that
 XX distinguishes between methylated and non-methylated CpG dinucleotides.

XX PS Claim 15; Page 65; 117pp; English.

XX CC The present invention describes a method for detecting and
 CC differentiating between haematopoietic cell proliferative disorders
 CC associated with at least 1 gene and/or their regulatory regions in a
 CC subject. The method comprises contacting a target nucleic acid in a
 CC biological sample obtained from the subject with at least 1 reagent,
 CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118
 CC represent specifically claimed nucleotide sequences from the present
 CC invention. Oligonucleotides from the present invention can be used: for
 CC differentiating between healthy haematopoietic cells and proliferative
 CC disorder haematopoietic cells; for differentiating between acute
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of haematopoietic cell proliferation disorder related DNA
 CC sequences. The nucleotide sequences from the present invention can also
 CC be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC haematopoietic cell proliferative disorders. The present method enables a
 CC highly specific classification of haematopoietic cell proliferative

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CC disorders allowing for improved and informed treatment of patients
XX
SQ Sequence 18 BP; 2 A; 0 C; 5 G; 11 T; 0 U; 0 Other;
    Query Match      0.6%; Score 13.2; DB 1; Length 18;
    Best Local Similarity 83.3%; Pred. No. 1.1e+03;
    Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1916 TTTTAGATTGGTTCGTT 1933
Db 1 TTTTATATTCGGTGTGTT 18

RESULT 1723
AAD56471/c
ID AAD56471 standard; DNA; 18 BP.
XX
AC AAD56471;
XX
DT 07-AUG-2003 (first entry)
XX
DE Target DNA used in the exemplification of the invention.
XX
KW Acyclic linker; gene expression; gene therapy; ds.
XX
OS Unidentified.
XX
FN WO2003037909-A1.
XX
PD 08-MAY-2003.
XX
PF 29-OCT-2002; 2002WO-CA001628.
XX
PR 29-OCT-2001; 2001US-0330719P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX
DR WPI; 2003-421516/39.
XX
PT Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS Example 4; Fig 3; 104pp; English.
XX
CC The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner, for hybridising to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is a target DNA, used in the exemplification of the invention
XX
SQ Sequence 18 BP; 12 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
    Query Match      0.6%; Score 13.2; DB 1; Length 18;
    Best Local Similarity 83.3%; Pred. No. 1.1e+03;
    Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1577 TTATATTTTCTATTTC 1594
Db 18 TTATATTTTCTATTCC 1

RESULT 1724
AAD56442
ID AAD56442 standard; DNA; 18 BP.
XX
AC AAD56442;
XX
DT 07-AUG-2003 (first entry)
XX
DE 2'F-ANA antisense oligo #7, to elicit RNase H degradation of target RNA.
XX
KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
XX
OS antisense; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers

```

```

XX
AC AAD56442;
XX
DT 07-AUG-2003 (first entry)
XX
DE CAT antisense oligo #1, to elicit RNase H degradation of target RNA.
XX
KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
XX
OS antisense; ss.
XX
OS Unidentified.
XX
FN WO2003037909-A1.
XX
PD 08-MAY-2003.
XX
PF 29-OCT-2002; 2002WO-CA001628.
XX
PR 29-OCT-2001; 2001US-0330719P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX
DR WPI; 2003-421516/39.
XX
PT Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS Example 2; Fig 3; 104pp; English.
XX
CC The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner, for hybridising to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
XX
SQ Sequence 18 BP; 2 A; 4 C; 0 G; 12 T; 0 U; 0 Other;
    Query Match      0.6%; Score 13.2; DB 1; Length 18;
    Best Local Similarity 83.3%; Pred. No. 1.1e+03;
    Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1577 TTATATTTTCTATTTC 1594
Db 1 TTATATTTTCTATTCC 18

RESULT 1725
AAD56452
ID AAD56452 standard; DNA; 18 BP.
XX
AC AAD56452;
XX
DT 07-AUG-2003 (first entry)
XX
DE 2'F-ANA antisense oligo #7, to elicit RNase H degradation of target RNA.
XX
KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
XX
OS antisense; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers

```

FT modified_base 1. .2
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT 3
FT modified_base
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinoadenosine"
FT 4
FT modified_base
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT 5
FT modified_base
FT /tag= d
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinoadenosine"
FT 6. .11
FT modified_base
FT /tag= e
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT 12
FT modified_base
FT /tag= f
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabincytidine"
FT 13. .15
FT modified_base
FT /tag= g
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT 16. .18
FT modified_base
FT /tag= h
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabincytidine"

WO2003037909-A1.

08-MAY-2003.

29-OCT-2002; 2002WO-CA001628.

29-OCT-2001; 2001US-0330719P.

(UYMC-) UNIV MCGILL.

Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;

WPI; 2003-421516/39.

Novel acyclic linker-containing oligonucleotide useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system, comprises a modified deoxyribonucleotide.

Example 2; Page 49; 104pp; English.

The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified deoxyribonucleotide. Oligonucleotides of the invention are useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequence-specific manner, for hybridising to and inducing cleavage of complementary mRNA or viral RNA, to hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is an antisense oligo used to elicit human RNase (ribonuclease) H degradation of target RNA. This sequence is used in the exemplification of the invention

Sequence 18 BP; 2 A; 4 C; 0 G; 12 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1577 TTATATTTCTATTTCTC 1594
|||||
Db 1 TTATATTTCTTTCTCC 18

RESULT 1726

AAD56445

ID AAD56445 standard; DNA; 18 BP.

XX AAD56445;

XX

DT 07-AUG-2003 (first entry)

XX

DE Antisense oligo #3, to elicit RNase H degradation of target RNA.

XX

KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;

KW antisense; ss.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT misc_feature

FT 9..10

FT /tag= a

FT /note= "Bases 9 and 10 are linked by a butanediol linker which is represented as B in page 49 of the specification"

XX

PN WO2003037909-A1.

XX

PD 08-MAY-2003.

XX

PF 29-OCT-2002; 2002WO-CA001628.

XX

PR 29-OCT-2001; 2001US-0330719P.

XX

PA (UYMC-) UNIV MCGILL.

XX

PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;

XX

XX WPI; 2003-421516/39.

DR

Novel acyclic linker-containing oligonucleotide useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system, comprises a modified deoxyribonucleotide.

Example 2; Page 91; 104pp; English.

The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified deoxyribonucleotide. Oligonucleotides of the invention are useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequence-specific manner, for hybridising to complementary RNA such as cellular mRNA or viral RNA, to hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is an antisense oligo used to elicit human RNase (ribonuclease) H degradation of target RNA. This sequence is used in the exemplification of the invention

Sequence 18 BP; 2 A; 4 C; 0 G; 12 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1577 TTATATTTCTATTTCTC 1594

|||||

Db 1 TTATATTTCTTTCTCC 18

RESULT 1727

AAD56456
ID AAD56456 standard; DNA; 18 BP.
XX
AC AAD56456;
XX
DT 07-AUG-2003 (first entry)
XX
DE 2'-ANA antisense oligo #11, to elicit RNase H degradation of target RNA.
XX
KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW antisense; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 1..2
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT modified_base 3
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinoadenosine"
FT modified_base 4
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT modified_base 5
FT /*tag= d
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinoadenosine"
FT modified_base 6..11
FT /*tag= e
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT misc_feature 9..10
FT /*tag= f
FT /note= "Bases 9 and 10 are linked by a butanediol linker
FT which is represented as B in page 49 and X in page 64 of
FT the specification"
FT modified_base 12
FT /*tag= g
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabincytidine"
FT modified_base 13..15
FT /*tag= h
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT modified_base 16..18
FT /*tag= i
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabincytidine"
FT
FT
XX W02003037909-A1.
XX
XX 08-MAY-2003.
XX
XX 29-OCT-2002; 2002WO-CA001628.
XX
XX 29-OCT-2001; 2001US-0330719P.
XX (UYMC-) UNIV MCGILL.
XX
XX Damha MJ, Viarovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
XX decreasing translation, reverse transcription and/or replication of a
XX target RNA in a system, comprises a modified deoxyribonucleotide.
XX
XX Example 2; Page 49; 104pp; English.
XX

CC The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner for hybridising to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
CC of the invention
XX

SQ Sequence 18 BP; 2 A; 4 C; 0 G; 12 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1577 TTATATTTCTATTTTC 1594
Db 1 TTATATTTTCTTTCCC 18
|||||

RESULT 1728

AAD56455

ID AAD56455 standard; DNA; 18 BP.

XX AAD56455;

XX 07-AUG-2003 (first entry)

DE 2'-F-ANA antisense oligo #10, to elicit RNase H degradation of target RNA.

KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW antisense; ss.

OS Unidentified.

FH Key Location/Qualifiers

FT modified_base 1..2

FT /*tag= a

FT /mod_base= OTHER

FT /note= "2'-deoxy-2'-fluoroarabinothymidine"

FT modified_base 3

FT /*tag= b

FT /mod_base= OTHER

FT /note= "2'-deoxy-2'-fluoroarabinoadenosine"

FT modified_base 4

FT /*tag= c

FT /mod_base= OTHER

FT /note= "2'-deoxy-2'-fluoroarabinothymidine"

FT modified_base 5

FT /*tag= d

FT /mod_base= OTHER

FT /note= "2'-deoxy-2'-fluoroarabinoadenosine"

FT modified_base 6..9

FT /*tag= e

FT /mod_base= OTHER

FT /note= "2'-deoxy-2'-fluoroarabinothymidine"

FT modified_base 11

FT /*tag= f

FT /mod_base= OTHER

FT /note= "2'-deoxy-2'-fluoroarabinothymidine"

FT modified_base 12

FT /*tag= g

FT /mod_base= OTHER

FT /note= "2'-deoxy-2'-fluoroarabincytidine"

FT modified_base 13..15

FT /*tag= h

FT /mod_base= OTHER

FT /note= "2'-deoxy-2'-fluoroarabinothymidine"


```

FT modified_base 16..18
FT /*tag= i
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinocytidine"
XX
XX WO2003037909-A1.
XX
XX 08-MAY-2003.
XX
XX 29-OCT-2002; 2002WO-CR001628.
XX
XX 29-OCT-2001; 2001US-0330719P.
XX (UYMC-) UNIV MCGILL.
XX
XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
XX decreasing translation, reverse transcription and/or replication of a
XX target RNA in a system, comprises a modified deoxyribonucleotide.
XX
XX Example 2; Page 49; 104pp; English.
XX
XX The invention relates to an acyclic linker-containing oligonucleotide
XX comprising at least one modified deoxyribonucleotide. Oligonucleotides of
XX the invention are useful for preventing or decreasing translation,
XX reverse transcription and/or replication of a target RNA in a system.
XX They are useful for selectively preventing gene expression in a sequence-
XX specific manner, for hybridising to complementary RNA such as cellular
XX mRNA or viral RNA, to hybridise to and induce cleavage of complementary
XX RNA. They are also useful therapeutically in formulations or medicaments
XX to prevent or treat a disease characterised by the expression of a
XX particular target RNA. The invention is used in gene therapy. The present
XX sequence is an antisense oligo used to elicit human RNase (ribonuclease)
XX H degradation of target RNA. This sequence is used in the exemplification
XX of the invention
XX
XX Sequence 18 BP; 2 A; 4 C; 0 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 18;
XX Best Local Similarity 83.3%; Pred. No. 1.1e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1577 TTATATTTTCTATTCTC 1594
XX ||||| |||||
XX 1 TTATATTTTCTTTCC 18
XX
XX RESULT 1729
XX AAD56467/c
XX ID AAD56467 standard; RNA; 18 BP.
XX
XX AC AAD56467;
XX
XX 07-AUG-2003 (first entry)
XX
XX Target RNA #2 used in the exemplification of the invention.
XX
XX Acyclic linker; gene expression; gene therapy; ss.
XX
XX Unidentified.
XX
XX WO2003037909-A1.
XX
XX 08-MAY-2003.
XX
XX 29-OCT-2002; 2002WO-CR001628.
XX
XX 29-OCT-2001; 2001US-0330719P.
XX (UYMC-) UNIV MCGILL.
XX

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XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
XX decreasing translation, reverse transcription and/or replication of a
XX target RNA in a system, comprises a modified deoxyribonucleotide.
XX
XX Example 2; Page 50; 104pp; English.
XX
XX The invention relates to an acyclic linker-containing oligonucleotide
XX comprising at least one modified deoxyribonucleotide. Oligonucleotides of
XX the invention are useful for preventing or decreasing translation,
XX reverse transcription and/or replication of a target RNA in a system.
XX They are useful for selectively preventing gene expression in a sequence-
XX specific manner, for hybridising to complementary RNA such as cellular
XX mRNA or viral RNA, to hybridise to and induce cleavage of complementary
XX RNA. They are also useful therapeutically in formulations or medicaments
XX to prevent or treat a disease characterised by the expression of a
XX particular target RNA. The invention is used in gene therapy. The present
XX sequence is a target RNA, used in the exemplification of the invention
XX
XX Sequence 18 BP; 12 A; 0 C; 4 G; 0 T; 2 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 18;
XX Best Local Similarity 83.3%; Pred. No. 1.1e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1577 TTATATTTTCTATTCTC 1594
XX ||||| |||||
XX 18 TTATATTTTCTTTCC 1
XX
XX RESULT 1730
XX ADB84616/c
XX ID ADB84616 standard; DNA; 18 BP.
XX
XX AC ADB84616;
XX
XX 04-DEC-2003 (first entry)
XX
XX Human mitogen-activated protein kinase kinase 2 primer #16.
XX
XX antiinflammatory; gene therapy; MEKK2; inflammatory reaction; human;
XX mitogen-activated protein kinase kinase 2; sequencing; ss; MEKK2;
XX primer.
XX
XX Homo sapiens.
XX
XX US2003064496-A1.
XX
XX 03-APR-2003.
XX
XX 05-JUN-2002; 2002US-00163811.
XX
XX 05-JUN-2002; 2002US-00163811.
XX (ATHE-) ATHEROGENICS INC.
XX
XX Whalen AM, Cook CK, Sikorski JA;
XX WPI; 2003-540788/51.
XX
XX New isolated nucleic acid molecule encoding a human MEKK2 protein, useful
XX for modulating the activity of the protein, such as regulation of
XX inflammatory reactions.
XX
XX Example 1; Page 18; 54pp; English.
XX
XX The invention describes an isolated nucleic acid molecule comprising a
XX 1857 base pair sequence, given in the specification and encoding a MEKK2
XX protein or its fragment, or encoding a fusion protein. The nucleic acid
XX

```

CC molecule is useful in modulating the activity of MEKK2 protein, such as
 CC regulation of inflammatory reactions. The MEKK2 protein is useful in
 CC identifying a compound that specifically modulates the expression or
 CC activity of a non-MEKK2 protein, where lack of expression or activity of
 CC the MEKK2 protein as compared to the expression or activity of the non-
 CC MEKK2 protein indicates that the compound specifically modulates the
 CC expression or activity of the non-MEKK2 protein. This sequence represents
 CC a sequencing primer used to verify the authenticity of human mitogen-
 CC activated protein kinase kinase 2 (MEKK2) clones.

XX Sequence 18 BP; 5 A; 3 C; 2 G; 8 T; 0 U; 0 Other;

SQ Query Match 0.6%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. NO. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 656 TTCATAGTATGGAGAGT 673

Db 18 TCCATAATATGGAAAGT 1

RESULT 1731

ADD56587/c

ID ADD56587 standard; DNA; 18 BP.

XX AC ADD56587;

XX 15-JAN-2004 (first entry)

XX Human gene expression analysis multiplex Start-PCR primer #107.

XX Gene expression; multiplex standardised reverse transcriptase-PCR;
 KW Start-PCR; high density oligonucleotide array; cDNA array;
 KW small biological sample; fine needle aspirate biopsy;
 KW laser captured microdissected material; human; primer; ss.

XX OS Homo sapiens.

XX US2003186246-A1.

XX 02-OCT-2003.

XX 28-MAR-2002; 2002US-00109349.

XX 28-MAR-2002; 2002US-00109349.

XX (WILL/) WILLEY J C.

XX (CRAW/) CRAWFORD E L.

XX Willey JC, Crawford EL;

XX WPI; 2003-811730/76.

XX Direct comparison of numerical gene expression values between samples of
 PT genes comprises using multiplex standardized reverse transcription-
 PT polymerase chain reaction.

PS Example 1; SEQ ID NO 107; 59pp; English.

XX The present invention relates to a method for the direct comparison of
 CC numerical gene expression values between samples of genes. The method
 CC comprises amplifying cDNA in the presence of a competitive template
 CC mixture and primer pairs for several genes and then amplifying aliquots
 CC of the PCR products using a primer pair specific for each gene. The
 CC method of amplification is by multiplex standardised reverse
 CC transcriptase-polymerase chain reaction (Start-PCR). High density
 CC oligonucleotide or cDNA arrays are used to measure PCR products following
 CC quantitative Start-PCR. The method is useful for the assessment of gene
 CC expression in small biological samples such as fine needle aspirate
 CC biopsies, and laser captured microdissected materials. The method allows
 CC for the standardised measurement of hundreds of genes from the same
 CC sample, which in prior art, could only be assessed for one gene. The
 CC present sequence represents a multiplex Start-PCR primer which can be

CC used in the method of the present invention.

XX Sequence 18 BP; 1 A; 4 C; 6 G; 7 T; 0 U; 0 Other;

SQ Query Match 0.6%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. NO. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 897 CAAAGGACACCCCAAGTG 914

Db 18 CAAAGGAAACCCCAAGTG 1

RESULT 1732

ADE14891/c

ID ADE14891 standard; DNA; 18 BP.

XX AC ADE14891;

XX 29-JAN-2004 (first entry)

XX Beer spoilage-associated primer SEQ ID 86.

XX ss; primer; detection; beer-spoilage; lactic acid bacteria;
 KW Gram-negative bacteria; spoilage bacteria.

XX OS Lactobacillus brevis.

XX WO2002103043-A2.

XX 27-DEC-2002.

XX 19-JUN-2002; 2002WO-EP006808.

XX 19-JUN-2001; 2001DE-01029410.

XX (VERM-) VERMICON AG.

XX Beimfohr C, Snaidr J;

XX WPI; 2003-175243/17.

XX New oligonucleotides, useful for rapid detection of beer-spoilage
 PT bacteria by in situ hybridization, are specific for type, genus or
 PT species.

PS Claim 1; SEQ ID NO 86; 88pp; German.

XX This invention describes novel oligonucleotides used in a method for
 CC detecting beer-spoilage bacteria in a sample. The bacteria detected
 CC include lactic acid bacteria of the genera Lactobacillus or Pediococcus,
 CC especially the species L. coryniformis, L. perolens, L. buchneri, L.
 CC plantarum, L. fructivorans, L. lindneri, L. casei, L. brevis or P.
 CC damnosus or Gram-negative bacteria of the genera Pectinatus and
 CC Megasphaera, specifically P. frisingensis, P. cerevisiphilus and M.
 CC cerevisiae. The oligonucleotides of the invention provide rapid detection
 CC of spoilage bacteria (typically within 48 hours, compared with 7-12 days
 CC for conventional culture methods), can detect all relevant bacteria in
 CC parallel, can differentiate between species of the same genus, and are
 CC easy to use. ADE14806-ADE15247 represent the oligonucleotides used in the
 CC method of the invention.

XX Sequence 18 BP; 5 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

SQ Query Match 0.6%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. NO. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1042 GAGCTTCACATCAATGAC 1059

Db 18 GAGCTTCGTTGATGAC 1

```
RESULT 1733
ADE14228
ID ADE14228 standard; DNA; 18 BP.
XX AC ADE14228;
XX DT 29-JAN-2004 (first entry)
XX DT Optineurin promoter motif, repeat element or regulatory region #337.
DE DE Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
XX KW SNP; glaucoma; progressive ocular hypertensive disorder;
XX KW glaucoma related disorder; motif; repeat element; regulatory region.
OS OS Homo sapiens.
XX US2003190617-A1.
PN 09-OCT-2003.
XX 06-MAR-2002; 2002US-00091281.
XX 06-MAR-2002; 2002US-00091281.
XX (SIEE/) SI E.
PA (RAYM/) RAYMOND V.
PA (MORI/) MORISSETTE J.
XX Raymond V, Morissette J, Si E;
XX WPI; 2003-864168/80.
DR New nucleic acid sequences of the optineurin gene are useful to detect
PT polymorphisms particularly single nucleotide polymorphisms in the
PT optineurin promoter to diagnose, prognosis and treat glaucoma and related
PT disorders.
XX Claim 11; SEQ ID NO 339; 159pp; English.
XX The invention relates to an isolated nucleic acid (NI) comprising at
CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
CC promoter appearing as ADE13890. Also included are the optineurin promoter
CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
CC detecting a single nucleotide polymorphism (SNP) in the optineurin
CC promoter, a host cell comprising the promoter operably linked to a
CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
CC in a promoter region of the optineurin gene, associated with a glaucoma
CC phenotype), detecting a SNP sequence variation in a sample containing
CC DNA, detecting the presence of an optineurin promoter sequence variation
CC in a sample containing DNA, determining the presence or increased
CC susceptibility to glaucoma or to a progressive ocular hypertensive
CC disorder resulting in loss of visual field in a patient (or the severity
CC or progression of glaucoma in a patient, comprising providing
CC amplification reaction primers that direct amplification of a selected
CC nucleic acid region containing the variation within the optineurin
CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
CC obtaining a sample containing human genomic DNA, providing a nucleic acid
CC capable of detecting a SNP located within an optineurin promoter, and
CC detecting the polymorphism). The invention is used to diagnose and
CC prognose glaucoma and also to treat glaucoma related disorders. The
CC present sequence is an optineurin promoter motif, repeat element or
CC putative regulatory region.
XX SQ Sequence 18 BP; 3 A; 5 C; 1 G; 9 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1586 CTATTTCTCTGTATTT 1603
Db 1 CCATTTCTCTGTATAT 18
```

```
RESULT 1734
AAQ10624/c
ID AAQ10624 standard; DNA; 19 BP.
XX AC AAQ10624;
XX DT 25-MAR-2003 (revised)
XX DT 29-APR-1991 (first entry)
XX DE HLA Class I locus-specific primer A2.2.
XX DE Human leukocyte antigen; major histocompatibility complex; MHC;
XX KW restriction fragment length polymorphic analysis; RFLP; tissue typing;
XX KW allele; PCR; ss.
XX OS Synthetic.
XX PN EP414469-A.
XX PD 27-FEB-1991.
XX 20-AUG-1990; 90EP-00309107.
XX 25-AUG-1989; 89US-00398217.
XX 11-SEP-1989; 89US-00405499.
XX 16-JAN-1990; 90US-00465863.
XX 11-JUL-1990; 90US-00551239.
XX (GENE-) GENETYPE AG.
PA (JEAN-) GENETYPE AG.
PA (SIMO/) SIMONS M J.
XX Simons MJ;
XX WPI; 1991-059664/09.
XX Detection of adjacent and non-adjacent locus, e.g. HLA alleles - by
XX amplifying genomic DNA, for direct determination of haplotype.
XX Claim 29; Page 49; 53pp; English.
XX The primer is specific for nt 1667-1685 of HLA Class I A2 locus. It is
XX used in a method for the prodn. of RFLP fragments for an HLA locus,
XX together with a second primer making up a locus-specific primer (LSP)
XX pair. It is pref. used with a Class I-specific primer which hybridises
XX with at least two different Class I loci, pref. at least one of each of
XX A, B, and C, and most pref. all of these. The Class I primer esp.
XX hybridises with intervening sequence (IVS) III or IVS I sequences. Direct
XX determination of the haplotype is possible, providing useful information
XX for identity of individuals for e.g. paternity case and forensic
XX investigations. See also AAQ10621-Q10669. (Updated on 25-MAR-2003 to
XX correct PA field.)
XX SQ Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 849 CTCAGACTCCCTATCTGG 866
Db 18 CTCAGAGTCACTCTCTGG 1
RESULT 1735
AAQ98612/c
ID AAQ98612 standard; DNA; 19 BP.
XX AC AAQ98612;
XX DT 25-MAR-2003 (revised)
```

```

DT 10-APR-1996 (first entry)
XX Human papilloma virus 42 specific oligonucleotide probe MY121.
XX
XX Human papilloma virus; probe; detection: diagnosis; genital; oral;
KW carcinomas; research; typing; HPV42; specific; MY121; ss.
XX
XX Synthetic.
XX
XX US5447839-A.
XX
XX 05-SEP-1995.
XX
XX 20-APR-1993; 93US-00050743.
XX
XX 09-SEP-1988; 88US-00243486.
XX
XX 10-MAR-1989; 89US-00322550.
XX
XX 09-SEP-1989; 89WO-US003747.
XX
XX 14-NOV-1990; 90US-00613142.
XX
XX (HOFF ) HOFFMANN LA ROCHE INC.
XX
XX Ting Y, Resnick RM, Greer CE, Manos MM, Bauer HM;
XX
XX WPI; 1995-319884/41.
XX
XX Detection of human papilloma virus DNA by amplification - using specific
XX consensus primer pairs and pref. detection with generic or type specific
XX probes for use in research and diagnosis.
XX
XX Claim 3; Col 49-50; 36pp; English.
XX
XX The human papilloma virus (HPV) specific probes AAQ98584-Q98650 are used
XX to detect, or type HPV for research or diagnostic purposes, e.g. to
XX identify HPV that are implicated in genital or oral carcinomas. (Updated
XX on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 19 BP; 5 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 19;
XX Best Local Similarity 83.3%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 560 ATCACCAGAGGTCGTGT 577
XX ||||| |||||
XX 19 ATCACCAGATGTCAGT 2
XX
XX RESULT 1736
XX AAT32499
XX ID AAT32499 standard; DNA; 19 BP.
XX
XX AC AAT32499;
XX
XX DT 02-DEC-1996 (first entry)
XX
XX DE Calpain large subunit 1 gene exon 19 splice acceptor site.
XX
XX KW Calpain; subunit; calcium; protease; mutation; treatment; detection;
XX identification; diagnosis; ling girdle muscular dystrophy; LGMD2;
XX calcium activated neutral protease; CANP; ss.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT misc_recomb 14..15
XX FT /*tag= a
XX FT /label= Splice acceptor site.
XX
XX WO9616175-A2.
XX
XX 30-MAY-1996.
XX
XX
XX 10-APR-1996; 95WO-EP004575.
XX
XX 22-NOV-1994; 94EP-00402668.
XX
XX (ASFR-) ASSOC FR CONTRE MYOPATHIES.
XX
XX Beckmann J, Richard I;
XX
XX WPI; 1996-268611/27.
XX
XX Human novel Calpain large subunit 1 gene encoding a calcium dependent
XX protease - used to develop prods. for the diagnosis and treatment of limb
XX -girdle muscular dystrophy 2 disease.
XX
XX Claim 16; Page 11; 66pp; English.
XX
XX The calpain large subunit 1 gene located on chromosome 15 codes for a
XX calcium activated neutral protease (CANP3) belonging to the calpain
XX family. Mutations in the gene induce limb-girdle muscular dystrophy
XX (LGMD) 2 disease. The gene, and fragments of it, can be used in the
XX prevention, treatment, diagnosis and detection of a predisposition to
XX LGMD2 disease. Fifty sequences (AAT32464-509) are given in the
XX CC amplification which correspond to the splice donor and splice acceptor
XX sites of the calpain large subunit 1 gene exons
XX
XX Sequence 19 BP; 5 A; 10 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 19;
XX Best Local Similarity 83.3%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 294 CTCATCCGTCAGATAA 311
XX ||||| |||||
XX 1 CTCATCCCCCGACACAA 18
XX
XX RESULT 1737
XX AAT44639/C
XX ID AAT44639 standard; DNA; 19 BP.
XX
XX AC AAT44639;
XX
XX DT 25-MAR-2003 (revised)
XX
XX DT 28-JAN-1997 (first entry)
XX
XX DE Human papillomavirus detection probe MY33 for HPV type 42.
XX
XX KW Probe; primer; PCR; polymerase chain reaction; amplification;
XX human papillomavirus; consensus; ss.
XX
XX OS Synthetic.
XX
XX PN US5527898-A.
XX
XX PD 18-JUN-1996.
XX
XX PF 07-JUN-1995; 95US-00474542.
XX
XX PR 09-SEP-1988; 88US-00243486.
XX
XX PR 10-MAR-1989; 89US-00322550.
XX
XX PR 09-SEP-1989; 89WO-US003747.
XX
XX PR 14-NOV-1990; 90US-00613142.
XX
XX PR 20-APR-1993; 93US-00050743.
XX
XX PR 24-SEP-1993; 93US-00126452.
XX
XX (HOFF ) HOFFMANN LA ROCHE INC.
XX
XX PA Bauer HM, Resnick RM, Greer CE, Manos MM, Zhang TV, Gravitt PE;
XX
XX WPI; 1996-299903/30.
XX
XX Nucleic acid hybridisation probes - specific for selected human papilloma
XX virus types.
XX

```

```

XX
PS Claim 1; Col 135; 96pp; English.
CC
CC The invention relates to new oligonucleotide probes and primers used for
CC the detection of human papillomaviruses which are not genital types 6,
CC 11, 16, 18 or 33. The probes and primers AAT44608-T44693 are esp. used to
CC detect HPV types 26, 31, 31B, 35, 39, 40, 43, 45, 51-59 and 68. The
CC primers can be used to detect these HPV types in conjunction with the
CC consensus primers and typing probes AAT44733-T44906, which are based on
CC and amplify fragments of the L1, E6, E7 and E1 regions of the HPV
CC sequences. This primer is targeted to the new HPV type 42. (Updated on 25
CC -MAR-2003 to correct PF field.)
XX
XX Sequence 19 BP; 5 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 560 ATCACCAGAGGGTGCTGT 577
DB 19 ATCACCAGATGTTGCAGT 2
RESULT 1738
AAT79910/c
ID AAT79910 standard; DNA; 19 BP.
XX
XX AAT79910;
XX
XX 09-OCT-1997 (first entry)
XX
XX Primer PCBAC for actin gene of Candida boidinii.
XX
XX Actin gene; promoter; Candida boidinii; Saccharomyces cerevisiae; primer;
XX terminator; chemical-resistant gene; polymerase chain reaction; amplify;
XX PCR; ss.
XX
XX Synthetic.
XX
XX JP09135694-A.
XX
XX 27-MAY-1997.
XX
XX 05-JUL-1996; 96JP-00176713.
XX
XX 12-SEP-1995; 95JP-00258305.
XX
XX (KIRI ) KIRIN BREWERY KK.
XX
XX WPI; 1997-335995/31.
XX
XX Promoter/terminator from the actin gene of Candida boidinii - used in a
XX vector, e.g. for expressing a chemical-resistance gene in yeast.
XX
XX Example 1; Page 10; 15pp; Japanese.
XX
XX AAT79910-T79917 represent amplification primers for the actin gene of
XX Candida boidinii (see AAT79909). The amplified sequence was isolated by
XX hybridisation to the Saccharomyces cerevisiae actin gene (amplified using
XX AAT79907 and AAT79908). The promoter and terminator regions of the
XX Candida actin gene (see AAT79905 and AAT79906 respectively) can be used
XX in a promoter/terminator gene expression cassette. The gene expression
XX cassette also contains a dominant gene marker, and an objective gene. The
XX promoter/terminator expresses the objective gene extensively and
XX constitutively. The construct can also express an exotic gene different
XX from a gene contained in the transformant, such as a chemical-resistant
XX gene in a yeast transformant
XX
XX Sequence 19 BP; 3 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 560 ATCACCAGAGGGTGCTGT 577
DB 19 ATCACCAGATGTTGCAGT 2
RESULT 1740
AAT62178/c
ID AAT62178 standard; DNA; 19 BP.
XX
XX AAT62178;
XX
XX 25-NOV-1997 (first entry)
XX
XX Primer PCBAC for Saccharomyces cerevisiae cDNA library.

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XX
PS Claim 1; Col 135; 96pp; English.
CC
CC The invention relates to new oligonucleotide probes and primers used for
CC the detection of human papillomaviruses which are not genital types 6,
CC 11, 16, 18 or 33. The probes and primers AAT44608-T44693 are esp. used to
CC detect HPV types 26, 31, 31B, 35, 39, 40, 43, 45, 51-59 and 68. The
CC primers can be used to detect these HPV types in conjunction with the
CC consensus primers and typing probes AAT44733-T44906, which are based on
CC and amplify fragments of the L1, E6, E7 and E1 regions of the HPV
CC sequences. This primer is targeted to the new HPV type 42. (Updated on 25
CC -MAR-2003 to correct PF field.)
XX
XX Sequence 19 BP; 5 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 560 ATCACCAGAGGGTGCTGT 577
DB 19 ATCACCAGATGTTGCAGT 2
RESULT 1738
AAT79910/c
ID AAT79910 standard; DNA; 19 BP.
XX
XX AAT79910;
XX
XX 09-OCT-1997 (first entry)
XX
XX Primer PCBAC for actin gene of Candida boidinii.
XX
XX Actin gene; promoter; Candida boidinii; Saccharomyces cerevisiae; primer;
XX terminator; chemical-resistant gene; polymerase chain reaction; amplify;
XX PCR; ss.
XX
XX Synthetic.
XX
XX JP09135694-A.
XX
XX 27-MAY-1997.
XX
XX 05-JUL-1996; 96JP-00176713.
XX
XX 12-SEP-1995; 95JP-00258305.
XX
XX (KIRI ) KIRIN BREWERY KK.
XX
XX WPI; 1997-335995/31.
XX
XX Promoter/terminator from the actin gene of Candida boidinii - used in a
XX vector, e.g. for expressing a chemical-resistance gene in yeast.
XX
XX Example 1; Page 10; 15pp; Japanese.
XX
XX AAT79910-T79917 represent amplification primers for the actin gene of
XX Candida boidinii (see AAT79909). The amplified sequence was isolated by
XX hybridisation to the Saccharomyces cerevisiae actin gene (amplified using
XX AAT79907 and AAT79908). The promoter and terminator regions of the
XX Candida actin gene (see AAT79905 and AAT79906 respectively) can be used
XX in a promoter/terminator gene expression cassette. The gene expression
XX cassette also contains a dominant gene marker, and an objective gene. The
XX promoter/terminator expresses the objective gene extensively and
XX constitutively. The construct can also express an exotic gene different
XX from a gene contained in the transformant, such as a chemical-resistant
XX gene in a yeast transformant
XX
XX Sequence 19 BP; 3 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 560 ATCACCAGAGGGTGCTGT 577
DB 19 ATCACCAGATGTTGCAGT 2
RESULT 1740
AAT62178/c
ID AAT62178 standard; DNA; 19 BP.
XX
XX AAT62178;
XX
XX 25-NOV-1997 (first entry)
XX
XX Primer PCBAC for Saccharomyces cerevisiae cDNA library.

```

KW Formate dehydrogenase; promoter; terminator; construction; expression; cassette; vector; primer; recombinant production; transformed yeast;
 KW Candida boidinii; polymerase chain reaction; PCR; amplification;
 KW Saccharomyces cerevisiae; library; acid phosphatase; ss.
 XX Synthetic.
 XX OS
 XX WO9710345-A1.
 PN
 XX
 XX 20-MAR-1997.
 PD
 XX
 XX 12-SEP-1996; 96WO-JP002597.
 PF
 XX
 XX 12-SEP-1995; 95JP-00234133.
 PR
 XX 29-FEB-1996; 96JP-00042536.
 PR
 XX (KIRI) KIRIN BEER KK.
 PA
 XX
 XX Komeda T, Suda H, Tamai Y, Iwamatsu A, Kato N, Sakai Y;
 PI
 XX WPI; 1997-202241/18.
 DR
 XX
 XX Candida boidinii formate dehydrogenase gene promoter and terminator - for
 PT efficient expression of foreign genes in yeast.
 PT
 XX Example 3; Page 48; 69pp; Japanese.
 PS
 XX
 XX The present sequence is a Saccharomyces cerevisiae cDNA library primer. A
 CC cassette vector (pHexAG) was constructed using pEdhp and pEdHT, which
 CC contain the promoter and terminator sequences from the Candida boidinii
 CC S2 AOU-1 formate dehydrogenase gene in pBluescriptII SK. The
 CC Saccharomyces cerevisiae S288C acid phosphatase gene (PHO5) was inserted
 CC into this cassette to give the expression vector pPHoAG, which was used
 CC to transform C. boidinii ATCC 48180. Culture of the transformant in a
 CC medium containing a 1.5% methanol carbon source, resulted in the
 CC accumulation of 0.70 U/ml acid phosphatase. No acid phosphatase was
 CC produced in a medium containing a glucose carbon source, or in a culture
 CC of untransformed C. boidinii ATCC 48180 in a medium containing either
 CC methanol or glucose
 CC
 XX Sequence 19 BP; 3 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 152 TGAAGCCTCACCAGATCC 169
 Db ||||| ||||| ||||| ||||| |||||
 18 TGAAGCCCCAATGATCC 1
 RESULT 1741
 AAX30684
 ID AAX30684 standard; DNA; 19 BP.
 XX
 XX AAX30684;
 AC
 XX
 XX 08-JUN-1999 (first entry)
 DT
 XX
 XX Oligonucleotide primer used for PCR amplification of H. pylori DNA.
 DE
 XX Vaccine; probe; diagnostic; ORF; cell envelope protein; secreted protein;
 KW cytoplasmic protein; cellular protein; ds.
 KW
 XX Helicobacter pylori.
 OS
 XX
 XX WO9824475-A1.
 PN
 XX
 XX 11-JUN-1998.
 PD
 XX
 XX 05-DEC-1997; 97WO-US022104.
 PF
 XX
 XX 05-DEC-1996; 96US-00759625.
 PR

PR 25-MAR-1997; 97US-00823745.
 PR 14-JUL-1997; 97US-00891928.
 XX (ASTR) ASTRA AB.
 PA
 XX Smith D, Alm RA, Doig PC, Kabok Z, Castriotta LM;
 PI
 XX WPI; 1998-333051/29.
 DR
 XX
 XX New isolated Helicobacter pylori nucleic acids - used to develop products
 PT for the diagnosis, prevention and treatment of infection by H. pylori and
 PT other Helicobacter species.
 PT
 XX Disclosure; Page 94; 339pp; English.
 PS
 XX Recombinant or substantially pure preparations of H. pylori polypeptides
 CC are disclosed, together with the nucleic acids encoding them. In all, 97
 CC ORFs are shown. The proteins are variously cell envelope proteins,
 CC cytoplasmic proteins, secreted proteins or other cellular proteins.
 CC Vaccines containing the nucleic acids or proteins are claimed, as are
 CC probes containing at least 8 nucleotides from the nucleic acid sequences.
 CC The vaccines are useful for treating or reducing the risk of H. pylori
 CC infections, and the probes can be used diagnostically for detecting the
 CC presence of Helicobacter in a sample. The products are also of use in
 CC screening for compounds having the ability to interfere with the H.
 CC pylori life cycle or to inhibit H. pylori infection
 XX
 XX Sequence 19 BP; 5 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 935 TTAACCTGCCTGCTGCTGA 952
 Db ||||| ||||| ||||| ||||| |||||
 2 TCAAGTTGCTGCTGCTGA 19
 RESULT 1742
 AAX09810/c
 ID AAX09810 standard; DNA; 19 BP.
 XX
 XX AAX09810;
 AC
 XX 24-MAR-1999 (first entry)
 DT
 XX
 XX Human biallelic polymorphic marker downstream primer #116.
 DE
 XX Polymorphism; biallelic; human; forensic; paternity testing; disease;
 KW detection; phenotypic typing; characteristic; infection; hereditary;
 KW autoimmune disease; cancer; inflammation; drug; therapy; medicament;
 KW treatment; marker; primer; ss.
 KW
 XX Synthetic.
 OS
 XX Homo sapiens.
 OS
 XX WO9820165-A2.
 PN
 XX
 XX 14-MAY-1998.
 PD
 XX
 XX 05-NOV-1997; 97WO-US020313.
 PF
 XX
 XX 06-NOV-1996; 96US-0030455P.
 PR
 XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA
 XX Lander ES, Wang D, Hudson T;
 PI
 XX WPI; 1998-286974/25.
 DR
 XX
 XX New isolated nucleic acid segments from the human genome - used for
 PT determining polymorphic forms for use in e.g. forensics, paternity
 PT testing or phenotypic typing for disease.
 PT

XX Claim 16; Page 59; 310pp; English.

XX CC AAX09121-X10268 are allele-specific oligonucleotide primers used in the

XX CC isolation of various biallelic polymorphic markers found in the human

XX CC genome (represented in AAX10269-X12937). These primers can be used in a

XX CC method for determining polymorphic forms in an individual for use in e.g.

XX CC forensics, paternity testing or for phenotypic typing for diseases such

XX CC as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular

XX CC dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial

XX CC hypercholesterolemia, polycystic kidney disease, hereditary

XX CC spirocytosis, von Willebrand's disease, tuberous sclerosis, hereditary

XX CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos

XX CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,

XX CC autoimmune diseases, inflammation, cancer, diseases of the nervous

XX CC system, infection by pathogenic microorganisms, and characteristics such

XX CC as longevity, appearance (e.g. baldness, obesity), strength, speed,

XX CC endurance, fertility, and susceptibility or receptivity to particular

XX CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid

XX CC segments can also be used to produce medicaments for the treatment or

XX CC prophylaxis of such diseases

SQ Sequence 19 BP; 2 A; 6 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 19;

Best Local Similarity 83.3%; Pred. No. 1.2e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1416 AGACCCGAGGAGAGAGAA 1433

DB 18 AGACCCCTGGGAGAAAAA 1

RESULT 1743

AAV17496/c

ID AAV17496 standard; DNA; 19 BP.

XX AC AAV17496;

XX DT 25-MAR-2003 (revised)

DT 04-JUN-1998 (first entry)

XX DT 04-JUN-1998 (first entry)

XX DE Probe MY121 for human papillomavirus typing.

XX KW Human papillomavirus; HPV; HPV detection; HPV typing;

XX KW L1 type-specific probe; ss.

XX OS Synthetic.

OS Human papillomavirus.

PN US5705627-A.

XX PD 06-JAN-1998.

XX PF 26-MAY-1995; 95US-00452055.

XX PR 09-SEP-1989; 88US-00243486.

PR 10-MAR-1989; 89US-00322550.

PR 14-NOV-1990; 90US-00613142.

XX PR 20-APR-1993; 93US-00050743.

XX PA (HOFF) ROCHE MOLECULAR SYSTEMS INC.

XX PI Ting Y, Resnick RM, Greer CE, Bauer HM, Manos MM;

XX DR WPI; 1998-192210/17.

XX PT Human papilloma probes and primers - useful for, e.g. detecting and

PT typing of human papilloma viruses.

XX PS Disclosure; Col 17-18; 37pp; English.

XX CC This sequence represents a human papillomavirus (HPV) L1 type-specific

CC probe of the invention. This sequence may be used in conjunction with L1

CC specific primers for detecting and typing HPV. Identification and typing

CC of HPV is important as different types of HPV pose different risks for

CC infected individuals. HPV16 and HPV18 have been more consistently

CC identified in higher grades of cervical dysplasia and carcinoma than

CC other HPV types. (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 19 BP; 5 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 19;

Best Local Similarity 83.3%; Pred. No. 1.2e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 560 ATCACCAGAGGGTGTGT 577

DB 19 ATCACCAGATGTTCAGT 2

RESULT 1744

AAX30525

ID AAX30525 standard; DNA; 19 BP.

XX AC AAX30525;

XX DT 08-JUN-1999 (first entry)

DT 08-JUN-1999 (first entry)

XX DE Oligonucleotide primer used for sequencing H. pylori DNA.

XX KW Vaccine; probe; diagnostic; ORF; cell envelope protein; secreted protein;

KW cellular protein; ds.

XX OS Helicobacter pylori.

XX PN WO9818323-A1.

XX PD 07-MAY-1998.

XX PF 28-OCT-1997; 97WO-US019575.

XX PR 28-OCT-1996; 96US-00739150.

PR 06-DEC-1996; 96US-00759739.

PR 14-JUL-1997; 97US-00891928.

XX PA (ASTR) ASTRA AB.

XX PI Smith D, Alm RA;

XX DR WPI; 1998-271811/24.

XX PT Helicobacter pylori nucleic acids and proteins - used to develop products

XX PT for the detection, prevention and treatment of H. pylori infections.

XX PS Disclosure; Page 78; 279pp; English.

XX CC Recombinant or substantially pure preparations of H. pylori polypeptides

CC are disclosed, together with the nucleic acids encoding them. In all, 73

CC ORFs are shown. The proteins are variously cell envelope proteins, the

CC secreted proteins or other cellular proteins. Vaccines containing the

CC nucleic acids or proteins are claimed, as are probes containing at least

CC 8 nucleotides from the nucleic acid sequences. The vaccines are useful

CC for treating or reducing the risk of H. pylori infections, and the probes

CC can be used diagnostically for detecting the presence of Helicobacter in

CC a sample. The products are also of use in screening for compounds having

CC the ability to interfere with the H. pylori life cycle or to inhibit H.

CC pylori infection

XX SQ Sequence 19 BP; 5 A; 4 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 19;

Best Local Similarity 83.3%; Pred. No. 1.2e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 935 TTAACCTGCCTATGCTGA 952


```

PR 15-JAN-1999; 99US-00231235.
XX (CHIR ) CHIRON CORP.
XX Johnston JC, Sauter SL, Hsu D, Sheridan PL, Hardy SF;
PI Dubensky JW, Yee J;
XX WPI; 1999-444391/37.
XX
XX New feline immunodeficiency virus vectors containing heterologous DNA
PT sequences for gene therapy in transformed hosts.
XX
XX Example 5A; Page 97; 170pp; English.
XX
XX The present sequence is FIV5 primer used to introduce a NotI restriction
CC enzyme recognition site into pF34deltaenv at nt 9168. Primers FIV5 and
CC FIV6 were used along with DNA polymerase, 10X buffer, pF34 plasmid DNA
CC template and dNTP in the first round of PCR involved in the construction
CC of packaging expression cassette, pCMVpFIVkho from pF34deltaenv. The PCR
CC products were then subjected to the second round of PCR employing primers
CC FIV5 and FIV8. The second round PCR products were digested with Nde I and
CC Sal I and the fragment obtained was ligated into pF34deltaenv to generate
CC pF34deltaenv which was digested with Tth111 I and NotI or XhoI and
CC Tth111. The fragments obtained were subsequently ligated into NotI/XhoI
CC fragment from pCMVBeta to create pCMVpFIVkho also referred to as pCFIVX
XX
XX Sequence 19 BP; 6 A; 2 C; 7 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1694 GCACCTTGCACCCATT 1711
DB 19 GCACATTGCCATTACCATT 2
RESULT 1748
AAAX75879
ID AAAX75879 standard; DNA; 19 BP.
XX AC
XX AAAX75879;
DT 03-AUG-1999 (first entry)
XX
XX H. pylori OMP DNA amplifying primer.
XX
XX Outer membrane polypeptide; OMP; vaccine; H. pylori infection; humoral;
KW cellular immune response; PCR primer; ss.
XX
XX Synthetic.
OS Helicobacter pylori.
XX
XX WO9921959-A2.
XX
XX 06-MAY-1999.
XX
XX 28-OCT-1998; 98WO-US022883.
XX
XX 28-OCT-1997; 97US-00959131.
XX
XX 17-DEC-1997; 97US-00993001.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Ellis RW, Noonan BM, Alm RA, Smith D, Guild BC;
XX WPI; 1999-326698/27.
XX
XX Cellular vaccine against Helicobacter pylori.
XX
XX Example 5; Page 90; 352pp; English.
XX
XX The invention relates to a vaccine for preventing or treating infections
CC
CC by Helicobacter pylori. The vaccine contains at least one isolated H.
CC pylori polypeptide, or its fragments, in a carrier, where the carrier is
CC a Salmonella, Vibrio cholerae or Shigella vector containing a nucleic
CC acid encoding the H. pylori polypeptide. The vaccines induce humoral and
CC cellular immune responses. The vaccines are used to treat or prevent
CC infections by H. pylori. The invention provides nucleic acid sequences
CC AAX75779 to AAX75837 encoding H. pylori outer membrane polypeptides
CC (OMPs) AAY17160 to AAY17218
XX
XX Sequence 19 BP; 5 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 935 TTAACCTGCTATGCTGA 952
DB 2 TCAAGTTGCTATGCTGA 19
RESULT 1749
AAV68658/c
ID AAV68658 standard; DNA; 19 BP.
XX AC
XX AAV68658;
XX
XX 24-MAY-1999 (first entry)
XX
XX Nucleotide sequence of the PCR primer 5.
DE areA gene; peptidase; Koji mold; L-glutamine; prolidase; PCR;
XX prolyl-dipeptidyl-peptidase; amplification; PCR primer; ss.
KW
XX Aspergillus oryzae.
OS Synthetic.
XX
XX WO9902691-A1.
XX
XX 21-JAN-1999.
XX
XX 01-MAY-1998; 98WO-EP002785.
XX
XX 05-JUL-1997; 97EP-00111378.
XX
XX (NEST ) SOC PROD NESTLE SA.
XX
XX Van Den Broek P, Affolter M;
XX WPI; 1999-120892/10.
XX
XX New koji mold capable of expressing two times more endo- and exo-
PT peptidases than wild-type strain Aspergillus oryzae CNCM I-1882 - useful
PT for hydrolyzing protein-containing materials, and producing food products
PT with improved organoleptic properties.
XX
XX Example 3; Page 32; 53pp; English.
XX
XX This is the nucleotide sequence of a PCR primer used for amplification in
CC the method of the invention involving the doubled expression of
CC peptidases in a new Koji mold. The koji mold is useful for hydrolyzing
CC protein-containing materials, and for over-producing proteolytic enzymes.
CC When hydrolyzing protein-containing material (containing 5 mM L-
CC glutamine), the mold may be used in combination with an enzyme and/or a
CC microorganism providing a prolidase activity. Additionally, the mold is
CC useful in fermentation processes for creating food products. The koji
CC mold is used to produce high levels of endopeptidases and exopeptidases,
CC including enhanced prolyl-dipeptidyl-peptidase activity, which may be
CC useful for releasing L-glutamine from peptides
XX
XX Sequence 19 BP; 8 A; 6 C; 4 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;

```

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 640 GTCATGACTGTCCTTT 657
 ||| ||||| |||||
 Db 19 GTCGTGACTGTTCTCTG 2

RESULT 1750

AAZ38277/c
 ID AAX38277 standard; DNA; 19 BP.

XX AC AAX38277;

XX 04-JUN-1999 (first entry)

XX Histocompatibility locus antigen PCR primer SEQ ID NO:433.

XX Human; histocompatibility locus antigen; HLA; determination; allele;
 KW HLA-B typing; PCR; HLA class I; cis/trans linkage resolution; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9907883-A1.

XX 18-FEB-1999.

XX 11-AUG-1998; 98WO-CA000768.

XX 11-AUG-1997; 97US-00909290.

XX (VISI-) VISIBLE GENETICS INC.

PA (BLAS/) BLASZYK R H.

XX Blasczyk RH, Leushner J;

XX WPI; 1999-167446/14.

XX Determination of HLA class I group type of a subject - using group
 PT specific untranslated region primer pair.

XX Example; Page 29; 195pp; English.

XX The present invention describes a method using novel primers involving
 CC the PCR-based determination of histocompatibility locus antigen B (HLA-B)
 CC Class I group type. Determining the HLA-B Class I group type of a subject
 CC comprises: (i) combining a group-specific untranslated region primer pair
 CC with a target DNA sample from the subject under conditions such that
 CC primer-based amplification of the target DNA may occur; and (ii)
 CC determining whether a nucleic acid product is produced by the
 CC amplification; where the ability of the primer pair to produce a nucleic
 CC acid product is associated with a particular HLA group type. The method
 CC can be used for HLA-B typing. In the method, the initial group specific
 CC amplification allows a PCR based separation of haplotypes in 95% of
 CC patient samples. It permits the resolution of cis/trans linkages of
 CC heterozygote sequencing results which cannot be achieved with other
 CC protocols. AAX37845 to AAX38286 represent DNA sequence used in the
 CC exemplification of the present invention

XX Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 779 CCATTTCACGCGGTCA 796

Db 18 CCATTTCACGCGGTCA 1

RESULT 1751

AAZ36558

ID AAZ36558 standard; DNA; 19 BP.

XX AAZ36558;

XX 22-FEB-2000 (first entry)

XX Probe hybridising to nucleotides of exon 28 of the MLL-1 gene.

XX Major breakpoint region; mbr; MLL-1 gene; chromosome aberration;
 KW acute lymphoblastic leukaemia-1; ALL-1; probe; peptide nucleic acid;
 KW haemopoietic malignancy; cancer; inborn constitutiel disease;
 KW herbicide resistance gene; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9957309-A1.

XX 11-NOV-1999.

XX 04-MAY-1999; 99WO-DK000245.

XX 04-MAY-1998; 98DK-00000615.

XX (DAKO-) DAKO AS.

XX Pluzek K, Nielsen KV, Adelhorst K;

XX WPI; 2000-038821/03.

XX Detection of chromosome aberrations, used for detecting diseases and
 PT disorders, infections, and plant alterations related to e.g. herbicide
 PT resistance.

XX Disclosure; Page 40; 63pp; English.

XX AAZ36520-41 (set 1) and AAZ36542-61 (set 2) represent two sets of probes
 CC which flank each site of the major breakpoint region (mbr) of the MLL-1
 CC gene. The MLL gene is associated with acute lymphoblastic leukaemia-1
 CC (ALL-1). The probes are selected from the lower strand of the MLL-1 gene,
 CC and so hybridise to the upper strand. The probes are used to demonstrate
 CC the method of the invention. The specification describes a method for the
 CC detection of chromosome aberrations in eukaryotic samples uses sets of
 CC peptide nucleic acid (PNA) probes in hybridisation reactions. The method
 CC comprises using at least 2 sets of hybridisation probes, where at least
 CC one set comprises one or more PNA probes capable of hybridising to a
 CC specific nucleic acid sequences related to a potential aberration in a
 CC chromosome. The methods can be used for the detection of chromosome
 CC aberrations. They can be used for the diagnosis of disorders and diseases
 CC related to chromosomal aberrations or abnormalities such as e.g.
 CC haemopoietic malignancies, cancers and inborn constitutiel diseases. The
 CC method may be used for detecting viral sequences and their localization
 CC in the chromosome. In plant biology, the methods can be used for
 CC monitoring the efficiency of transferring herbicide resistance genes to a
 CC plant

XX Sequence 19 BP; 3 A; 4 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1913 CATTTTAGATTGGTTCT 1930

Db 1 CATTTTAGATTGGTTCT 18

RESULT 1752

AAZ93343

ID AAZ93343 standard; DNA; 19 BP.

XX AAZ93343;

DT 11-JAN-2001 (first entry)

XX DE Human cystic fibrosis-associated sequence CF3.
 XX KW Human; cystic fibrosis; nucleic acid detection; genomic typing;
 KW mutation detection; viral load determination; species identification;
 OS forensic analysis; ss.
 XX OS Homo sapiens.
 XX PN WO200049181-A1.
 XX PD 24-AUG-2000.
 XX PF 18-FEB-2000; 2000WO-US004243.
 XX PR 18-FEB-1999; 99US-00252436.
 PR 11-MAR-1999; 99WO-US005304.
 PR 21-JUL-1999; 99US-00358972.
 PR 27-SEP-1999; 99US-00406064.
 XX (PROM-) PROMEGA CORP.
 PA Lewis MK, Kephart D, Rhodes RB, Shultz JW, Leippe D, Mandrekar M;
 PI Andrews CA, Hartnett JR, Gu T, Wood KV, Welch R;
 XX WPI; 2000-565378/52.
 DR Determining the presence of predetermined nucleic acid target sequences
 PT useful for detecting single nucleotide polymorphisms by depolymerizing
 PT the 3' end of an oligonucleotide probe hybridized to a nucleic acid
 PT target sequence.
 XX Disclosure; Page 80; 220pp; English.
 XX The present sequence may be used in a method for determining the presence
 CC of a known exogenous nucleic acid target sequence in a nucleic acid
 CC sample. The method comprises admixing a treated sample with a
 CC depolymerising enzyme which releases one or more nucleotides from the 3'-
 CC end of a hybridised nucleic acid probe. The method is used for assaying
 CC nucleic acids for a particular native or mutant sequence, and for genomic
 CC typing. It is useful for detecting mutations, translocations, and single
 CC nucleotide polymorphisms, determination of viral load, species
 CC identification, detection of sample contamination, and analysis of
 CC forensic samples. Compared with previous methods of detecting nucleic
 CC acid hybrids, the new method has higher sensitivity without the need for
 CC radiochemicals or electrophoresis. It is quantitative, highly
 CC reproducible and can be automated. The method can reliably detect as few
 CC as 10 copies of a virus in a sample, and is capable of providing multiple
 CC analyses in a single assay (multiplex assay)
 XX Sequence 19 BP; 9 A; 5 C; 3 G; 2 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 895 ATCAGGACACGCCAAG 912
 DB 2 ATCATAGGAACACCAAG 19
 RESULT 1753
 AAA86059/c
 ID AAA86059 standard; DNA; 19 BP.
 XX AC AAA86059;
 XX DT 04-DEC-2000 (first entry)
 XX Cdc 25 hs ribozyme binding site #167.
 DE Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
 KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
 XX

OS Mammalia.
 XX WO200032765-A2.
 XX PD 08-JUN-2000.
 XX PF 06-DEC-1999; 99WO-US028772.
 PR 04-DEC-1998; 98US-0110954P.
 XX (IMMU-) IMMUSOL INC.
 XX Tritz R, Welch PJ, Barber JR, Robbins JM;
 WPI; 2000-412314/35.
 XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1.
 XX Disclosure; Page 102; 109pp; English.
 XX The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells. The
 CC ribozyme is resistant to endonuclease activity and hence is efficient in
 CC restenosis treatment
 XX Sequence 19 BP; 7 A; 5 C; 5 G; 2 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 376 GGCCTGTTTGAGTTCTGT 393
 DB 19 GGCCTGTTTGAGTTCTGT 2
 RESULT 1754
 AAA82457
 ID AAA82457 standard; DNA; 19 BP.
 XX AC AAA82457;
 XX DT 04-DEC-2000 (first entry)
 XX cdk1 ribozyme binding site #43.
 XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
 XX Mammalia.
 XX WO200032765-A2.
 XX PD 08-JUN-2000.
 XX PF 06-DEC-1999; 99WO-US028772.
 PR 04-DEC-1998; 98US-0110954P.
 XX (IMMU-) IMMUSOL INC.
 XX Tritz R, Welch PJ, Barber JR, Robbins JM;
 WPI; 2000-412314/35.
 XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1.
 XX

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XX PS Disclosure; Page 46; 109pp; English.
XX CC The present invention relates to a hairpin or hammerhead ribozyme,
XX CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX CC Representative examples of ribozyme recognition sites are given in
XX CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
XX CC inhibiting restenosis by introduction of the ribozyme into cells. The
XX CC ribozyme is resistant to endonuclease activity and hence is efficient in
XX CC restenosis treatment
XX SQ Sequence 19 BP; 6 A; 2 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1051 TACAATGACTTCTTGAA 1068
DB 1 TACAATGATTCTTGAA 18
RESULT 1755
AAA82418/C
ID AAA82418 standard; DNA; 19 BP.
XX AC AAA82418;
XX XX 04-DEC-2000 (first entry)
XX DT 04-DEC-2000 (first entry)
XX DE cdk1 ribozyme binding site #4.
XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX OS Mammalia.
XX PN WO200032765-A2.
XX PD 08-JUN-2000.
XX PF 06-DEC-1999; 99WO-US028772.
XX PR 04-DEC-1998; 98US-0110954P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX XX WPI; 2000-412314/35.
XX XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX XX PCNA and Cyclin B1.
XX PS Disclosure; Page 46; 109pp; English.
XX CC The present invention relates to a hairpin or hammerhead ribozyme,
XX CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX CC Representative examples of ribozyme recognition sites are given in
XX CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
XX CC inhibiting restenosis by introduction of the ribozyme into cells. The
XX CC ribozyme is resistant to endonuclease activity and hence is efficient in
XX CC restenosis treatment
XX SQ Sequence 19 BP; 5 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 831 GGTGGTCTTACAGTGTG 848
```

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DB 18 GGTGGTCTTACCGAGG 1
|||||
RESULT 1756
AAA83336/C
ID AAA83336 standard; DNA; 19 BP.
XX AC AAA83336;
XX XX 04-DEC-2000 (first entry)
XX DT 04-DEC-2000 (first entry)
XX DE cdk8 ribozyme binding site #56.
XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX OS Mammalia.
XX PN WO200032765-A2.
XX PD 08-JUN-2000.
XX PF 06-DEC-1999; 99WO-US028772.
XX PR 04-DEC-1998; 98US-0110954P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX XX WPI; 2000-412314/35.
XX XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX XX PCNA and Cyclin B1.
XX PS Disclosure; Page 60; 109pp; English.
XX CC The present invention relates to a hairpin or hammerhead ribozyme,
XX CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX CC Representative examples of ribozyme recognition sites are given in
XX CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
XX CC inhibiting restenosis by introduction of the ribozyme into cells. The
XX CC ribozyme is resistant to endonuclease activity and hence is efficient in
XX CC restenosis treatment
XX SQ Sequence 19 BP; 7 A; 4 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 421 AGTGCTGTGAACCTTAAT 438
DB 19 AGCTCTGTGAACCTTGAT 2
|||||
RESULT 1757
AAA83813/C
ID AAA83813 standard; DNA; 19 BP.
XX AC AAA83813;
XX XX 04-DEC-2000 (first entry)
XX DT 04-DEC-2000 (first entry)
XX DE cdk-we-hu ribozyme binding site #288.
XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX OS Mammalia.
XX PN WO200032765-A2.
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XX 08-JUN-2000.
XX
XX 06-DEC-1999; 99WO-US028772.
XX
XX 04-DEC-1998; 98US-0110954P.
XX (IMMU-) IMMUSOL INC.
XX
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PCNA and Cyclin B1.
XX
XX Disclosure; Page 67; 109pp; English.
XX
XX The present invention relates to a hairpin or hammerhead ribozyme,
XX designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX Representative examples of ribozyme recognition sites are given in
XX AAA82415 to AAA86787. The ribozyme of the invention is useful for
XX inhibiting restenosis by introduction of the ribozyme into cells. The
XX ribozyme is resistant to endonuclease activity and hence is efficient in
XX restenosis treatment
XX
XX Sequence 19 BP; 8 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 19;
XX Best Local Similarity 83.3%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1579 ATATTTCTATTCTCTG 1596
Db 18 AGAGTTCTATTACTCTG 1
XX
RESULT 1758
AAA84187
ID AAA84187 standard; DNA; 19 BP.
XX
XX AAA84187;
XX
XX 04-DEC-2000 (first entry)
XX
XX Cyclin C ribozyme binding site #159.
XX
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX Mammalia.
XX
XX WO200032765-A2.
XX
XX 08-JUN-2000.
XX
XX 06-DEC-1999; 99WO-US028772.
XX
XX 04-DEC-1998; 98US-0110954P.
XX (IMMU-) IMMUSOL INC.
XX
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PCNA and Cyclin B1.
XX
XX Disclosure; Page 73; 109pp; English.
XX
XX The present invention relates to a hairpin or hammerhead ribozyme,
XX designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX Representative examples of ribozyme recognition sites are given in
XX AAA82415 to AAA86787. The ribozyme of the invention is useful for
XX inhibiting restenosis by introduction of the ribozyme into cells. The
XX ribozyme is resistant to endonuclease activity and hence is efficient in
XX restenosis treatment
XX
XX Sequence 19 BP; 8 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 19;
XX Best Local Similarity 83.3%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1579 ATATTTCTATTCTCTG 1596
Db 18 AGAGTTCTATTACTCTG 1
XX
RESULT 1758
AAA84187
ID AAA84187 standard; DNA; 19 BP.
XX
XX AAA84187;
XX
XX 04-DEC-2000 (first entry)
XX
XX Cyclin C ribozyme binding site #159.
XX
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX Mammalia.
XX
XX WO200032765-A2.
XX
XX 08-JUN-2000.
XX
XX 06-DEC-1999; 99WO-US028772.
XX
XX 04-DEC-1998; 98US-0110954P.
XX (IMMU-) IMMUSOL INC.
XX
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PCNA and Cyclin B1.
XX
XX Disclosure; Page 73; 109pp; English.
XX
XX The present invention relates to a hairpin or hammerhead ribozyme,
XX designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX Representative examples of ribozyme recognition sites are given in
XX AAA82415 to AAA86787. The ribozyme of the invention is useful for
XX inhibiting restenosis by introduction of the ribozyme into cells. The
XX ribozyme is resistant to endonuclease activity and hence is efficient in
XX restenosis treatment
XX
XX Sequence 19 BP; 4 A; 4 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 19;
XX Best Local Similarity 83.3%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 929 AGAGCTTTAACTGCTTA 946
Db 2 ATAGCTTTAGCTTGCTTA 19
XX
RESULT 1759
AAA83288
ID AAA83288 standard; DNA; 19 BP.
XX
XX AAA83288;
XX
XX 04-DEC-2000 (first entry)
XX
XX cdk8 ribozyme binding site #8.
XX
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX Mammalia.
XX
XX WO200032765-A2.
XX
XX 08-JUN-2000.
XX
XX 06-DEC-1999; 99WO-US028772.
XX
XX 04-DEC-1998; 98US-0110954P.
XX (IMMU-) IMMUSOL INC.
XX
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PCNA and Cyclin B1.
XX
XX Disclosure; Page 59; 109pp; English.
XX
XX The present invention relates to a hairpin or hammerhead ribozyme,
XX designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX Representative examples of ribozyme recognition sites are given in
XX AAA82415 to AAA86787. The ribozyme of the invention is useful for
XX inhibiting restenosis by introduction of the ribozyme into cells. The
XX ribozyme is resistant to endonuclease activity and hence is efficient in
XX restenosis treatment
XX
XX Sequence 19 BP; 4 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 19;
XX Best Local Similarity 83.3%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 486 TCGAAAGAGTCCGAGGC 503
Db 2 TCGAAAGTTGCCGAGGC 19
```

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RESULT 1760
AAAAA82809/C
ID AAA82809 standard; DNA; 19 BP.
XX
XX
XX
XX
04-DEC-2000 (first entry)
XX
XX
XX
XX
cdk3 ribozyme binding site #94.
DE
DE
XX
XX
Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
KW
XX
Mammalia.
XX
XX
WO200032765-A2.
XX
XX
08-JUN-2000.
XX
XX
06-DEC-1999; 99WO-US028772.
XX
XX
04-DEC-1998; 98US-0110954P.
XX
XX
(IMMU-) IMMUSOL INC.
XX
XX
Tritz R, Welch P, Barber JR, Robbins JM;
XX
XX
WPI; 2000-412314/35.
XX
XX
New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX
XX
RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX
XX
PCNA and Cyclin B1.
XX
XX
Disclosure; Page 52; 109pp; English.
XX
XX
The present invention relates to a hairpin or hammerhead ribozyme,
XX
XX
designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX
XX
other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX
XX
Representative examples of ribozyme recognition sites are given in
XX
XX
AAAG2415 to AAAG6787. The ribozyme of the invention is useful for
XX
XX
inhibiting restenosis by introduction of the ribozyme into cells. The
XX
XX
ribozyme is resistant to endonuclease activity and hence is efficient in
XX
XX
restenosis treatment
XX
XX
Sequence 19 BP; 4 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1193 CTGGGTCCCAATGCAGG 1210
|||
|||
DB 19 CTGGGGTCACTGCAGG 2
RESULT 1761
AAZ69694/C
ID AAZ69694 standard; DNA; 19 BP.
XX
XX
AAZ69694;
XX
XX
AC
XX
XX
10-SEP-2001 (first entry)
XX
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:4050.
XX
XX
Human genome; biallelic marker; high density disequilibrium map;
XX
XX
genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX
XX
haplotyping; hybridisation; identification; characterisation;
XX
XX
amplification; single nucleotide polymorphism; SNP; PCR primer;
XX
XX
diagnosis; ss.
XX
XX
Homo sapiens.
OS

```

XX (GEST) GENSET.
 XX Cohen D, Blumenfeld M, Chumakov I;
 PI WPI; 2000-013267/01.
 XX Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome.
 XX Claim 8; Page 1291; 2745pp; English.
 XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX Sequence 19 BP; 10 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1587 TATTCTCTGCTGATTTA 1604
 DB |||||
 18 TATTCTCTGGGCTTTA 1

RESULT 1763
 AAZ72944
 ID AAZ72944 standard; DNA; 19 BP.
 XX AAZ72944;
 AC AAZ72944;
 XX 10-SEP-2001 (first entry)
 DT Human biallelic marker upstream amplification primer SEQ ID NO:7300.
 XX Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.
 XX Homo sapiens.
 OS WO9954500-A2.
 XX 28-OCT-1999.
 PD 21-APR-1999; 99WO-IB000822.
 XX 21-APR-1998; 98US-0082614P.
 PR 23-NOV-1998; 98US-0109732P.
 XX (GEST) GENSET.
 PA Cohen D, Blumenfeld M, Chumakov I;
 XX WPI; 2000-013267/01.
 XX Novel biallelic markers used to construct a high density disequilibrium

PT map of the human genome.
 XX Claim 9; Page 1787; 2745pp; English.
 XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX Sequence 19 BP; 11 A; 0 C; 8 G; 0 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1394 AAACAGAGGATGAAAAAG 1411
 DB |||||
 2 AAAGAGGAGGAAAAAGG 19

RESULT 1764
 AAZ71736/C
 ID AAZ71736 standard; DNA; 19 BP.
 XX AAZ71736;
 AC AAZ71736;
 XX 10-SEP-2001 (first entry)
 DT Human biallelic marker upstream amplification primer SEQ ID NO:6092.
 DE Human genome; biallelic marker; high density disequilibrium map;
 XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.
 XX Homo sapiens.
 OS WO9954500-A2.
 XX 28-OCT-1999.
 PD 21-APR-1999; 99WO-IB000822.
 XX 21-APR-1998; 98US-0082614P.
 PR 23-NOV-1998; 98US-0109732P.
 XX (GEST) GENSET.
 PA Cohen D, Blumenfeld M, Chumakov I;
 XX WPI; 2000-013267/01.
 XX Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome.
 XX Claim 8; Page 1529; 2745pp; English.
 XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention

XX Sequence 19 BP; 0 A; 4 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1119 CCAGAACACGATGAGTA 1136
 |||||
 Db 19 CCAGAACACCAAGAGAA 2

RESULT 1765

AAZ73298
 ID AAZ73298 standard; DNA; 19 BP.

XX AAZ73298;

XX 10-SEP-2001 (first entry)

XX Human biallelic marker upstream amplification primer SEQ ID NO:7654.

XX Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.

XX Homo sapiens.

XX WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

XX 23-NOV-1998; 98US-0109732P.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium
 XX map of the human genome.

XX Claim 9; Page 1862; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.

CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention

XX Sequence 19 BP; 6 A; 5 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 19;

Best Local Similarity 83.3%; Pred. No. 1.2e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 889 CTAACATCAAGGACAC 906

|||||

Db 2 CTAACATGTAAGGACTC 19

RESULT 1766

AAZ74528
 ID AAZ74528 standard; DNA; 19 BP.

XX AAZ74528;

XX 10-SEP-2001 (first entry)

XX Human biallelic marker downstream amplification primer SEQ ID NO:8884.

XX Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.

XX Homo sapiens.

XX WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

XX 23-NOV-1998; 98US-0109732P.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium
 XX map of the human genome.

XX Claim 8; Page 2125; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention

XX Sequence 19 BP; 4 A; 5 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 19;

Best Local Similarity 83.3%; Pred. No. 1.2e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 847 GGCTCAGACCTCCCTATCT 864
 Db 1 GGCTTAGACTCCATATTT 18

RESULT 1767
 AAA97306
 ID AAA97306 standard; DNA; 19 BP.
 XX
 AC AAA97306;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human MG-UC1 (UNK3) quantitative real-time PCR primer, SEQ ID NO:15.
 XX
 KW Differential gene expression; organelle; mitochondrion; disease state;
 KW metabolic state; respiratory state; apoptotic state; cybrid cell line;
 KW cytoplasmic hybrid; organelle-associated disease; autoimmune disease;
 KW hyperproliferative disorder; hyperproliferative disorder; human;
 KW Alzheimer's disease; quantitative real-time PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200055323-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 16-MAR-2000; 2000WO-US007311.
 XX
 PR 16-MAR-1999; 99US-0124673P.
 PR 15-MAR-2000; 2000US-00526977.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Herrnstadt C, Miller SW, Davis RE;
 XX
 DR WPI; 2000-638202/61.
 XX
 PT Identifying factor encoded by gene that is differentially expressed
 PT comprises comparing expression of genes in cell in first and second
 PT state.
 XX
 PS Claim 32; Page 84; 176pp; English.
 XX
 CC The invention relates to a method of identifying factors, including
 CC organellar factors encoded by genes that are differentially expressed
 CC when cells in different states (e.g., metabolic, respiratory, diseased,
 CC or apoptotic states) are compared. The invention also encompasses a
 CC method of diagnosing a disease by contacting a sample from an individual
 CC with the differentially expressed gene product or an antibody which binds
 CC to it; and a cell line a cell line selected from cybrid (cytoplasmic
 CC hybrid) cell line 1685, ARCC 207149 or ARCC 207150. The invention also
 CC discloses examples of organellar factors which are differentially
 CC expressed in organelle-associated disease, including a variety of human
 CC genes which are differentially expressed in Alzheimer's disease. The
 CC method of the invention is useful for identifying factors which are
 CC differentially expressed in organelle-associated diseases as compared
 CC with the healthy state. The organelle-associated diseases include
 CC mitochondria-associated diseases such as neurodegenerative disorders
 CC (e.g., Alzheimer's disease, Parkinson's disease), autoimmune diseases,
 CC diabetes mellitus, arthritis, NARP (neuropathy, ataxia, retinitis
 CC pigmentosa), Kearns-Sayre disease, Pearson's Syndrome, PEO (progressive
 CC external ophthalmoplegia), Wolfram syndrome, Leigh's Syndrome,
 CC schizophrenia, stroke, mitochondrial diabetes and deafness (MIDD) and
 CC hyperproliferative disorders, such as cancer, tumours and psoriasis.
 CC Sequences AAA97304-A97313 represent PCR primers used in quantitative real
 CC -time PCR of the Alzheimer's disease-associated genes AAA97298-A97302
 XX
 SQ Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 906 CGCCAAAGTGTGTGAATT 923
 Db 1 CGCCAAAGTGTGTGAATT 18

RESULT 1768
 AAA86903
 ID AAA86903 standard; DNA; 19 BP.
 XX
 AC AAA86903;
 XX
 DT 15-JAN-2001 (first entry)
 XX
 DE Probe for human cystic fibrosis gene.
 XX
 KW Detection; nucleic acid hybrid; depolymerisation; analysis; SNP;
 KW single nucleotide polymorphism; identification; viral load; probe;
 KW genotyping; medical marker diagnostic; primer; target; mutation;
 KW genetic disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200049180-A1.
 XX
 PD 24-AUG-2000.
 XX
 PF 18-FEB-2000; 2000WO-US004242.
 XX
 PR 18-FEB-1999; 99US-00252436.
 PR 21-JUL-1999; 99US-00358972.
 PR 25-AUG-1999; 99US-00383316.
 XX
 PA (PROM-) PROMEGA CORP.
 XX
 PI Shultz JW, Lewis MK, Leippe D, Mandrekar M, Kephart D, Rhodes RB;
 PI Andrews CA, Hartnett JR, Gu T, Olson RU, Wood KV, Welch R;
 XX
 DR WPI; 2000-565377/52.
 XX
 PT Determining presence or absence of a predetermined endogenous nucleic
 PT acid sequence by using an enzyme that depolymerizes the 3' end of an
 PT oligonucleotide probe hybridized to a target sequence to release
 PT identifier nucleotides.
 XX
 PS Example; Page 325; 389pp; English.
 XX
 CC The present invention describes a method (M1) for determining the
 CC presence or absence of a predetermined endogenous nucleic acid target
 CC sequence (ENAR). The method comprises hybridising a probe having an
 CC identifier nucleotide (IN) with ENAR which is treated with an enzyme that
 CC depolymerizes the 3' end of hybridised NA to release the INs. M1 is used
 CC for determining the number of known sequence repeats present in a nucleic
 CC acid target sequence in a nucleic acid sample. The method is also useful
 CC for determining whether a nucleic acid target sequence in a sample is an
 CC allele from a homozygous or heterozygous locus. The method is also useful
 CC for detection of mutations, translocations and SNPs in nucleic acids
 CC (including those associated with genetic disease), determination of viral
 CC load, species identification, sample contamination, and analysis of
 CC forensic samples. AAA86903 to AAA87079 and AAB12817 represent sequence
 CC which are used in the exemplification of the present invention. N.B.
 CC There is a discrepancy between the SEQ ID NO: and sequences given in the
 CC examples, and the SEQ ID NO: and sequences given in the sequence listing
 CC from the present invention
 XX
 SQ Sequence 19 BP; 9 A; 5 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 895 ATCAAAGGACACGCCAAG 912
 DB 2 ATCATAGGAACACCAAG 19

RESULT 1769
 AAS07540/c
 ID AAS07540 standard; DNA; 19 BP.
 XX
 AC AAS07540;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE REVOLUTA cDNA PCR primer FIL-2.
 XX
 KW Revoluta; Rev; corn; barley; rice; tomato; PCR primer; apical meristem;
 KW leaf; floral organ; stem; transgenic plant; crop yield; cereal; fruit;
 KW pharmaceutical; industrial; ss.
 XX
 OS Arabidopsis thaliana.
 OS Synthetic.
 XX
 PN WO200133944-A1.
 XX
 PD 17-MAY-2001.
 XX
 PF 10-NOV-2000; 2000WO-US030794.
 XX
 PR 10-NOV-1999; 99US-0164587P.
 XX
 PA (SLAD/) SLADE A.
 PA (MADI/) MADISEN L.
 PA (COMA/) COMAI L.
 XX
 PI Slade A, Madisen L, Comai L;
 XX
 DR WPI; 2001-328861/34.
 XX
 PT Isolated DNA molecule comprising a sequence that encodes a REVOLUTA
 PT protein, useful for producing transgenic plants with modulated cell
 PT division.
 XX
 PS Example 4; Page 57; 149pp; English.
 XX
 CC AAS07401-AAS07571 represent REVOLUTA (REV) coding sequences and PCR
 CC primers of the invention. The REV nucleic acid sequences were isolated
 CC from plants such as Arabidopsis thaliana, tomato, corn, barley and rice.
 CC The REV gene is required to promote the growth of apical meristems, but
 CC has an opposite effect on meristems of leaves, floral organs and stems,
 CC such that it acts to limit cell division reducing the rate of plant
 CC growth and final size of the tissue. Therefore, loss of functional REV
 CC leads to increases in the size of floral organs, leaf and stem tissue.
 CC DNA encoding the REV protein is useful for modulating plant cell
 CC division. The mutant REV DNA is also useful for producing transgenic
 CC plants with modulated cell division. These transgenic plants can be used
 CC to increase crop yield in cereals and fruits, and as a potential source
 CC of pharmaceuticals and industrial products
 XX
 SQ Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 542 TCCTGGAACCTGCTAAAGT 559
 DB 19 TCCTGACGCTGCTACGT 2

RESULT 1770
 AAF60204
 ID AAF60204 standard; DNA; 19 BP.
 XX

AC AAF60204;
 XX
 DT 27-APR-2001 (first entry)
 XX
 DE Human ATM gene exon 47 forward primer.
 XX
 KW Human; ATM; ataxia telangiectasia; mutation detection;
 KW single-stranded conformation polymorphism; SSCP; electrophoresis;
 KW PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200107660-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 21-JUL-2000; 2000WO-US020011.
 XX
 PR 23-JUL-1999; 99US-00360416.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Gatti RA;
 XX
 DR WPI; 2001-168574/17.
 XX
 PT Detecting a mutation or polymorphism in human ataxia telangiectasia gene
 PT or polyexonic eukaryotic gene, involves using mega-single stranded
 PT conformation polymorphism analysis.
 XX
 PS Claim 7; Page 54; 118pp; English.
 XX
 CC The present sequence is one of a number of primers used in a method for
 CC detecting a mutation or a polymorphism in the human ATM gene, which is
 CC associated with the disease ataxia telangiectasia, or a polyexonic
 CC eukaryotic gene of at least 4 kb. The method uses an improved version of
 CC single-stranded conformation polymorphism (SSCP) electrophoresis that
 CC allows electrophoresis of two or three amplified segments in a single
 CC lane. The method is useful for screening large, complex polyexonic
 CC eukaryotic genes such as the ATM gene for mutations and polymorphisms.
 CC The new mutations and polymorphisms in the ATM gene are useful for
 CC performing more accurate screening of human DNA samples for mutations,
 CC for distinguishing mutations from polymorphisms, and for improving the
 CC efficiency of automated screening methods. The mega-SSCP method provides
 CC a screening method of genes for multiple polymorphisms and mutations at
 CC once. The method is particularly suitable for large, polyexonic,
 CC eukaryotic genes, having mutations and polymorphisms at many points and
 CC not merely at one or a few hot spots. Note: the SEQ ID assigned to this
 CC sequence in the disclosure and claims of the the specification is one
 CC number lower than the number given in the sequence listing
 XX
 SQ Sequence 19 BP; 8 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 234 CAAGCCCAATGCTGAGGA 251
 DB 1 CAAGCCCTATGATGAGAA 18

RESULT 1771
 AAH56776
 ID AAH56776 standard; DNA; 19 BP.
 XX
 AC AAH56776;
 XX
 DT 06-SEP-2001 (first entry)
 XX
 DE S. aureus groE operon antisense oligonucleotide SEQ ID NO:424.
 XX
 KW Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth;

KW sickle cell retinopathy; ss.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200130362-A2.
 PN 03-MAY-2001.
 XX 26-OCT-2000; 2000WO-US029500.
 PF 26-OCT-1999; 99US-0161532P.
 PR (IMMU-) IMMUSOL INC.
 XX Robbins JM, Tritz R;
 PI WPI; 2001-300427/31.
 DR Treating proliferative skin or eye diseases and scarring, using ribozymes
 XX that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.
 XX Example 1; Page 200; 408pp; English.
 PS The present invention describes a method for treating a proliferative
 XX skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antiskidling,
 CC ophthalmological, vulnary, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 XX exemplification of the present invention
 SQ Sequence 19 BP; 4 A; 4 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 929 AGAGCTTTAACTGCTTA 946
 Db 2 ATAGCTTTAGCTTGCTTA 19
 RESULT 1774
 AAH57580/c
 ID AAH57580 standard; DNA; 19 BP.
 XX AAH57580;
 AC 10-SEP-2001 (first entry)
 XX Cell-cycle dependent kinase cdk1 ribozyme binding site SEQ ID NO:4.
 DE Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antiskidling; ophthalmological; keratolytic; gene therapy; viral wart;

KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 XX sickle cell retinopathy; ss.
 OS Homo sapiens.
 OS Synthetic.
 XX WO200130362-A2.
 PN 03-MAY-2001.
 XX 26-OCT-2000; 2000WO-US029500.
 PF 26-OCT-1999; 99US-0161532P.
 PR (IMMU-) IMMUSOL INC.
 XX Robbins JM, Tritz R;
 PI WPI; 2001-300427/31.
 DR Treating proliferative skin or eye diseases and scarring, using ribozymes
 XX that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.
 XX Example 1; Page 72; 408pp; English.
 PS The present invention describes a method for treating a proliferative
 XX skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antiskidling,
 CC ophthalmological, vulnary, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 XX exemplification of the present invention
 SQ Sequence 19 BP; 5 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 831 GGTGCTTTCACAGTGTGG 848
 Db 18 GGTGCTTTCACAGG 1
 RESULT 1775
 AAH57971/c
 ID AAH57971 standard; DNA; 19 BP.
 XX AAH57971;
 AC 10-SEP-2001 (first entry)
 XX Cell-cycle dependent kinase cdk3 ribozyme binding site SEQ ID NO:395.
 DE Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antiskidling; ophthalmological; keratolytic; gene therapy; viral wart;

antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisking; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200130362-A2.
 XX
 XX 03-MAY-2001.
 XX
 XX 26-OCT-2000; 2000WO-US029500.
 XX
 XX 26-OCT-1999; 99US-0161532P.
 XX
 XX (IMMU-) IMMUSOL INC.
 XX
 XX Robbins JM, Tritz R;
 XX
 XX WPI; 2001-300427/31.
 XX
 XX Treating proliferative skin or eye diseases and scarring, using ribozymes
 PT that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.
 XX
 XX Example 1; Page 100; 408pp; English.
 PS
 CC The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisking,
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 19 BP; 4 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1193 CTGGGTCCTCAATGCAGG 1210
 Db ||||| ||||| |||||
 19 CTGGGTCATCTGCAGG 2
 RESULT 1776
 AAH58450
 ID AAH58450 standard; DNA; 19 BP.
 XX
 AC AAH58450;
 XX
 XX 10-SEP-2001 (first entry)
 DT
 XX Cell-cycle dependent kinase cdk8 ribozyme binding site SEQ ID NO:874.
 DE
 XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;

cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisking; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200130362-A2.
 XX
 XX 03-MAY-2001.
 XX
 XX 26-OCT-2000; 2000WO-US029500.
 XX
 XX 26-OCT-1999; 99US-0161532P.
 XX
 XX (IMMU-) IMMUSOL INC.
 XX
 XX Robbins JM, Tritz R;
 XX
 XX WPI; 2001-300427/31.
 XX
 XX Treating proliferative skin or eye diseases and scarring, using ribozymes
 PT that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.
 XX
 XX Example 1; Page 135; 408pp; English.
 PS
 CC The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisking,
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 19 BP; 4 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 486 TCGAAGAGTCCGAGGC 503
 Db ||||| ||||| |||||
 2 TCGAAGTTCGCGAGGC 19
 RESULT 1777
 AAH58975/c
 ID AAH58975 standard; DNA; 19 BP.
 XX
 AC AAH58975;
 XX
 XX 10-SEP-2001 (first entry)
 DT
 XX Cdk-we-hu ribozyme binding site SEQ ID NO:1399.
 DE
 XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;

Cell-cycle dependent kinase cdk8 ribozyme binding site SEQ ID NO:922.

Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnery; proliferative disease; skin disease; psoriasis; diabetic retinopathy; cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP; matrix metalloproteinase; growth factor; reductase; scarring; cytotatic; antipsoriatic; dermatological; antiseborrheic; keratolytic; cytostatic; antisking; ophthalmological; antiseborrheic; antidiabetic; virucide; atopic dermatitis; actinic keratosis; gene therapy; viral wart; basal cell carcinoma; seboreic wart; squamous cell carcinoma; sickle cell retinopathy; ss.

Homo sapiens.
OS Synthetic.
XX
OS
XX
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029500.
XX
PF 26-OCT-1999; 99US-0161532P.
XX
XX (IMMU-) IMMUSOL INC.
PA
XX
PI Robbins JM, Tritz R;
XX
XX WPI; 2001-300427/31.
DR
XX
PT Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.
PT
XX
PS Example 1; Page 139; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme (I) which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid segment encoding (I). (I) can have antipsoriatic, dermatological, cytostatic, antiseborrheic, antidiabetic, antisking, ophthalmological, vulnery, keratolytic and virucide activities, and cleaves RNA encoding cytokine involved in inflammation. (I) can be used in gene therapy. (I) and (II) are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, squamous or basal cell carcinoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing scarring such as keloid, adhesion and hypertrophic or hypertrophic burn scar. AAH57577 to AAH62099 represent sequences used in the exemplification of the present invention
CC
CC
SQ Sequence 19 BP; 7 A; 4 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 421 AGTCTGTGAACCTTAAT 438
Db 19 AGCTCTGTGAACCTTGAT 2
|| |||||
RESULT 1780
AAH61221/c
ID AAH61221 standard; DNA; 19 BP.
XX
AC AAH61221;

XX OS Feline immunodeficiency virus.
XX PN WO200242482-A2.
XX PD 30-MAY-2002.
XX PF 27-NOV-2001; 2001WO-US044617.
XX PR 27-NOV-2000; 2000US-0253419P.
XX PA (CHIR) CHIRON CORP.
XX PI Dubensky TW, Gasmí M, Sauter SL;
XX DR WPI; 2002-471730/50.
XX PT Chimeric murine leukemia virus-feline leukemia virus vector construct,
XX PT useful in gene therapy for treating diabetes, cystic fibrosis, cancer,
XX PT hypercholesterolemia, hyperlipidemia, anemia, hemophilia, hepatitis.
XX PS Example 5; Page 88; 108pp; English.
XX XX The invention relates to a chimeric murine leukemia virus (MLV)-feline
XX CC immunodeficiency virus (FIV) vector construct (I), comprising an MLV
XX CC vector backbone and an FIV vector construct. (I) is useful for delivering
XX CC a desired heterologous sequence to a vertebrate or insect e.g. cat, to
XX CC establish an animal model for studying the parameters of gene delivery in
XX CC vivo, and also useful in veterinary application. (I) is also useful in
XX CC therapeutic or productive purposes e.g. for stimulating a specific immune
XX CC response, inhibiting the interaction of an agent with a host cell
XX CC receptor, to express a toxic palliative (conditional toxic palliatives),
XX CC to immunologically regulate the immune system to express markers
XX CC (phosphatase gene, beta-galactosidase gene or luciferase gene) for
XX CC replacement gene therapy and/or to produce a recombinant protein. (I) is
XX CC useful for preventing, inhibiting, stabilizing or reversing infectious,
XX CC cancerous, autoimmune or immune diseases e.g. viral infections such as
XX CC human immunodeficiency virus (HIV), hepatitis B virus (HBV), hepatitis C
XX CC virus (HCV), melanomas, diabetes, diabetes, graft versus host disease, Alzheimer's
XX CC disease and heart disease (myocardial infarction), for stimulating an
XX CC immune response against pathogenic agents such as bacteria, fungi, virus
XX CC and cancer cells. (I) is involved in inhibiting viral assembly and is
XX CC useful for treating Goucher's disease, hemophilia, hereditary disorders
XX CC such as thalassemia, phenylketonuria, cystic fibrosis, Duchenne's
XX CC muscular dystrophy, emphysema, hypercholesterolemia, hyperlipidemia,
XX CC anemia, obesity, autoimmune disease, anorexia, inflammation, hepatitis,
XX CC lentiviral infection. (I) is useful for preventing the spread of
XX CC metastatic tumour and also for modulating transcription factor activity.
XX CC Sequences ABL60721-24 represent primers for constructing a packaging
XX CC expression cassette pCMV-FIVXho
XX SQ Sequence 19 BP; 6 A; 2 C; 7 G; 4 T; 0 U; 0 Other;
XX Query Match 0.6%; Score 13.2; DB 1; Length 19;
XX Best Local Similarity 83.3%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1694 GCCACCTTGCACCCATT 1711
DB 19 GCCACATTGCCTACCAT 2
RESULT 1783
AAD22914
ID AAD22914 standard; DNA; 19 BP.
XX AC AAD22914;
XX DT 26-FEB-2002 (first entry)
XX XX Murine leukemia virus; MLV; feline immunodeficiency virus; FIV; chimeric;
XX DE cytostatic; virucide; hepatotropic; antiinflammatory; antileptic;
XX XX antidiabetic; immunosuppressive; nootropic; neuroprotective; cardiac;
XX XX antibacterial; fungicide; haemostatic; antianemic; anorectic; anti-HIV;
XX KW gene therapy; mutagenic; PCR; primer; ss.

XX AC AAF97791;
XX DT 31-MAY-2001 (first entry)
XX DE Human nerve growth factor beta (lp13) PCR primer SEQ ID NO:5.
XX KW Human; chromosome 1; lp36; neuroblastoma cell line; NB-1; anticancer;
XX KW tumour suppressor; human lp36 homozygosity deletion domain; tumour;
XX KW diagnosis; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200116311-A1.
XX PD 08-MAR-2001.
XX PF 31-AUG-2000; 2000WO-JP005930.
XX PR 31-AUG-1999; 99JP-00245962.
XX PR 09-MAY-2000; 2000JP-00136266.
XX PA (HISM) HISAMITSU PHARM CO LTD.
XX PA (CHIB-) CHIBA PREFECTURE.
XX PI Nakagawara A;
XX DR WPI; 2001-226686/23.
XX XX Human lp36 homozygosity deletion domain from the 36-position of first
XX PT chromosome short arm in human neuroblastoma cell lines, applicable e.g.
XX PT in gene diagnosis of tumors as well as in developing anti-cancer drugs.
XX PS Example 4; Page 15; 226pp; Japanese.
XX XX The present invention describes a homozygosity deletion domain co-
XX CC existing in the 36-position of the first chromosome short arm (lp36) in
XX CC human neuroblastoma. Also described are base sequences from the lp36
XX CC position of human neuroblastoma cell lines (NB-1 and MASS-NB-SCH-1),
XX CC which are tumour suppressor genes in human neuroblastoma. The genes are
XX CC tumour suppressor genes, base sequence data of which are applicable as
XX CC tumour markers and reagents in studying mechanism of tumour body
XX CC formation, and gene diagnosis of tumours as well as in developing anti-
XX CC cancer drugs. AAF97787 to AAF97829 represent PCR primers used in the
XX CC exemplification of the present invention, and AAF97830 to AAF97874
XX CC represent sequences given in the exemplification of the present invention
XX SQ Sequence 19 BP; 5 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
XX Query Match 0.6%; Score 13.2; DB 1; Length 19;
XX Best Local Similarity 83.3%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 737 ACTACCGCTCGGAGCG 754
DB 1 ACTAACAGCTCGGTGACG 18
RESULT 1782
ABL60721/c
ID ABL60721 standard; DNA; 19 BP.
XX AC ABL60721;
XX DT 27-AUG-2002 (first entry)
XX DE Packaging expression cassette pCMV-FIVXho generating primer FIV5.
XX XX Murine leukemia virus; MLV; feline immunodeficiency virus; FIV; chimeric;
XX KW cytostatic; virucide; hepatotropic; antiinflammatory; antileptic;
XX KW antidiabetic; immunosuppressive; nootropic; neuroprotective; cardiac;
XX KW antibacterial; fungicide; haemostatic; antianemic; anorectic; anti-HIV;
XX KW gene therapy; mutagenic; PCR; primer; ss.

KW OS Unidentified.
 XX PN WO200177153-A2.
 XX PD 18-OCT-2001.
 XX 10-APR-2001; 2001WO-US011630.
 XX PR 10-APR-2000; 2000US-0195785P.
 XX PA (UMOR) UNIV MISSOURI.
 XX English JT, Schmidt FU, Smith GP, Morris RO, Bishop-Hurley S;
 XX WPI; 2002-025897/03.
 XX Identification of fungicidal peptides involves constructing peptide phage
 PT display libraries using degenerate oligonucleotides, contacting the
 PT peptide library with fungi followed by isolation of bound phage and
 PT identification.
 XX Example 5; Page 22; 72pp; English.
 XX The invention relates to identification of non-immunoglobulin peptides
 CC having an affinity for the surface of fungi. The method involves
 CC constructing peptide phage display libraries using degenerate
 CC oligonucleotides; contacting a vector expressing the peptide library with
 CC a target fungus; eluting the bound vector from fungi; sequencing the
 CC oligonucleotides from eluted vectors; deducing an amino acid sequence of
 CC peptide and selecting the non-immunoglobulin peptides. The method is
 CC useful for identification of antifungal peptides. The method is
 CC plants for the pathogens, preferably members of genus Phytophthora, to
 CC treat soil and to confer immunity of the plant against the pathogen. The
 CC present sequence is a primer used to isolate, sequence and analyse f8
 CC phage-displayed peptide DNA clones
 XX SQ Sequence 19 BP; 8 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1460 AGGAGGAGGAGGAGGAGGAGG 1477
 Db 1 AGTAGCAGAGGCTGTGAG 18
 RESULT 1784
 ABK89999
 ID ABK89999 standard; DNA; 19 BP.
 XX AC ABK89999;
 XX 21-OCT-2002 (first entry)
 XX Mouse beta-actin, PCR primer #1.
 XX Mouse; immune response; chronic B-lymphoproliferative disorder; CDR3;
 KW complementarity determining region 3; hypervariable region; B-cell;
 KW immunoglobulin heavy chain; VH-CDR3; idiotype immunoglobulin;
 KW cytotostatic; beta-actin; PCR; primer; ss.
 XX OS Mus sp.
 XX WO200255559-A1.
 XX 18-JUL-2002.
 XX 15-JAN-2001; 2001WO-IT000014.
 XX 15-JAN-2001; 2001WO-IT000014.

XX (FAZI/) FAZIO V M.
 PA (SAGL/) SAGLIO G.
 XX Fazio VM, Saglio G;
 XX WPI; 2002-583654/62.
 XX Use of DNA sequences coding for hypervariable region (VH- complementarity
 PT determining region 3 (CDR3)) of idiotype immunoglobulin expressed on B-
 PT cells of chronic B- lymphoproliferative disorders, as therapeutic
 PT vaccine.
 XX Example 5; Page 16; 30pp; English.
 XX The present invention relates to a method for inducing an immune response
 CC against B-lymphoproliferative disorders. The method comprises DNA
 CC sequences encoding for the complementarity determining region 3 (CDR3)
 CC hypervariable region of immunoglobulin heavy chain (VH-CDR3) alone or in
 CC combination with at least another immunomodulating sequence. The DNA
 CC sequences are useful as therapeutic vaccines for chronic B-
 CC lymphoproliferative disorders in mammals, preferably humans. A
 CC recombinant plasmid expression vector containing a DNA sequence of the
 CC vaccine is useful as a therapeutic vaccine or for the manufacture of a
 CC expressing the surface idiotype immunoglobulin on B-cells in mammals,
 CC preferably humans. An efficient, safe and easily reproducible DNA-based
 CC immune response against B-lymphoproliferative pathologies can be
 CC achieved. The present sequence represents a PCR primer used to amplify
 CC mouse beta-actin cDNA in the examples of the present invention
 XX SQ Sequence 19 BP; 2 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 774 TGAGGCCATTTCAGCC 791
 Db 1 TGAGGCTCTTTCCAGCC 18
 RESULT 1785
 ABT11233
 ID ABT11233 standard; DNA; 19 BP.
 XX AC ABT11233;
 XX 12-DEC-2002 (first entry)
 XX TRC8 related PCR primer SEQ ID No 38.
 XX TRC8; Translocation in Renal cancer from Chromosome 8; fused DNA; 3 2;
 KW FHIT/TRC8 fusion DNA; sporadic renal cell carcinoma; TRC8/FHIT; TRC8FHIT;
 KW human chromosomal translocation; PCR; primer; ss.
 XX Homo sapiens.
 XX US2002106656-A1.
 XX 08-AUG-2002.
 XX 02-JUL-2001; 2001US-00898533.
 XX 12-MAR-1998; 98US-0077723P.
 XX 12-MAR-1999; 99US-00268140.
 XX (GENM/) GEMMILL R M.
 PA (DRAB/) DRABKIN H A.
 XX Gemmill RM, Drabkin HA;
 XX WPI; 2002-712395/77.

CC and/or cleavable element. The series of nested primers comprise primers
CC complementary to different portions of the template and are 5' to one
CC another with respect to the template and do not overlap with one another
CC at the position of the non-replicable and cleavable elements. The method
CC of the invention may be used for amplifying nucleic acid sequences of
CC interest contained in the complementary first and second nucleic acid
CC strands which are prepared from RNA by reverse transcription. This method
CC is capable of producing large quantities of a specific nucleic acid
CC sequence of interest. The products are single stranded and do not have to
CC be denatured prior to detection. As the products accumulate linearly,
CC they can be accurately identified. The occurrence of false positives will
CC be reduced in comparison with exponential processes that use newly
CC synthesised DNA as template in subsequent rounds using the same primer.
CC The present sequence represents the linked linear amplification related
CC oligonucleotide #30 of the invention
XX
SQ Sequence 19 BP; 8 A; 6 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 808 ATGAGATGTTCCAGCT 825
DB 19 ATGAGTGTGTTCTGCT 2
RESULT 1787
ABL55870/c
ID ABL55870 standard; DNA; 19 BP.
XX ABL55870;
AC ABL55870;
DT 15-JUL-2002 (first entry)
XX Hepatitis B virus primer pIespHBV-2.
DE Hepatitis B virus; HBV; vaccine; hepatitis B surface antigen; HBsAg;
KW Hepatitis B virus.
KW primer; ss.
XX Hepatitis B virus.
OS KR2001095658-A.
PN KR2001095658-A.
XX 07-NOV-2001.
PD 11-APR-2000; 2000KR-00018946.
PF 11-APR-2000; 2000KR-00018946.
PR 11-APR-2000; 2000KR-00018946.
XX (ILYA-) IL YANG PHARM CO LTD.
PA Jung SG, Kim HJ;
XX WPI; 2002-301914/34.
DR Producing HBsAg pres2 and S proteins and HBV vaccine comprises use of
PT recombinant technology and affinity chromatography.
XX Example 1; Page 6; 12pp; Korean.
XX The sequence represents a primer used in the invention. The invention
CC relates to a novel method for producing hepatitis B surface antigen
CC (HBsAg) pres2 and S proteins and hepatitis B virus (HBV) vaccine
XX Sequence 19 BP; 2 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1448 AGGAGAAACCAAGGAGG 1465
DB 1448 AGGAGAAACCAAGGAGG 1465

XX Novel Translocation in Renal cancer from Chromosome 8 genes, useful for
PT detection of tumors, comprises rearrangements in the t(3;8)(p14.2;q24.1)
PT chromosomal translocation which occurs in renal and thyroid carcinomas.
XX
PS Claim 9; Page 10; 49pp; English.
XX The invention relates to an isolated TRC8 (Translocation in Renal cancer
CC from Chromosome 8) nucleic acid molecule, encoding a polypeptide
CC comprising a sequence of 664 amino acids fully defined in the
CC specification and comprising a sequence located in the 5' flanking region
CC to the coding region of TRC8 and a sequence which occurs in certain
CC sporadic renal cell carcinomas. The methods are useful for detecting the
CC presence of the TRC8 gene in a biological sample, detecting alterations
CC to the gene, such as a 3:2 human chromosomal translocation, and fused DNA
CC containing the fused site of TRC8/PHIT. A nucleic acid probe is useful
CC for detecting the 3:8 human chromosomal translocation, by contacting the
CC nucleic acid probe with a biological sample to be tested, and determining
CC whether the nucleic acid probe specifically hybridises to the TRC8/PHIT or
CC PHIT/TRC8 fusion DNA. This polynucleotide sequence represents a TRC8
CC related PCR primer of the invention
XX
SQ Sequence 19 BP; 7 A; 8 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 144 CCACCCCAATGAAGCTCA 161
DB 1 CCACCCCAATGAAGCTCA 18
RESULT 1786
ABK14617/c
ID ABK14617 standard; DNA; 19 BP.
XX ABK14617;
AC ABK14617;
XX 08-MAY-2002 (first entry)
DT Linked linear amplification related oligonucleotide #30.
DE Nucleic acid amplification; linked linear amplification; LLA; ss.
XX Homo sapiens.
OS US6335184-B1.
PN 01-JAN-2002.
PD 11-JAN-1999; 99US-00228324.
PF 23-JUL-1993; 93US-00095442.
PR 02-APR-1997; 97US-00826532.
XX (BIRA) BIO-RAD LAB INC.
PA Reyes AA, Wallace RB, Ugozzoli LA;
XX WPI; 2002-163204/21.
DR Linked linear amplification of nucleic acid sequence of interest
PT contained within complementary nucleic acids by using series of nested
PT primers each of which contains a non-replicable element and/or cleavable
PT element.
XX Disclosure; Col 41; 42pp; English.
PS This invention relates to a novel method of nucleic acid amplification
XX called linked linear amplification (LLA). The method involves
CC simultaneously combining a series of nested primers by combining nucleic
CC acid template with nested primer each containing non-replicable element

Db 19 AGGATAAAACCTAGCAGG 2

RESULT 1788
ABK10455

ID ABK10455 standard; DNA; 19 BP.
XX
AC ABK10455;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human TRC8 coding region SSCP PCR primer 9F.
XX
KW Human; ss; translocation in renal cancer from chromosome 8; 9F; TRC8;
KW fragile histidine triad; FHIT; renal cell carcinoma; t(3; 8);
KW single-stranded conformational polymorphism; thyroid tumour; PCR; primer;
XX SSCP.
XX
OS Homo sapiens.
XX
FN US6268176-B1.
XX
PD 31-JUL-2001.
XX
PF 12-MAR-1999; 99US-00268140.
XX
PR 12-MAR-1998; 98US-0077723P.
XX
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI Gemmill RM, Drabkin HA;
XX
DR WPI; 2002-224110/28.
XX

New TRC8 (Translocation in Renal Cancer from Chromosome 8) polypeptide,
PT useful for diagnosing tumors, particularly for determining TRC8 gene
PT expression in samples.
XX
PS Example 5; Col 17; 45pp; English.
XX

The invention relates to a polypeptide (which is the product of the
CC expression in a host cell of a DNA) TRC8 (translocation in Renal Cancer
CC from Chromosome 8). Also included are a polypeptide product of the
CC expression in a host cell of a DNA, comprising (a) culturing a host cell
CC containing a vector comprising a nucleic acid molecule encoding the
CC polypeptide comprising TRC8 and (b) recovering the polypeptide. The gene
CC encoding TRC8 is located in the chromosomal translocation region t(3;8),
CC resulting in a fusion with the fragile histidine triad gene, FHIT. This
CC region is associated with renal and thyroid tumors (especially renal
CC cell carcinoma, RCC). The polypeptide is useful for diagnosing tumors,
CC particularly for determining if the TRC8 gene is expressed in samples.
CC The present sequence is an single-stranded conformational polymorphism
CC (SSCP) PCR primer used to identify tumour specific mutations in TRC8 in
CC sporadic renal cell carcinoma samples
XX

SQ Sequence 19 BP; 7 A; 8 C; 2 G; 2 T; 0 U; 0 Other;
XX

Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 144 CCACCCCAATGAAGCCTCA 161
|||||
1 CCACCCCAATGAAGCCTCA 18

Db

RESULT 1789
ABK13429

ID ABK13429 standard; DNA; 19 BP.
XX
AC ABK13429;
XX
DT 23-APR-2002 (first entry)

XX OS Homo sapiens.
XX PN WO200248369-A2.
XX PD 20-JUN-2002.
XX PF 01-NOV-2001; 2001WO-US050726.
XX PR 02-NOV-2000; 2000US-0245366P.
XX PR 21-DEC-2000; 2000US-0257851P.
XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX PI Feder JN, Lee LM, Chen J, Jackson D, Ramanathan C, Siemers N;
XX PI Chang H;
XX DR WPI; 2002-583519/62.
XX XX Novel human potassium channel beta-subunit, KMBETAL polypeptide and
XX PT polynucleotides for diagnosing, prognosing, preventing, treating immune,
XX PT hyperproliferative, cardiovascular disorder and for identifying
XX PT modulators.
XX PS Example 3; Page 210; 316pp; English.
XX CC The present invention describes the human potassium channel beta-subunit
XX CC K-Mbeta1 (I). (I) has immunosuppressive, nephrotropic, neuroprotective,
XX CC antithyroid, dermatological, antiinflammatory, cardiant, vasotropic,
XX CC anticoagulant, antimigraine, cytostatic, vulnary and antibacterial
XX CC activities, and can be used in gene therapy and antisense therapy. (I)
XX CC can be used for screening candidate compounds (small molecules) capable
XX CC of binding to and/or modulating activity of a potassium channel beta-
XX CC subunit, by contacting a test compound with a substantially or partially
XX CC purified (I) and selecting a candidate compound those test compounds
XX CC that bind to and/or modulate activity of the polypeptide. (I) stimulates
XX CC neuronal growth which can be used to treat, prevent, and/or diagnose
XX CC neuronal damage which occurs in certain neuronal disorders or neuro-
XX CC degenerative conditions. (I) can be used in treating, preventing and/or
XX CC diagnosing diseases, disorders or conditions associated with: autoimmune
XX CC diseases; inflammatory conditions; hyperproliferative diseases; cancer;
XX CC cardiovascular disorders; cerebrovascular disease; inflammation; and
XX CC bacterial, fungal or parasitic infection. (I) is also useful as a vaccine
XX CC adjuvant that enhances immune responsiveness to an antigen, as a vaccine
XX CC to enhance tumour-specific immune responses. Further (I) is useful as a
XX CC anti-fungal, anti-parasitic immune responses. Further (I) is useful as a
XX CC stimulator of B cell responsiveness to pathogens, as an activator of T
XX CC cells, as an agent to boost immunoresponsiveness among aged populations
XX CC and/or neonates, as a stimulator of cytokines, to enhance or inhibit
XX CC complement mediated cell lysis, for stimulating wound and tissue repair,
XX CC angiogenesis, and the repair of vascular or lymphatic diseases or
XX CC disorders. The present sequence represents a PCR primer for (I), which is
XX CC used in an example from the present invention
XX SQ Sequence 19 BP; 1 A; 3 C; 8 G; 7 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1670 TGTGCTGGGTGAGCTCTT 1687
DB 1 TGTGCTGCTGGGCACTT 18
RESULT 1791
ABQ73687
ID ABQ73687 standard; DNA; 19 BP.
XX AC ABQ73687;
XX 17-OCT-2002 (first entry)
XX DT

XX Key Location/Qualifiers
XX modified_base 1 /*tag= a
XX FT /*note= "Blotynlated"
XX PN WO200220837-A2.
XX PD 14-MAR-2002.
XX PF 10-SEP-2001; 2001WO-GB004042.
XX PR 08-SEP-2000; 2000GB-00022069.
XX PA (PYRO-) PYROSEQUENCING AB.
XX PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX PA (GARD/) GARDNER R.
XX PI Ronaghi M, Ekstroem B, Pourmand N;
XX DR WPI; 2002-393849/42.
XX XX Typing nucleic acid for obtaining information about several variable
XX PT sites involves simultaneously or sequentially performing two or more
XX PT primer extension reactions, and determining the pattern of nucleotide
XX PT incorporation.
XX PS Example 2; Page 47; 86pp; English.
XX CC The invention relates to a novel method for obtaining typing information
XX CC about several variable sites within target nucleic acid, or typing one or
XX CC more nucleic acid molecules. The methods of the invention are useful for
XX CC typing one or more nucleic acid molecules containing two or more variable
XX CC sites, preferably nucleic acid molecules containing three or more
XX CC variable sites are typed, where three or more primer extension reactions
XX CC are performed. The method is also useful for diagnosis of pathological
XX CC conditions characterized by the presence of specific nucleic acid
XX CC molecule(s). The methods are particularly suited for identifying
XX CC microbial species or their subtypes, and in typing procedures e.g. typing
XX CC of polymorphisms, tissue typing or in clinical applications. The sequence
XX CC represents a PCR primer used in the invention to amplify a specific
XX CC target region of genomic DNA
XX SQ Sequence 19 BP; 2 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1134 GTACTCTGGAGAGATCAA 1151
DB 19 GTACTCTGGAGAGAGCGA 2
RESULT 1791
ABQ73687
ID ABQ73687 standard; DNA; 19 BP.
XX AC ABQ73687;
XX 04-OCT-2002 (first entry)
XX DT Human potassium channel beta-subunit K-Mbeta1 PCR primer SEQ ID NO: 6.
XX DE Human; potassium channel beta-subunit; K-Mbeta1; potassium channel;
XX KW immunosuppressive; nephrotropic; neuroprotective; antiinflammatory;
XX KW antithyroid; dermatological; cardiant; vasotropic; anticoagulant;
XX KW antimigraine; cytostatic; vulnary; antibacterial; gene therapy;
XX KW antisense therapy; neuronal growth; neuronal damage; neuronal disorder;
XX KW neurodegenerative condition; autoimmune disease; inflammatory condition;
XX KW hyperproliferative disease; cancer; cardiovascular disorder; infection;
XX KW cerebrovascular disease; inflammation; vaccine; lymphatic disease;
XX KW angiogenesis; vascular disease; PCR primer; ss.

```

DE Human CD23 + A1261 oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Disclosure; SEQ ID NO 13583; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytosstatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 19 BP; 3 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 19;
XX Best Local Similarity 83.3%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 560 ATCACCAGAGGGTGTGT 577
XX ||| ||||| ||||| |||||
XX 2 ATCTGAGAGGGTGTGT 19
XX
XX RESULT 1793
XX ABZ97606/c
XX ID ABZ97606 standard; DNA; 19 BP.
XX
XX AC ABZ97606;
XX
XX 17-OCT-2003 (first entry)
XX
DE Human IL5-R oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Disclosure; SEQ ID NO 12848; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytosstatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 19 BP; 4 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 19;
XX Best Local Similarity 83.3%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1003 TATGAGACAGCTGTGCC 1020
XX ||||| ||||| ||||| |||||
XX 18 TATGAGAAAGCTGGTCC 1
XX
XX RESULT 1794
XX ABT21412/c
XX ID ABT21412 standard; DNA; 19 BP.
XX
XX AC ABT21412;
XX
XX 16-APR-2003 (first entry)
XX

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DE Multiplex group PCR primer #159.
XX Racing potential; horse; grandpaternal DNA; over-represented; breeding;
KW grandmother; performance; progeny horse; PCR; primer; ss.
XX
XX Unidentified.
OS
XX WO200292851-A2.
PN
XX
XX 21-NOV-2002.
PD
XX
XX 15-MAY-2002; 2002WO-GB002273.
PF
XX
XX 15-MAY-2001; 2001GB-00011886.
PR
XX
XX (ANIM-) ANIMAL HEALTH TRUST.
PA (BRHO-) BRITISH HORSE RACING BOARD.
PA
PI Binns MM, Swinburne JE;
XX
XX WPT; 2003-129314/12.
DR
XX Determining the racing potential of a horse comprises measuring whether
XX grandpaternal or grandmaternal DNA from the selected grandmother DNA is
XX over-represented in the genome of the horse.
XX
XX Example 2; Page 24; 49pp; English.
PS
XX The invention relates to a novel method for determining racing potential
XX of a horse. The method comprises measuring: whether grandpaternal DNA is
XX over-represented in the genome of the horse; or in the case where one of
XX the grandmothers was selected for breeding on the basis of racing
XX performance, whether grandmaternal DNA from the selected grandmother is
XX over-represented in the genome of the horse which indicates that the
XX horse has good racing potential. The method of the invention is useful
XX for determining the racing potential of a horse or for obtaining a
XX progeny horse with good racing potential. This polynucleotide sequence
XX represents a PCR primer used in the detection method of over-
XX representation of DNA from male grandparents of the invention
XX
XX Sequence 19 BP; 6 A; 2 C; 7 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1544 GTCCTCAGGTTCTTCC 1561
DB 19 GTCCTCAGGTTCTTCC 2
RESULT 1795
ABT16464/c
ID ABT16464 standard; DNA; 19 BP.
XX
XX AC ABT16464;
XX
XX 20-MAR-2003 (first entry)
DT
DE Human neurokinin 1 receptor gene related PCR primer SEQ ID No 45.
DE
XX Cytostatic; antiasthmatic; antiinflammatory; cardiant; polymorphic site;
KW human neurokinin 1 receptor; TACR1; disease phenotype; forensics;
KW TACR1 ligand mediated disease; asthma; paternity testing; cancer;
KW inflammation; heart disease; central nervous system; infection; PCR;
KW primer; ss.
XX
XX Unidentified.
OS
XX EP1262565-A2.
PN
XX 04-DEC-2002.
PD
XX

PF 23-MAY-2002; 2002EP-00253662.
XX
XX 25-MAY-2001; 2001US-0293425P.
XX
XX (PFIZ) PFIZER PROD INC.
PA
XX Affourtit JP, Nelson DL, Seymour AB, Webb SM;
PI
XX WPT; 2003-150228/15.
DR
XX Novel nucleic acid segment from human neurokinin 1 receptor, including
XX polymorphic sites for diagnosing and treating asthma, and in forensics,
XX paternity testing, and genetic mapping of the traits.
XX
XX Example; Page 12; 27pp; English.
PS
XX The invention relates to a nucleic acid segment from the human neurokinin
XX 1 receptor (TACR1) gene of 10-100 nucleotides comprising a fragment
XX having a polymorphic site or a complement of the fragment. The TACR1
XX segment is useful for analysing a nucleic acid, by obtaining the nucleic
XX acid from an individual, and determining the base occupying any one of
XX the polymorphic sites in the segment. The nucleic acid is obtained from
XX several individuals, and the base occupying one of the polymorphic sites
XX is determined in each of the individuals, and further involves testing
XX each of the individuals for the presence of a disease phenotype, and
XX correlating the presence with the base. The TACR1 segment is useful for
XX diagnosing and treating TACR1 ligand mediated diseases, such as asthma.
XX The TACR1 segment is also useful in forensics, paternity testing,
XX correlating polymorphisms with phenotypic traits, and genetic mapping of
XX phenotypic traits. The TACR1 segment is useful in diagnosing and
XX monitoring of diseases such as cancer, inflammation, heart disease,
XX diseases of central nervous system, and susceptibility to infection to
XX microorganisms. The TACR1 segment is also useful in the manufacture of a
XX medicament for the treatment of the diseases. This polynucleotide
XX sequence represents a PCR primer of the human neurokinin 1 receptor
XX (TACR1) gene of the invention
XX
XX Sequence 19 BP; 2 A; 9 C; 2 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 326 GCACGACATGCAGAGAT 343
DB 19 GCGACGACATGCAGAGAT 2
RESULT 1796
ACA90054/c
ID ACA90054 standard; DNA; 19 BP.
XX
XX AC ACA90054;
XX
XX 10-JUL-2003 (first entry)
DT
DE Cardiovascular disease differential gene expression related primer #101.
DE
XX Cardiovascular disease; arteriosclerosis; ischaemia; angina pectoris;
KW myocardial infarction; cardiant; antiarteriosclerotic; antianginal;
KW gene therapy; differential gene expression; PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX WO2003031650-A2.
PN
XX 17-APR-2003.
PD
XX 02-OCT-2002; 2002WO-EP011034.
PF
XX 08-OCT-2001; 2001GB-00024145.
PR
XX (FARB) BAYER AG.
PA

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XX
PI Munnes M, Gehrman M, Wick M, Schmitz G;
DR WPI; 2003-403108/38.
XX
XX Predicting, diagnosing or prognosing a cardiovascular disease, e.g.
XX PT angina, ischemia, myocardial infarction or arteriosclerosis by detection
XX PT of a polynucleotide in a biological sample comprises detecting a
XX PT hybridization complex.
XX
XX Example 3; Page 105; 454pp; English.
XX
XX The invention describes a method of predicting, diagnosing or prognosing
XX CC a cardiovascular disease by detection of a polynucleotide in a biological
XX CC sample comprises hybridising at least one of the polynucleotide to a
XX CC nucleic acid material of a biological sample, thus forming a
XX CC hybridisation complex, and detecting the hybridisation complex. The
XX CC polynucleotides, polypeptides, antisense molecule, antibody and reagent
XX CC are useful for preparing compositions for preventing, predicting or
XX CC diagnosing, or a medicament for treating a cardiovascular disease, e.g.
XX CC arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction.
XX CC This sequence represents a primer used to identify genes differentially
XX CC regulated in individuals with cardiovascular disease
XX
XX SQ Sequence 19 BP; 6 A; 6 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1542 GAGTCCCTCAGTTCTT 1559
DB 18 GGGTCCCTCAGTTCTT 1
RESULT 1797
ABZ58621
ID ABZ58621 standard; DNA; 19 BP.
XX
XX AC ABZ58621;
XX
XX DT 14-APR-2003 (first entry)
XX
XX DE Cytochrome P450 (CYP450) cDNA probe specific primer.
XX
XX KW CYP450; cytochrome P450; isoform; primer; PCR; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO2002101031-A1.
XX
XX PD 19-DEC-2002.
XX
XX PF 11-JUN-2001; 2001WO-BP007056.
XX
XX PR 11-JUN-2001; 2001WO-BP007056.
XX
XX PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX PI De Waziers I, Couteau C, Gros C, Moncion A, Beaune P;
XX
XX DR WPI; 2003-175177/17.
XX
XX New polynucleotide, useful for detecting Cytochromes P450 (CYP450)
XX PT isoforms and for evaluating the toxicity or pathogenicity of a product
XX PT and predicting drug in vivo interactions or efficiency.
XX
XX PS Claim 2; Fig 2; 52pp; English.
XX
XX The invention relates to a set of new cDNA probes which enables the
XX CC specific and simultaneous detection of the main fourteen CYP450
XX CC (cytochrome P450) isoforms and to new primers specific for the probes.
XX CC The probes and primers are useful for detecting CYP450 isoforms and for

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CC evaluating the toxicity or pathogenicity of a product and predicting drug
CC in vivo interactions or efficiency. Sequences ABZ58615-642 represent
CC specific examples of the primers specific for the CYP450 cDNA probes
XX
XX SQ Sequence 19 BP; 5 A; 3 C; 10 G; 1 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1341 GGGAGAGGGGGCGCCAA 1358
DB 1 GGGAGAGGGGGCGCAGCTA 18
RESULT 1798
ADD69492
ID ADD69492 standard; DNA; 19 BP.
XX
XX AC ADD69492;
XX
XX DT 15-JAN-2004 (first entry)
XX
XX DE PCR primer 13 used to distinguish Basmati and semi dwarf rice varieties.
XX
XX KW inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;
XX KW animal; Basmati rice; ss.
XX
XX OS Unidentified.
XX
XX PN WO2003085133-A2.
XX
XX PD 16-OCT-2003.
XX
XX PF 09-JAN-2003; 2003WO-IB000041.
XX
XX PR 08-APR-2002; 2002IN-CH000260.
XX
XX PA (DNAP-) CENT DNA FINGERPRINTING & DIAGNOSTICS.
XX
XX PI Nagaraju JG;
XX
XX DR WPI; 2003-804317/75.
XX
XX PT New set of inter-simple sequence repeats (ISSR)-PCR primers for
XX PT genotyping eukaryotes, useful for genotyping diverse genomes of plant and
XX PT animal systems.
XX
XX PS Disclosure; Page 21; 60pp; English.
XX
XX CC The invention relates to a novel set of inter-simple sequence repeats
XX CC (ISSR)-PCR primers for genotyping eukaryotes. The primers of the
XX CC invention may be useful for genotyping diverse genomes of plant and
XX CC animal systems, in particular for distinguishing Basmati rice varieties
XX CC from non-Basmati rice varieties and traditional Basmati rice varieties
XX CC from evolved Basmati rice varieties. The current sequence is that of the
XX CC PCR primer of the invention which may be used to distinguish Basmati and
XX CC semi dwarf rice varieties.
XX
XX SQ Sequence 19 BP; 5 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1639 ACAGAAACCAAGGCCCG 1656
DB 1 ACAGTATCCAGGCCCTG 18
RESULT 1799
ADD15353
ID ADD15353 standard; DNA; 19 BP.

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QY 728 ATGCTGTTAACTACCGC 745
 DB 16 ATGCTACTAACCAGC 1

RESULT 1801
 ADE14131
 ID ADE14131 standard; RNA; 19 BP.
 AC ADE14131;
 XX
 DT 29-JAN-2004 (first entry)
 DE Human c-fos siRNA lower strand, SEQ ID NO:203.
 XX
 KW RNA interference; short interfering nucleic acid; siRNA;
 KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
 KW short hairpin RNA; shRNA; expression modulation; gene therapy;
 KW drug screening; diagnosis; therapeutic target identification;
 KW pharmacogenomics; gene function analysis; gene mapping;
 KW central nervous system disorder; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; epilepsy; dementia;
 KW amyotrophic lateral sclerosis; cancer; proliferative disease; restenosis;
 KW polycystic kidney disease; inflammatory disease; allergic disease;
 KW viral infection; HIV infection; autoimmune disease; transplant rejection;
 KW vasotropic; nontropic; antiparkinsonian; neuroprotective; cytostatic;
 KW antiinflammatory; anti-allergic; virucide; anti-HIV; immunosuppressive;
 KW anticonvulsant; nephrotropic; human; c-fos; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003070914-A2.
 XX
 PD 28-AUG-2003.
 XX
 PF 20-FEB-2003; 2003WO-US005162.
 XX
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX
 PA (SIRN-) SIRNA THERAPEUTICS INC.
 XX
 PI Mcswiggen J, Beigelman L;
 XX
 DR WPI; 2003-679877/64.
 XX
 PT New short interfering nucleic acid downregulates expression of the c-fos
 PT gene useful for treatment and diagnosis of diseases, e.g. cancer and
 PT inflammation.
 XX
 PS Example 3; SEQ ID NO 203; 145bp; English.
 XX
 CC The invention relates to short interfering nucleic acids (siRNA) which
 CC downregulate expression of the human c-fos gene by RNA interference. The
 CC siRNAs may or may not comprise ribonucleotides and may be double or single
 CC stranded. They further comprise sense and antisense regions, or
 CC alternatively are assembled from a sense oligonucleotide and an antisense
 CC oligonucleotide. Specifically, the siRNAs include short interfering RNA
 CC (siRNA), double-stranded RNA, micro-RNA (miRNA) and short hairpin RNA
 CC (shRNA). The siRNAs can be unmodified or chemically modified, can contain
 CC deoxyribonucleotides, and can be chemically synthesised, expressed from a
 CC vector or enzymatically synthesised. The invention also relates to kits
 CC for the in vitro or in vivo delivery of siRNA; conjugates and/or complexes
 CC of siRNA; and vectors that express siRNA. The siRNAs are used to modulate
 CC expression of the c-fos gene in cells, tissue explants or organisms
 CC (e.g., by ex vivo gene therapy), or in grafts and transplants for the
 CC treatment of a variety of conditions. They may be used for treating
 CC central nervous system lesions and injuries (e.g., Alzheimer's disease,

CC Parkinson's disease, Huntington's disease, epilepsy, dementia or
 CC amyotrophic lateral sclerosis); various cancers; other proliferative
 CC diseases (e.g., restenosis and polycystic kidney disease); inflammatory
 CC and/or allergic diseases; viral infections (including HIV infection);
 CC autoimmune diseases; and transplant rejection. The siRNAs are also useful
 CC for drug screening, diagnosis, therapeutic target identification and
 CC validation, genetic engineering, pharmacogenomics, studying gene
 CC function, and gene mapping (e.g., of single nucleotide polymorphisms).
 CC The present sequence represents the lower strand of a human c-fos-
 CC targeted double-stranded siNA.
 XX
 SQ Sequence 19 BP; 6 A; 7 C; 2 G; 0 T; 4 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 61.1%; Pred. No. 1.2e+03;
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 728 ATGCTGTTAACTACCGC 745
 DB 16 ATGCTACTAACCAGC 19
 RESULT 1802
 ADE14131
 ID ADE14131 standard; DNA; 19 BP.
 XX
 AC ADE14131;
 XX
 DT 29-JAN-2004 (first entry)
 DE Optineurin promoter motif, repeat element or regulatory region #240.
 XX
 KW Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
 KW SNP; glaucoma; progressive ocular hypertensive disorder;
 KW glaucoma related disorder; motif; repeat element; regulatory region.
 XX
 OS Homo sapiens.
 XX
 PN US2003190617-A1.
 XX
 PD 09-OCT-2003.
 XX
 PF 06-MAR-2002; 2002US-00091281.
 XX
 PR 06-MAR-2002; 2002US-00091281.
 XX
 PA (SIE/) SI E.
 PA (RAYM/) RAYMOND V.
 PA (MORI/) MORISSETTE J.
 XX
 PI Raymond V, Morissette J, Si E;
 XX
 DR WPI; 2003-864168/80.
 XX
 PT New nucleic acid sequences of the optineurin gene are useful to detect
 PT polymorphisms particularly single nucleotide polymorphisms in the
 PT optineurin promoter to diagnose, prognose and treat glaucoma and related
 PT disorders.
 XX
 PS Claim 11; SEQ ID NO 242; 159pp; English.
 XX
 CC The invention relates to an isolated nucleic acid (N1) comprising at
 CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
 CC promoter appearing as ADE13890. Also included are the optineurin promoter
 CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
 CC detecting a single nucleotide polymorphism (SNP) in the optineurin
 CC promoter, a host cell comprising the promoter operably linked to a
 CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
 CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
 CC in a promoter region of the optineurin gene, associated with a glaucoma
 CC phenotype), detecting a SNP sequence variation in a sample containing
 CC DNA, detecting the presence of an optineurin promoter sequence variation
 CC in a sample containing DNA, determining the presence or increased

This invention relates to a novel method for the concurrent interrogation of a number of polymorphic sites in the presence of, and without interference from, non-designated polymorphic sites. Specifically, it comprises conducting a multiplexed elongation assay by applying one or more temperature cycles to achieve linear amplification of the target or a combination of annealing and elongation steps under temperature-

CC that
CC by PN:

XX The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC by RNA interference.

CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 3 C; 4 G; 0 T; 7 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2064 CCTCTTTGTAATAAATG 2081
||||| ||||| |||||
Db 18 CCTCATAGTAATAAGATG 1

RESULT 1805
ADE27185
ID ADE27185 standard; RNA; 19 BP.
XX AC ADE27185;
XX DT 29-JAN-2004 (first entry)
XX DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:129.
XX short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX OS Synthetic.
XX PN WO2003070885-A2.
XX PD 28-AUG-2003.
XX PF 13-FEB-2003; 2003WO-US004317.
XX PR 20-FEB-2002; 2002US-0358580P.
XX PR 11-MAR-2002; 2002US-0363124P.
XX PR 06-JUN-2002; 2002US-0386782P.
XX PR 29-AUG-2002; 2002US-0406784P.
XX PR 05-SEP-2002; 2002US-0408378P.
XX PR 09-SEP-2002; 2002US-0409293P.
XX PR 15-SEP-2002; 2002US-0412304P.
XX PR 15-JAN-2003; 2003US-0440129P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Mcswiggen J, Beigelman L, Thompson J;
XX WPI; 2003-721687/68.
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX Example 3; SEQ ID NO 129; 139pp; English.
XX The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)

CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 4 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 1.2e+03;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2064 CCTCTTTGTAATAAATG 2081
||||| ||||| |||||
Db 2 CCUCAUAGUAUAAGAUG 19

RESULT 1806
ADE29458/c
ID ADE29458 standard; RNA; 19 BP.
XX AC ADE29458;
XX DT 29-JAN-2004 (first entry)
XX DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:80.
XX short interfering nucleic acid; siNA; downregulation; inhibition;
KW mitogen-activated protein kinase; MAP kinase; RNA interference;
KW cytostatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
KW psoriasis; inflammatory bowel disease; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX OS Synthetic.
XX PN WO2003072590-A1.
XX PD 04-SEP-2003.
XX PF 28-JAN-2003; 2003WO-US002510.
XX PR 20-FEB-2002; 2002US-0358580P.
XX PR 11-MAR-2002; 2002US-0363124P.
XX PR 06-JUN-2002; 2002US-0386782P.
XX PR 29-AUG-2002; 2002US-0406784P.
XX PR 05-SEP-2002; 2002US-0408378P.
XX PR 09-SEP-2002; 2002US-0409293P.
XX PR 15-JAN-2003; 2003US-0440129P.
XX PA (SIRN-) SIRNA THERAPEUTICS INC.
XX PI Mcswiggen J, Beigelman L, Usman N, Haerberli P, Chowrira B;
XX WPI; 2003-689980/65.
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of mitogen-activated
PT protein kinase genes.
XX Example 3; SEQ ID NO 80; 164pp; English.
XX The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of a mitogen-activated protein kinase
CC (MAPK) genes by RNA interference. Also described: (1) a method for

CC modulating expression of MAPK genes in cells, tissue explants or
CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
CC vectors that express siNA and cells containing these vectors. MAPK siNAs
CC have cytostatic, anorectic, antidiabetic, antiinflammatory,
CC antiasthmatic, immunosuppressive, antibacterial, antirheumatic,
CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
CC siNAs can be used to modulate the expression of MAPK genes, in cells,
CC tissue explants or organisms. e.g. for treating obesity; diabetes types I
CC and II; a wide range of tumours and inflammatory diseases (asthma,
CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
CC disease). They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents a MAPK siNA which is used
CC in the exemplification of the present invention.

SQ Sequence 19 BP; 3 A; 6 C; 2 G; 0 T; 8 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1479 CAAAGGGGTCAAGGAGGA 1496
Db 19 CAAAGGAGTCAAGGTGGA 2
||||| ||||| |||||

RESULT 1807
ADE29543
ID ADE29543 standard; RNA; 19 BP.
XX
AC ADE29543;
XX
DT 29-JAN-2004 (first entry)
XX
DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:165.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition;
KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
KW cytostatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
KW psoriasis; inflammatory bowel disease; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003072590-A1.
XX
PD 04-SEP-2003.
XX
PF 28-JAN-2003; 2003WO-US002510.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0366782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Usman N, Haerberli P, Chowrira B;
XX WPI; 2003-689980/65.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of mitogen-activated
PT protein kinase genes.
XX

PS Example 3; SEQ ID NO 165; 164pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of a mitogen-activated protein kinase
CC (MAPK) genes by RNA interference. Also described: (1) a method for
CC modulating expression of MAPK genes in cells, tissue explants or
CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
CC vectors that express siNA and cells containing these vectors. MAPK siNAs
CC have cytostatic, anorectic, antidiabetic, antiinflammatory,
CC antiasthmatic, immunosuppressive, antibacterial, antirheumatic,
CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
CC siNAs can be used to modulate the expression of MAPK genes, in cells,
CC tissue explants or organisms. e.g. for treating obesity; diabetes types I
CC and II; a wide range of tumours and inflammatory diseases (asthma,
CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
CC disease). They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents a MAPK siNA which is used
CC in the exemplification of the present invention.

SQ Sequence 19 BP; 2 A; 6 C; 10 G; 0 T; 1 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 34 GACTGACGGTAGGACGG 51
Db 1 GACUGACGGCGGCGCGG 18
||||| ||||| |||||

RESULT 1808
ADE29621
ID ADE29621 standard; RNA; 19 BP.
XX
AC ADE29621;
XX
DT 29-JAN-2004 (first entry)
XX
DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:243.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition;
KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
KW cytostatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
KW psoriasis; inflammatory bowel disease; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003072590-A1.
XX
PD 04-SEP-2003.
XX
PF 28-JAN-2003; 2003WO-US002510.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0366782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Usman N, Haerberli P, Chowrira B;
XX WPI; 2003-689980/65.
XX

XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of mitogen-activated
PT protein kinase genes.
XX Example 3; SEQ ID NO 243; 164pp; English.

XX The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of a mitogen-activated protein kinase
CC (MAPK) genes by RNA interference. Also described: (1) a method for
CC modulating expression of MAPK genes in cells, tissue explants or
CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
CC vectors that express siNA and cells containing these vectors. MAPK siNAs
CC have cytostatic, anorectic, antidiabetic, antibacterial, antirheumatic,
CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
CC siNAs can be used to modulate the expression of MAPK genes, in cells,
CC tissue explants or organisms, e.g. for treating obesity; diabetes types I
CC and II; a wide range of tumours, and inflammatory diseases (asthma,
CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
CC disease). They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents a MAPK siNA which is used
CC in the exemplification of the present invention.

XX Sequence 19 BP; 8 A; 2 C; 6 G; 0 T; 3 U; 0 Other;
SQ Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1479 CAAAGGGGTCAAGGAGGA 1496
||||| :||| ||||
Db 1 CAAAGGAGUCAAGUGGA 18

RESULT 1809
ADE29811/c
ID ADE29811 standard; RNA; 19 BP.
XX AC ADE29811;
XX DT 29-JAN-2004 (first entry)
XX DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:433.
XX short interfering nucleic acid; siNA; downregulation; inhibition;
KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
KW cytostatic; anorectic; antidiabetic; antiinflammatory; antiarthritic;
KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
KW psoriasis; inflammatory bowel disease; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX Synthetic.
OS WO2003072590-A1.
XX PN WO2003072590-A1.
XX PD 04-SEP-2003.
XX PF 28-JAN-2003; 2003WO-US002510.
XX PR 20-FEB-2002; 2002US-0358580P.
XX PR 11-MAR-2002; 2002US-0363124P.
XX PR 06-JUN-2002; 2002US-0386782P.
XX PR 29-AUG-2002; 2002US-0406784P.
XX PR 05-SEP-2002; 2002US-0408378P.
XX PR 09-SEP-2002; 2002US-0409293P.
XX PR 15-JAN-2003; 2003US-0440129P.

PA (SIRN-) SIRNA THERAPEUTICS INC.
XX Mcswiggen J, Beigelman L, Usman N, Haerberli P, Chowrira B;
XX WPI; 2003-689980/65.
XX DR New short interfering nucleic acid, useful e.g. for treatment and
XX PT diagnosis of cancer, downregulates expression of mitogen-activated
XX PT protein kinase genes.
XX Example 3; SEQ ID NO 433; 164pp; English.

XX The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of a mitogen-activated protein kinase
CC (MAPK) genes by RNA interference. Also described: (1) a method for
CC modulating expression of MAPK genes in cells, tissue explants or
CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
CC vectors that express siNA and cells containing these vectors. MAPK siNAs
CC have cytostatic, anorectic, antidiabetic, antibacterial, antirheumatic,
CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
CC siNAs can be used to modulate the expression of MAPK genes, in cells,
CC tissue explants or organisms, e.g. for treating obesity; diabetes types I
CC and II; a wide range of tumours, and inflammatory diseases (asthma,
CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
CC disease). They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents a MAPK siNA which is used
CC in the exemplification of the present invention.

XX Sequence 19 BP; 1 A; 12 C; 4 G; 0 T; 2 U; 0 Other;
SQ Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 GCCGCGGGCGGAGGGCG 25
||||| :||| |||||
Db 18 GCCGTGGGGAGGAGGGCG 1

RESULT 1810
ADE29380/c
ID ADE29380 standard; RNA; 19 BP.
XX AC ADE29380;
XX DT 29-JAN-2004 (first entry)
XX DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:2.
XX short interfering nucleic acid; siNA; downregulation; inhibition;
KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
KW cytostatic; anorectic; antidiabetic; antiinflammatory; antiarthritic;
KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
KW psoriasis; inflammatory bowel disease; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX Synthetic.
OS WO2003072590-A1.
XX PN WO2003072590-A1.
XX PD 04-SEP-2003.
XX PF 28-JAN-2003; 2003WO-US002510.
XX PR 20-FEB-2002; 2002US-0358580P.
XX PR 11-MAR-2002; 2002US-0363124P.
XX PR 06-JUN-2002; 2002US-0386782P.

PF 28-JAN-2003; 2003WO-US002510.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 19-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Meswiggen J, Beigelman L, Usman N, Haeberli P, Chowrira B;
PI
XX WPI; 2003-689980/65.
DR
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of mitogen-activated
PT protein kinase genes.
XX
XX Example 3; SEQ ID NO 328; 164pp; English.
PS
XX The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of a mitogen-activated protein kinase
CC (MAPK) genes by RNA interference. Also described: (1) a method for
CC modulating expression of MAPK genes in cells, tissue explants or
CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
CC vectors that express siNA and cells containing these vectors. MAPK siNAs
CC have cytostatic, anorectic, antidiabetic, antitumoral, antiinflammatory,
CC antiasthmatic, immunosuppressive, antibacterial, antirheumatic,
CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
CC siNAs can be used to modulate the expression of MAPK genes, in cells,
CC tissue explants or organisms, and inflammatory diseases (asthma,
CC and II; a wide range of tumours, and psoriasis and inflammatory bowel
CC disease). They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents a MAPK siNA which is used
CC in the exemplification of the present invention.
XX
XX Sequence 19 BP; 2 A; 4 C; 12 G; 0 T; 1 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 8 GCCGCGCGCGGAGGGCG 25
DB 2 GCCGUGGGAGGAGGGCG 19
RESULT 1812
ABV72766/c
ID ABV72766 standard; DNA; 20 BP.
XX
XX AC ABV72766;
XX
XX 06-DEC-2002 (first entry)
DT Human zinc finger protein BiczFP71 PCR primer 2.
XX Human zinc finger protein; BiczFP71; immune disorder; cancer; PCR;
XX primer; ss.
XX Homo sapiens.
XX CNL293247-A.
XX
XX 02-MAY-2001.
PD
XX 14-OCT-1999; 99CN-00116966.
PF

PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
PA
XX Meswiggen J, Beigelman L, Usman N, Haeberli P, Chowrira B;
PI
XX WPI; 2003-689980/65.
DR
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of mitogen-activated
PT protein kinase genes.
XX
XX Example 3; SEQ ID NO 2; 164pp; English.
PS
XX The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of a mitogen-activated protein kinase
CC (MAPK) genes by RNA interference. Also described: (1) a method for
CC modulating expression of MAPK genes in cells, tissue explants or
CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
CC vectors that express siNA and cells containing these vectors. MAPK siNAs
CC have cytostatic, anorectic, antidiabetic, antitumoral, antiinflammatory,
CC antiasthmatic, immunosuppressive, antibacterial, antirheumatic,
CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
CC siNAs can be used to modulate the expression of MAPK genes, in cells,
CC tissue explants or organisms, and inflammatory diseases (asthma,
CC and II; a wide range of tumours, and psoriasis and inflammatory bowel
CC disease). They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents a MAPK siNA which is used
CC in the exemplification of the present invention.
XX
XX Sequence 19 BP; 1 A; 10 C; 6 G; 0 T; 2 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 34 GACTGACGGTGGGCGG 51
DB 19 GACTGACGGGCGGGCGG 2
RESULT 1811
ADE29706
ID ADE29706 standard; RNA; 19 BP.
XX
XX AC ADE29706;
XX
XX 29-JAN-2004 (first entry)
DT Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:328.
XX
XX short interfering nucleic acid; siNA; downregulation; inhibition;
KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
KW cytostatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
KW psoriasis; inflammatory bowel disease; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
XX Synthetic.
XX
XX WO2003072590-A1.
PN
XX 04-SEP-2003.
PD
XX

XX PR 14-OCT-1999; 99CN-00116966.
XX PA (SHEN-) SHENGYUAN GENE DEV CO LTD SHANGHAI.
XX PI Mao Y, Xie Y;
XX DR WPI; 2001-418927/45.
XX PT Human zinc finger protein and its coding sequence.
XX PS Example 3; Page 12 (Disclosure); 21pp; Chinese.
XX CC The invention relates to a novel human zinc finger protein (BioZFP71),
CC and the polynucleotide encoding it. The protein is useful for treating
CC immune disorder and cancers. The antagonist of BioZFP71, and its medical
CC action are also disclosed. The present sequence represents a PCR primer
CC used in the invention to amplify the human zinc finger protein
XX SQ Sequence 20 BP; 7 A; 1 C; 0 G; 12 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1606 ATAAAGATTTTATTAAATA 1623
Db 19 ATAAAGATTTTATTAAATA 2
RESULT 1813
ID ABA82490 standard; DNA; 20 BP.
XX AC ABA82490;
XX DT 25-JAN-2002 (first entry)
XX DE Zmax1 gene region physical map preparation STS marker #449.
XX KW Human; high bone mass; HBM gene; Zmax1 gene; chromosome 11; 11q13.3;
KW sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
KW antisense therapy; vaccine; bone disorder; Paget's disease; adapter;
KW sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200177327-A1.
XX PD 18-OCT-2001.
XX PF 21-JUN-2000; 2000WO-US016951.
XX PR 05-APR-2000; 2000US-00543771.
XX PR 05-APR-2000; 2000US-00544398.
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX WPI; 2001-657171/75.
XX DR New high bone mass (HBM) and Zmax1 genes and proteins useful for
XX PT modulating bone mass for the treatment of e.g. osteoporosis.
XX PS Disclosure; Page 36; 443pp; English.
XX CC The present invention describes the human Zmax1 gene and the high bone
CC mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM
CC genes have osteopathic activities. The genes can be used in gene therapy,
CC antisense therapy and in the production of vaccines. They can be used in
CC the diagnosis and treatment of bone disorders including osteoporosis,
XX CC

CC CC Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.
CC ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences used in
CC the exemplification of the present invention
XX SQ Sequence 20 BP; 8 A; 4 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1140 GGAGAAGATCAACACAGCG 1157
Db 3 GGAGAAGATCCACAGCG 20
RESULT 1814
ID ABK23287 standard; DNA; 20 BP.
XX AC ABK23287;
XX DT 09-APR-2002 (first entry)
XX DE Human Zmax1 cDNA forward PCR primer #225.
XX KW Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke;
KW lipid-associated condition; arteriosclerosis; cardiovascular disease; ss;
KW osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up;
KW neurovascular condition; wound healing; gene therapy; PCR primer; probe;
KW bone development disorder; antiarteriosclerotic; cardiovascular;
KW osteopathic; cerebroprotective.
XX OS Homo sapiens.
XX PN WO200192891-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US016946.
XX PR 26-MAY-2000; 2000US-00578900.
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
XX PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX WPI; 2002-097784/13.
XX PT Identifying molecules involved in lipid regulation, useful for
XX PT diagnosing, treating or preventing e.g., arteriosclerosis, comprises
XX PT identifying a molecule that binds to high bone mass gene or its
XX PT corresponding wild type gene.
XX PS Disclosure; Page 41; 409pp; English.
XX CC The invention relates to a method for identifying a molecule involved in
CC lipid regulation comprising identifying a molecule that binds to or
CC inhibits binding of a molecule to high bone mass (HBM) or its wild type
CC gene, Zmax1. Compounds identified by the method are useful for treating,
CC diagnosing, preventing or screening for normal and abnormal lipid-
CC associated conditions, including arteriosclerosis, cardiovascular
CC disease, stroke, and osteoporosis. The compounds may also be used in the
CC treatment or prevention of diabetic atherosclerosis, neurovascular
CC conditions caused by plaque build-up, poor circulation due to plaque
CC build-up and associated poor wound healing. The methods may be used in
CC gene therapy, pharmaceutical development, and diagnostic assays for bone
CC development disorders. Molecules identified by comparison of Zmax1 and
CC HBM systems can be used as surrogate markers in pharmaceutical
CC development, in diagnosis of human or animal bone disease, and in the
CC treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA
CC molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers
CC and adapters of the invention

XX Sequence 20 BP; 8 A; 4 C; 7 G; 1 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1140 GGAGAGATCAACACGCG 1157
 |||||
 Db 3 GGAGAGATCCACACGCG 20

RESULT 1815
 ACC45870
 ID ACC45870 standard; DNA; 20 BP.
 XX AC ACC45870;
 XX 02-JUN-2003 (first entry)
 XX Human HBM STS marker forward primer #225.
 DE Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;
 KW gene therapy; bone density modulation; bone strength; trabecular number;
 KW bone size; bone tissue connectivity; bone disease; osteoporosis; PCR;
 KW osteomalacia; rickets; Paget's disease; neoplasm of the bone; primer; ss.
 XX Homo sapiens.
 OS WO200292764-A2.
 XX 21-NOV-2002.
 XX 13-MAY-2002; 2002WO-US014876.
 XX 11-MAY-2001; 2001US-0290071P.
 XX 17-MAY-2001; 2001US-0291311P.
 PR 01-FEB-2002; 2002US-0353058P.
 PR 04-MAR-2002; 2002US-0361293P.
 XX (GENO-) GENOME THERAPEUTICS CORP.
 PA (AMHP) WYETH.
 XX Babij P, Bex FJ, Yaworsky PJ, Bodine PV;
 PI WPI; 2003-129278/12.
 XX New transgenic animals (e.g. mice), useful as models for studying bone
 PT density modulation, developing drugs for treating or preventing bone
 PT diseases (e.g. osteoporosis), or diagnosing diseases characterized by
 PT reduced bone density.
 XX Disclosure; Page 57; 603pp; English.
 PS The invention relates to novel transgenic animals expressing the high
 CC bone mass (HBM) gene, expressing the corresponding wild type HBM gene,
 CC comprising an alteration of the gene encoding LRP5 or LRP6, or expressing
 CC an LRP5 that is modulated by an altered gene control sequence introduced
 CC by homologous or non-homologous recombination. The transgenic animals are
 CC for the study of bone density modulation or bone mass modulation. The
 CC invention has osteopathic and cytostatic activity. The polynucleotides of
 CC the invention may have a use in gene therapy. The transgenic animals and
 CC nucleic acids are for the study of bone density modulation, where the
 CC bone mass is modulated relative to non-transgenic animals of the same
 CC species in more than one parameter selected from bone density, bone
 CC strength, trabecular number, bone size, or bone tissue connectivity. The
 CC transgenic animals, nucleic acids and methods are useful for identifying
 CC molecules involved in bone development, and for developing pharmaceutical
 CC compositions, which may be employed for treating or preventing bone
 CC diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or
 CC neoplasms of the bone. The transgenic animals and nucleic acids are also
 CC useful in methods for diagnosing diseases involved in bone development,
 CC or characterised by reduced bone density or mass. The present sequence is

CC used in the exemplification of the invention
 XX Sequence 20 BP; 8 A; 4 C; 7 G; 1 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1140 GGAGAGATCAACACGCG 1157
 |||||
 Db 3 GGAGAGATCCACACGCG 20

RESULT 1816
 ADB98568
 ID ADB98568 standard; DNA; 20 BP.
 XX AC ADB98568;
 XX 04-DEC-2003 (first entry)
 XX Sequence tagged site #449 used to prepare Zmax1 (LRP5) gene region map.
 DE Osteopathic; Gene therapy; High Bone Mass; HBM; LRP5; Zmax1; LRP6;
 KW bone mass modulation; osteoporosis; STS; sequence tagged site; ds.
 XX Homo sapiens.
 OS WO200292000-A2.
 XX 21-NOV-2002.
 XX 13-MAY-2002; 2002WO-US014877.
 XX 11-MAY-2001; 2001US-0290071P.
 PR 17-MAY-2001; 2001US-0291311P.
 PR 01-FEB-2002; 2002US-0353058P.
 PR 04-MAR-2002; 2002US-0361293P.
 XX (GENO-) GENOME THERAPEUTICS CORP.
 PA (AMHP) WYETH.
 XX Allen K, Anisowicz A, Graham JR, Morales A, Yaworsky PJ, Liu W;
 PI WPI; 2003-129214/12.
 XX New nucleic acid comprising a mutation in LRP5 or LRP6, useful for
 PT diagnosing a HBM-like phenotype in a subject and for preparing a
 PT composition for modulating bone mass and/or lipid levels in a subject
 PT suffering from e.g. osteoporosis.
 XX Example 2; Page 64; 629pp; English.
 PS The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and
 CC LRP6 mutants, which results in a HBM-like phenotype when expressed in a
 CC cell. The HBM-like phenotype results in bone mass modulation and/or lipid
 CC level modulation. The invention is useful for diagnosing a HBM-like
 CC phenotype in a subject and for preparing a composition for modulating
 CC bone mass and/or lipid levels in a subject suffering from e.g.
 CC osteoporosis. The present sequence is a sequence tagged site (STS)
 CC marker, which was used to prepare a physical map of the Zmax1 (LRP5) gene
 CC region.
 XX Sequence 20 BP; 8 A; 4 C; 7 G; 1 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1140 GGAGAGATCAACACGCG 1157
 |||||
 Db 3 GGAGAGATCCACACGCG 20

CC this method, 370 STSs specific for human chromosome 11 were generated and
CC most of them were regionally mapped. This procedure illustrates a novel
CC method for sequencing complex genomes. Designated "sequence sampled
CC mapping". The sequence sampled mapping method is useful for the
CC completion of high density sequence-based maps, and ultimately, for the
CC complete sequencing of genomic DNA directly from cosmid clones. See
CC AAQ82001-Q82706 for STS primers. (Also see AAQ91325-58). (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
XX Sequence 20 BP; 3 A; 3 C; 8 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1968 AAACACTGCTGCCCTCT 1985
DB 19 AAGCACTGACTGCCACT 2
RESULT 1821
AAQ84319/c
ID AAQ84319 standard; DNA; 20 BP.
XX AC AAQ84319;
XX 25-MAR-2003 (revised)
DT 02-OCT-1995 (first entry)
XX Murine APP mRNA PCR primer.
XX PCR primer; murine APP mRNA; transgenic; interleukin-1 beta;
KW animal model; chronic inflammatory disease; Alzheimer's; ss.
XX Synthetic.
XX WO9503402-A1.
XX 02-FEB-1995.
PD 19-JUL-1994; 94WO-US008111.
PF 22-JUL-1993; 93US-00096943.
XX (MERI) MERCK & CO INC.
XX Chen HY, Hofmann KJ, Van Der Ploeg LHT, Shaw AR, Trumbauer ME;
PI Zheng H;
XX WPI; 1995-075230/10.
XX Transgenic animal contg. a transgene encoding human IL-1 beta - useful to
PT study e.g. chronic inflammatory diseases and Alzheimer's disease.
XX Example 3; Page 12; 23pp; English.
XX AAQ84319 and AAQ84320 are a pair of primers for the PCR amplification of
CC the murine APP mRNA. They were used in the construction of a plasmid for
CC the expression of human IL-1beta in a non-human animal (pref. a mouse).
CC The transgenic animal is useful as a model for the study of chronic
CC inflammatory diseases, Alzheimer's disease and diseases in which IL-1beta
CC plays a role. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 20 BP; 1 A; 10 C; 3 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1331 CTGAACAGGAGGAGGAGG 1348
DB 19 CCGAAGAGGAGGAGGAGTGG 2

DR WPI; 1994-358248/44.
XX
PT DNA encoding chondroitinase I and II of Proteus vulgaris - and related
PT vectors, transformed cells and recombinant polypeptide(s) are produced in
PT large quantities and are protease free.
XX
XX Example 2; Page 45; 153pp; English.
XX
XX The Proteus vulgaris chondroitinase-I (CI) gene (AAQ74988) was isolated
CC by PCR amplification of genomic DNA using primers based on fragments of
CC the isolated enzyme. Primers AAQ74992-Q74999 are based on a generic
CC sequence (AAQ74991) corresponding to the N-terminus (given in AAR62536)
CC of CI, primers AAQ75001-Q75008 on a generic sequence (AAQ75000)
CC corresponding to the N-terminus of a 18 kDa obtained from CI by
CC proteolytic cleavage, and primers AAQ75011-Q75018 on generic sequences
CC AAQ75009-Q75010 corresponding to the N-terminus of a 90 kDa peptide
CC obtained from the same cleavage reaction. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX Sequence 20 BP; 6 A; 9 C; 2 G; 2 T; 0 U; 1 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 406 GGTGGTCTCTGGCAAGTG 424
DB 19 GGTGGTCTCTGGCAAGTG 1
RESULT 1820
AAQ82476/c
ID AAQ82476 standard; DNA; 20 BP.
XX AC AAQ82476;
XX 25-MAR-2003 (revised)
DT 13-SEP-1995 (first entry)
XX Chromosome 11 (locus D11S1222) STS primer CSRL-6b1-tz.
XX sequence sampled mapping; genomic analysis; complex genome mapping;
XX cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
XX Synthetic.
XX WO9429486-A1.
XX 22-DEC-1994.
PD 15-JUN-1994; 94WO-US006810.
PF 15-JUN-1993; 93US-00078471.
PR 07-SEP-1993; 93US-00117952.
XX (SALK) SALK INST BIOLOGICAL STUDIES.
XX Evans GA, Smith MW;
PI WPI; 1995-036508/05.
XX Sequencing complex genomes, present as fragments in a cosmid library - by
PT sequencing end-specific nucleotides of each clone then correlating with
PT spatial relationship of cosmid, esp. for mammalian chromosomes.
XX
XX Example 4; Page 83; 128pp; English.
XX
XX Sequences were determined from the ends of chromosome 11-specific cosmids
CC by automated sequencing without intermediate subcloning. A sample of 371
CC DNA sequence fragments were determined and of these, 277 were suitable
CC for STS primer prediction by computer analysis (using the "Primer"
CC program available from E. Lander, MIT). The STSs and cosmids were mapped
CC by in situ hybridisation, somatic cell hybrid analysis or both. Using

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RESULT 1822
AAQ91649
ID AAQ91649 standard; cDNA; 20 BP.
XX
AC AAQ91649;
XX
DT 03-MAY-1996 (first entry)
XX
DE CShh detection primer 924.
XX
KW Chicken; sonic hedgehog gene; nested polymerase chain reaction;
KW stage 22/22 limb bud; transgenic mouse screening; probe; primer; PCR;
KW diagnostic; nervous system disorder; gene therapy; antibody; ss.
XX
OS Synthetic.
XX
XX WO9518856-A1.
XX
XX 13-JUN-1995.
XX
XX 30-DEC-1994; 94WO-US014992.
XX
XX 30-DEC-1993; 93US-00176427.
XX
XX 14-DEC-1994; 94US-00356060.
XX
PA (HARD ) HARVARD COLLEGE.
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
XX
XX Ingham PW, McMahon AP, Tabin CJ;
XX
XX WPI; 1995-255060/33.
XX
XX Hedgehog-like protein(s) and nucleic acid(s) encoding them - useful to
XX treat degenerative nervous system disorder(s) and in gene therapy.
XX
XX Example 2; Page 79; 210pp; English.
XX
XX The sequences given in AAQ91646-49 are primers which were used in the
XX screening of transgenic mice containing WXP2-lacZ and WEXP2-CShh
XX constructs. The WXP2-CShh construct encodes the chicken sonic hedgehog
XX protein, homologous to a Drosophila hedgehog protein (AAR77337). The
XX chicken sonic hedgehog gene was isolated by nested polymerase chain
XX reaction using primers VHH50 (AAQ91643), VHH30 (AAQ91644) and VHH31
XX (AAQ91645). A clone resulting from the amplification (encoding AAR77348)
XX was used to isolate the full-length cDNA from a stage 22/22 limb bud cDNA
XX library. Primer AAQ91649 is derived from the chicken cDNA sequence, and
XX is used to screen transgenic mice. Probes and primers derived from the
XX sonic hedgehog sequence may be used as diagnostic agents for
XX neuromuscular, autonomic or central nervous system disorders, and the
XX gene may also be used in gene therapy. Antibodies generated from the
XX encoded protein may be used as therapeutic or research reagents
XX
XX Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1436 AAGTCACCGAGGAGGA 1453
DB 1 AAGTCAGCCCCAGGAGGA 18

RESULT 1823
AAQ95455
ID AAQ95455 standard; DNA; 20 BP.
XX
AC AAQ95455;
XX
DT 13-FEB-1996 (first entry)
XX
DE Primer A (Group 3, set C) for marker D1S192, chromosome 1.

XX primer; polymerase chain reaction; PCR; linkage study; locus;
XX microsatellite marker sequence; automated genotyping; allele;
XX polymorphism; detection; Homo sapiens; ss.
XX
XX Synthetic.
XX
XX WO9515400-A1.
XX
XX 08-JUN-1995.
XX
XX 05-DEC-1994; 94WO-US013945.
XX
XX 03-DEC-1993; 93US-00160837.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Levitt RC;
XX
XX WPI; 1995-215278/28.
XX
XX Kit for automated genotyping contg. pairs of PCR primers - designed to
XX amplify polymorphic nucleotide repeat sequences, arranged in sets each
XX with a characteristic fluorescence label, useful e.g. in detection of
XX disease related genetic rearrangement.
XX
XX Disclosure; Fig 7C-2; 104pp; English.
XX
XX The method aims to provide a collection of highly reproducible
XX microsatellite marker sequences (MMS) at approx. 10-50 cM intervals
XX throughout the human genome which can be detectably labelled. The MMS are
XX polymorphic, simple sequence repeats and can be used in automated
XX genotyping, esp. fluorescence repeats, and PCR is used to detect each
XX DNA sequence surrounding each marker, and PCR is used to detect each
XX polymorphism. When the MMS show considerable polymorphism (ie. a
XX difference in the number of repeats) between individuals, the markers can
XX be particularly informative. The MMS can be ideal for linkage studies.
XX Kits comprise at least 4 groups, of at least 3 sets, each comprising
XX labelled primers for PCR amplification of the DNA. Group 3 primer pairs
XX are shown in AAQ95417-464. The published size range of the D1S192 allele
XX is 203-211 bp, and the degree of heterozygosity in the population is
XX about 67%
XX
XX Sequence 20 BP; 9 A; 7 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1618 TAAATATAAATATCCCCA 1635
DB 1 TTAATAAATAATACCCCCA 18

RESULT 1824
AAQ03263
ID AAQ03263 standard; DNA; 20 BP.
XX
XX
AC AAQ03263;
XX
DT 02-APR-1996 (first entry)
XX
DE
XX
XX Mycobacterium tuberculosis 19kD antigen gene primer/probe.
XX
XX Mycobacterium; tuberculosis; primer; probe; detection; rapid; direct;
XX 19kD antigen gene; ss.
XX
XX Synthetic.
XX
XX JP07203997-A.
XX
XX 08-AUG-1995.
XX

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QY 1470 GCCAGAAGCCAAAGGGT 1487
DB 2 GCCAGCAGCCACAGTGGT 19

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RESULT 1827
AAT42103
ID AAT42103 standard; DNA; 20 BP.
XX AC AAT42103;
XX DT 25-MAR-2003 (revised)
XX DT 22-MAY-1997 (first entry)
XX DE Primer pair H-1, primer 2, binds to nucleotides 1020-1039.
XX KW limbic system associated membrane protein; LAMP; self binding domain;
XX KW antibody-like; cell surface adhesion protein; neuron;
XX KW monoclonal antibody; 2G9; growth; differentiation; epilepsy;
XX KW Alzheimer's disease; schizophrenia; neural stem cell; ss.
XX OS Synthetic.
XX FN WO9630052-A1.
XX PD 03-OCT-1996.
XX PF 29-MAR-1996; 96WO-US004397.
XX PR 31-MAR-1995; 95US-00414657.
XX PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
XX PI Levitt P, Pimenta A, Fischer I, Zhukareva V;
XX DR WPI; 1996-455009/45.
XX PT DNA encoding limbic system associated membrane protein self binding
XX PT domain - useful in treatment of excessive neural growth in limbic system,
XX PT e.g. in animal having epilepsy, Alzheimer's disease or schizophrenia.
XX PS Example 2; Page 26; 87pp; English.
XX CC The sequences given in AAT42102-13 are primers which were used to amplify
XX CC fragments of the human limbic system associated membrane protein (LAMP)
XX CC self binding domain. These primers used human cerebral cortex cDNA as a
XX CC template. Primer pair H-1 specifically amplified an 888 bp fragment. LAMP
XX CC is a self-binding, antibody-like cell surface adhesion protein, which
XX CC causes the formation of connections between adjacent neurons. LAMP is
XX CC bound by the monoclonal antibody 2G9 and is thought to be involved in the
XX CC growth and differentiation of certain neurons. The protein is highly
XX CC conserved and the human and rat sequences differ in only four amino
XX CC acids. LAMP nucleic acids, or soluble LAMP analogues, can be used to
XX CC treat an animal with excessive neural growth in the limbic region, i.e.
XX CC where the animal has epilepsy, Alzheimer's disease or schizophrenia.
XX CC Neural stem cells transformed with an expression vector comprising one of
XX CC these nucleic acids, can be used to treat neuropathologies involving the
XX CC limbic system. (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 20 BP; 5 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1470 GCCAGAGCCCAAGGGGT 1487
DB 2 GCCAGAGCCCAAGTGGT 19

RESULT 1828
AAT44467/c
ID AAT44467 standard; DNA; 20 BP.
XX AC AAT44467;
XX DT 31-JAN-1997 (first entry)
XX XX

Primer for p80 gene detection.
XX KW primer; polymerase chain reaction; PCR; detection; screening; diagnosis;
XX KW bovine viral diarrhoea-mucosal diseases virus; ss.
XX OS Synthetic.
XX FN JP08214883-A.
XX PD 27-AUG-1996.
XX PF 09-FEB-1995; 95JP-00021980.
XX PR 09-FEB-1995; 95JP-00021980.
XX PA (ZENK-) ZENKOKU NOGYO KYODO KUMIAI RENGOKAI.
XX DR WPI; 1996-436938/44.
XX PT New PCR primer(s) directed toward the p80 gene in BVD-MDV - used for the
XX PT diagnosis of bovine viral diarrhoea (BVD) and mucosal diseases virus
XX PT (MDV) infection.
XX PS Claim 1; Page 2; 6pp; Japanese.
XX CC AAT44467-68 are synthetic oligonucleotide primers which amplify the p80
XX CC gene which is used to detect bovine viral diarrhoea (BVD)-mucosal disease
XX CC virus (MDV). The primers provide rapid and specific diagnosis of BVD-MDV
XX SQ Sequence 20 BP; 9 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 526 GATATCGTCTTGGCCATC 543
DB 20 GTTATCTCTTGACCAATC 3

RESULT 1829
AAX32946
ID AAX32946 standard; RNA; 20 BP.
XX AC AAX32946;
XX DT 30-JUN-1999 (first entry)
XX DE Seq ID No: 13 of US5495009.
XX KW OCH2O linkage; analogue; 2,6-diethylpyridine; DEP; molecular sieve;
XX KW tetrabutylammonium fluoride; TBAP; tetrahydrofuran; chemical synthesis;
XX KW THF; thioformacetal linkage; diagnostic agent; ss.
XX OS Synthetic.
XX FN US5495009-A.
XX PD 27-FEB-1996.
XX PF 24-APR-1992; 92US-00874334.
XX PR 24-OCT-1989; 89US-00426286.
XX PR 11-DEC-1989; 89US-00448941.
XX PR 30-JUL-1990; 90US-00559957.
XX PR 24-APR-1991; 91US-00690786.
XX PA (GILE-) GILEAD SCI INC.
XX PI Lin K, Jones B, Matteucci M;
XX DR WPI; 1996-178794/18.
XX XX

```

PT Prodn. of nucleoside dimers with methylenedioxy linkage - by reacting 5'-
PT protected nucleoside 3'-methylthio:methyl ether and 3'-protected
PT nucleoside with bromine.

XX
XX
XX Example 2; Col 27; 27pp; English.

XX The invention relates to a method for linking a first nucleoside or
CC oligonucleotide to a second nucleoside or nucleotide through an OCH2O
CC linkage, starting with a 5'-protected nucleoside or nucleotide which is
CC derivatised in the 3' position with an OCH2SMe group. The method
CC comprises (a) treating the derivatised nucleoside or nucleotide and a 3'-
CC protected nucleoside or nucleotide with bromine in the presence of 2,6-
CC diethylpyridine (DEP) and molecular sieves; and (b) treating the product
CC with tetraethylammonium fluoride (TEPAF) in tetrahydrofuran (THF). The
CC OCH2O-linked dimers can be used in the synthesis of oligonucleotide
CC analogues (containing thioformacetal linkages) e.g. useful as diagnostic
CC agents (see WO9106629)

XX
XX Sequence 20 BP; 13 A; 0 C; 5 G; 0 T; 2 U; 0 Other;

SQ Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1393 AAAACAGAGGATGAAAA 1410
Db 2 AAAGAAAGGAGGAAAA 19

RESULT 1830
AAT41913
ID AAT41913 standard; cDNA to mRNA; 20 BP.

XX
XX AAT41913;
XX
XX 10-DEC-1996 (first entry)
XX
XX Thrombopoietin PCR amplification primer TPOs.

XX Human; thrombopoietin; TPO; variant; deletion mutant; megakaryocyte;
KW growth factor; platelet production; thrombocytopoiesis;
KW polymerase chain reaction; ss.
XX
XX Synthetic.

XX
XX JP08168386-A.
XX
XX 02-JUL-1996.
XX
XX 13-JUL-1995; 95JP-00199299.
XX
XX 19-OCT-1994; 94JP-00278657.
XX
XX (SNOW) SNOW BRAND MILK PROD CO LTD.
XX
XX WPI; 1996-357243/36.
XX
XX Thrombopoietin variants having megakaryocyte growth factor activity -
PT useful for promoting growth of megakaryocytes and platelets, also as
PT biochemical assay reagent.

XX
XX Example 7; Page 6; 21pp; Japanese.

XX Eight deletion variants of thrombopoietin (TPO), designated dTPO-1 to
CC dTPO-8, were engineered. The first four variants contained the first 132
CC residues from the N-terminal region of human TPO and the last four
CC variants contained residues 1-131 of human TPO. All 8 variants promoted
CC formation and growth of human megakaryocytes. Proteins comprising at
CC least residues 1-131 of TPO are useful for promoting platelet production.
CC The present sequence is that of a PCR primer used in the construction of
CC cDNA coding for the dTPO variants

XX
XX Sequence 20 BP; 3 A; 3 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 465 TTGGGCTGGGGCGCTGCA 482
Db 2 TTGGACTGGGACTTGA 19

RESULT 1831
AAT85335
ID AAT85335 standard; DNA; 20 BP.

XX
XX AAT85335;
AC
XX
XX 09-DEC-1997 (first entry)
XX
XX Human S182 gene, PS1 locus, PCR primer KM 7673.
XX
XX Mutant; antisense; antibody; vaccine; Alzheimer's disease;
KW polymerase chain reaction; ss.
XX
XX Synthetic.

XX
XX WO9708319-A1.
XX
XX 06-MAR-1997.
XX
XX 03-SEP-1996; 96WO-US014114.
XX
XX 31-AUG-1995; 95US-0003054P.
XX
XX 30-AUG-1996; 96US-00706344.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX
XX Tanzi RE, Masco W;
XX
XX WPI; 1997-179276/16.

XX
XX Chromosome 14 early-onset familial Alzheimer's disease gene PS1 mutants -
PT useful for diagnosing likelihood of developing Alzheimer's disease, also
PT anti-sense sequences, antibodies and vaccines to delay onset.

XX
XX Example 1; Page 63; 99pp; English.

XX The present sequence represents the PCR primer KM 7673 used to screen the
CC human S182 gene, PS1 locus. Mutant PS1 produces a gene product that
CC increases the probability of Alzheimer's disease. A nucleic acid sequence
CC able to hybridise to sequences coding for a mutant PS1 polypeptide can be
CC used as probes for diagnosing an increased likelihood of contracting
CC Alzheimer's disease. Antibodies against the mutant polypeptide can also
CC be used for this purpose. Vectors containing or expressing a nucleic acid
CC molecule, protein or antibody specific for mutant PS1 can be administered
CC to a patient to reduce the likelihood, or delay the onset, of Alzheimer's
CC disease, e.g. anti-sense RNA expression can be used to decrease
CC expression of the PS1 peptide. Transgenic animals expressing the
CC Alzheimer's disease protein can be used to test candidate therapeutics
CC and to investigate the normal role of PS1. The PS1 peptide may also be
CC included in pharmaceutical compositions (vaccines) for Alzheimer's
CC disease therapy

XX
XX Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 414 TGTGGCAAGTGGCTGAA 431
Db 3 TGAGACAAAGTGGCTGAA 20

```

RESULT 1832
AAT60511/c
ID AAT60511 standard; DNA; 20 BP.
XX
AC AAT60511;
XX
DT 10-JUN-1997 (first entry)
XX
DE Primer EC01.1.
XX
XX PCR; polymerase chain reaction; amplify; infection; forensic science;
KW infectious pathogen; genetic disorder; genetic variance; primer; ss.
XX
OS Synthetic.
XX
XX US5612473-A.
XX
XX 18-MAR-1997.
XX
XX 16-JAN-1996; 96US-00587209.
XX
XX 16-JAN-1996; 96US-00587209.
XX
XX (GULL-) GULL LAB.
XX
XX Glass MJ, Coombs J, Wu L, Malmstrom SL;
XX WPI; 1997-192163/17.
XX
XX Processing samples for amplification of nucleic acid target sequences -
PT using extraction buffer containing at least one detergent and a salt
PT composition of greater than 1 molar concentration.
XX
XX Example 3; Col 17; 21pp; English.
XX
XX AAT60503-T60514 represent amplification primers for DNA sequences present
CC in a sample processed by the method of the invention. The processing
CC method of the invention comprises obtaining a sample of material
CC potentially containing the target nucleic acid sequences, and mixing the
CC sample with an external buffer solution. The buffer solution comprises
CC two detergents, and at least one salt. Composition present in a greater
CC than 1 M concentration. The mixture is then centrifuged to obtain a
CC supernatant portion, which is then heated before being centrifuged to
CC precipitate the proteins, and obtaining a second supernatant portion,
CC from which nucleic acids are precipitated. The isolated nucleic acids are
CC then dissolved. The method provides a rapid means of preparing a sample
CC for amplification so that multiple analytes can be detected and
CC differentiated within a relatively short time period (typically less than
CC 5 hours with the novel pre-processing step taking less than 5 minutes).
CC Typical applications of nucleic acid amplification include detection of
CC infections in patients, foodstuffs and for diagnostic/forensic or quality
CC control purposes, to discriminate between multiple potential infectious
CC pathogens, to diagnose genetic disorders or to identify genetic variances
XX
XX Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1450 GAGAAACCCAGGAGGAG 1467
DB 18 GAGAAACCCATGGAAGAG 1
|||||
|||||
RESULT 1833
AAT89759
ID AAT89759 standard; DNA; 20 BP.
XX
AC AAT89759;
XX
DT 06-FEB-1998 (first entry)
XX
XX

```

```

DE Alpha amylase B gene promoter region PCR primer, Pr12.
XX
KW Promoter; secretion signal; genetic engineering; vector; amplification;
KW recombinant secreted protein; lactic acid bacteria; wide host spectrum;
KW Streptococcus thermophilus; Lactobacillus delbrueckii; primer; PCR; ss.
XX
OS Synthetic.
OS Streptococcus bovis; 148.
XX
XX JP09234078-A.
XX
XX 09-SEP-1997.
XX
XX 04-MAR-1996; 96JP-00073168.
XX
XX 04-MAR-1996; 96JP-00073168.
XX
XX (MEIP ) MEIJI MILK PROD CO LTD.
XX
XX WPI; 1997-497319/46.
XX
XX Vector for recombinant expression and secretion of proteins in lactic
PT acid bacteria - has Streptococcus bovis alpha-amylase secretion signal
PT sequence upstream of restriction site for insertion of gene encoding
PT protein to be secreted.
XX
XX Example 8; Fig 5; 13pp; Japanese.
XX
XX AAT89758 and AAT89759 are PCR primers used in the amplification of the
CC promoter region of the S. bovis 148 alpha-amylase B gene (including the
CC secretion signal) and the incorporation of this region into a vector. The
CC vector is used for the production of secreted proteins from transformed
CC lactic acid bacteria of the species Streptococcus thermophilus or
CC Lactobacillus delbrueckii. The vector is used to permit hosts to secrete
CC a product of an extraneous gene. The extraneous gene may be any gene,
CC including genes for e.g. enzymes such as amylase, protease, peptidase
CC etc. as well as biologically active substances. The vector used for
CC secretion in lactic acid bacteria is applicable to a wide spectrum of
CC hosts
XX
XX Sequence 20 BP; 8 A; 6 C; 5 G; 1 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 61 AAGATGGCGCAGCAGCAG 78
DB 2 AACATGGCACACGAG 19
|||||
|||||
RESULT 1834
AAT85960/c
ID AAT85960 standard; cDNA; 20 BP.
XX
AC AAT85960;
XX
XX 09-JAN-1998 (first entry)
XX
XX Human neuroblastoma-specific thymosin-beta primer #1.
XX
XX Human; neuroblastoma; thymosin-beta; G-actin; binding activity; glioma;
KW probe; diagnosis; detection; tumour; primer; PCR; amplification;
KW polymerase chain reaction; ss.
XX
OS Synthetic.
XX
XX JP09191881-A.
XX
XX 29-JUL-1997.
XX
XX 16-JAN-1996; 96JP-00004717.
XX

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16-JAN-1996; 96JP-00004717.
(NISE) JAPAN TOBACCO INC.
WPI; 1997-429181/40.
DNA encoding human neuroblastoma specific-thymosin-beta protein - useful
for detecting glioma(s) and tumours.
Claim 7; Page 2; 11pp; Japanese.
The invention relates to a novel gene encoding the human neuroblastoma-
specific thymosin-beta protein having G-actin binding activity, which is
expressed on human glioma cells. The gene was isolated from a 3' directed
cDNA library prepared from human neuroblastoma cell line CHP134. The
screen isolated a clone designated GS008703 whose insert contained the
coding sequence and the 5' and 3' sequences of the gene (AAT85957-9
respectively). Expression of the gene was detected in neuroblastoma cell
lines. Oligonucleotides such as the PCR primers AAT85960-1, derived from
the sequence of the thymosin-beta gene, can be used for diagnosing human
gliomas, and in the detection of new tumours. This primer corresponds to
nucleotides 7-26 of the 3' untranslated region (AAT85959)
Sequence 20 BP; 6 A; 8 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 949 CTGATGCTGGAGGCGGT 966
DB 19 CTGCTGTTGGAGGCGAT 2
RESULT 1835
AAT43240/c
ID AAT43240 standard; DNA; 20 BP.
AC AAT43240;
XX
XX 26-FEB-1997 (first entry)
XX Arabidopsis FCA alpha-beta gene PCR primer fca-3'a.
XX FCA; flowering; transgenic plant; polymerase chain reaction; PCR; primer;
XX Arabidopsis thaliana; ss.
XX Synthetic.
XX WO9638560-A2.
XX 05-DEC-1996.
XX 03-JUN-1996; 96WO-CB001332.
XX 02-JUN-1995; 95GB-00011196.
XX (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX Dean C, Macknight RC, Bancroft I, Lister CK;
XX WPI; 1997-034373/03.
XX Methods of influencing flowering characteristics of plants - by
XX administration of FCA protein, DNA or anti-sense transcripts.
XX Example 1; Page 60; 97pp; English.
XX PCR primers (AAT43229-41) are used to generate cDNA sequences based on
XX the FCA alpha-beta variant gene (AAT43226) of Arabidopsis thaliana.
XX Primer fca-3'a (AAT43240) is complementary to bases 4941-4960 of the FCA
XX alpha-beta sequence. It was used to generate cDNA from mutant FCA alleles
XX ; fca-1, fca-3 and fca-4 mutations were detected. FCA genes (see also

AAT43224-26) and alleles can be used to modulate flowering time in
transgenic plants
Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1042 GAGCTTCATACATGAC 1059
DB 20 GAGCTGCCAACAATGCG 3
RESULT 1836
AAT88923/c
ID AAT88923 standard; cDNA; 20 BP.
XX
AC AAT88923;
XX
XX 09-FEB-1998 (first entry)
XX Nos promoter PCR primer.
XX
XX Scaffold attachment region; RB7 SAR; transgenic plant; tobacco;
XX gene expression; nos; promoter; neomycin phosphotransferase; nptII gene;
XX PCR; primer; ss.
XX Synthetic.
XX WO9727207-A1.
XX 31-JUL-1997.
XX 24-JAN-1997; 97WO-US001278.
XX 26-JAN-1996; 96US-00592658.
XX (UNNC-) UNIV NORTH CAROLINA STATE.
XX Thompson WF, Hall G, Spiker S, Allen GC;
XX WPI; 1997-393609/36.
XX Isolated tobacco scaffold attachment region - used in DNA constructs to
XX transform plants to increase the expression of heterologous structural
XX genes.
XX Example 1; Page 16; 53pp; English.
XX This oligonucleotide comprises a PCR primer located in the nos gene
XX promoter. It was used with a primer (see AAT88924) from the translated
XX region of the nptII gene for nptII gene copy number analysis in tobacco
XX NT-1 cells. The cells had been subjected to microprojectile-mediated co-
XX transformation with GUS expression plasmid pGHCN11, containing scaffold
XX attachment region RB7 SAR (see AAT88920) and the GUS gene under control
XX of the CaMV 35S promoter, and with nptII selection plasmid pGHCN10
XX containing the nptII gene under control of the nos promoter. When used in
XX conjunction with a transgene, the RB7 SAR can increase the average
XX expression per gene copy by more than 100-fold in stably transformed cell
XX lines
Sequence 20 BP; 8 A; 6 C; 5 G; 1 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 381 GTTTCAGTTCTGTTCAGTT 398
DB 20 GTTTCAGTTCTGTTCAGTT 3

RESULT 1837
AAV09312
ID AAV09312 standard; DNA; 20 BP.
XX AC AAV09312;
XX XX
XX 14-MAY-1998 (first entry)
XX DE Delta-globin gene amplifying primer DG07.
XX XX
XX Chimeric repair vector; CRV; treatment; genetic mutation; repair;
XX KW sickle cell disease; beta-thalassemia; Gaucher disease; PCR primer;
XX KW hypercholesterolaemia; haemophilia; delta-globin; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9741141-A1.
XX XX
XX 06-NOV-1997.
XX PD
XX 01-MAY-1997; 97WO-US007362.
XX PF
XX 01-MAY-1996; 96US-00640517.
XX PR
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX PA
XX Kniec EB, Cole-Strauss A, Yoon K;
PI WPI; 1997-549675/50.
DR
XX Chimeric nucleic acid repair vectors - used for treating diseases such as
PT sickle cell disease, beta-thalassemia, Gaucher disease,
PT hypercholesterolaemia, emphysema or haemophilia.
XX PS
XX Example 2; Page 27; 79pp; English.
XX
XX This primer is used for the PCR amplification of a delta-globin gene
CC sequence. This is used in a method for determining the use of a chimeric
CC repair vector (CRV) to repair a mutation found in Sickle Cell disease
CC beta-globin. The CRV contains a nucleic acid having at most one 3' end
CC and one 5' end comprising a segment of unpaired bases disposed. The
CC unpaired bases separate the nucleic acid into a first strand and a second
CC strand, comprising a first region and a second region respectively, each
CC region having at least 15 nucleotides. Each nucleotide of the first
CC region is Watson-Crick paired to a nucleotide of the second region and
CC the first region comprises at least 8 ribonucleotides, which are Watson-
CC Crick paired to 2'-deoxynucleotides, which ribonucleotides form at least
CC one ribonucleotide segment of at least 3 ribonucleotides and the sequence
CC of the first or the second region is the sequence of a fragment of a wild
CC -type allele of a human gene. The CRVs can be used for repairing genetic
CC mutations in cells for re-introducing into a patient for treating
CC diseases. They can be used for treating, sickle cell disease, beta-
CC thalassemia, familial hypercholesterolaemia, Gaucher disease, emphysema
CC or haemophilia. This primer is used in the PCR amplification for
CC sequencing an episomal alkaline phosphatase DNA. This is used to in a
CC method for determining the use of a chimeric repair vector (CRV) to
CC repair episomal alkaline phosphatase. The CRV contains a nucleic acid
CC having at most one 3' end and one 5' end comprising a segment of unpaired
CC bases disposed. The unpaired bases separate the nucleic acid into a first
CC strand and a second strand, comprising a first region and a second region
CC respectively, each region having at least 15 nucleotides. Each nucleotide
CC of the first region is Watson-Crick paired to a nucleotide of the second
CC region and the first region comprises at least 8 ribonucleotides, which
CC are Watson-Crick paired to 2'-deoxynucleotides, which ribonucleotides
CC form at least one ribonucleotide segment of at least 3 ribonucleotides
CC and the sequence of the first or the second region is the sequence of a
CC fragment of a wild-type allele of a human gene. The CRVs can be used for
CC repairing genetic mutations in cells for re-introducing into a patient
CC for treating diseases. They can be used for re-introducing into a patient
CC disease, beta-thalassemia, familial hypercholesterolaemia, Gaucher
CC disease, emphysema or haemophilia.XX

SQ Sequence 20 BP; 9 A; 5 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1625 AATATATCCCGGACAG 1642
DB 3 AACAGCCCAAGGACAG 20
RESULT 1838
AAT95681/C
ID AAT95681 standard; DNA; 20 BP.
XX AC AAT95681;
XX XX
XX 20-APR-1998 (first entry)
XX DT
XX 3' primer for the first LTR-RRE fragment of the packaging vector.
XX KW Packaging vector; gag-pol fragment; LTR; HIV-packagable RNA;
XX KW HIV-based gene therapy vector; resistance; HIV infection; LTR-RRE;
XX KW PCR primer; ss.
XX OS Synthetic.
XX XX
XX WO9736481-A1.
XX PN
XX 09-OCT-1997.
XX PD
XX 26-MAR-1997; 97WO-US005272.
XX PF
XX 02-APR-1996; 96US-0015555P.
XX PR
XX 24-MAR-1997; 97US-00822516.
XX PR
XX (REGC) UNIV CALIFORNIA.
XX PA
XX Corbeau P, Kraus G, Wong-Staal F;
PI WPI; 1997-502768/46.
DR
XX New high efficiency packaging vectors - comprising HIV packaging
PT sequences, used for transduction of target cells, particularly for gene
PT therapy.
XX PS
XX Disclosure; Page 53; 85pp; English.
XX CC
XX PCR primers AAT95680-81 were used to detect a transduced high efficiency
CC packaging vector by amplification of the first LTR-RRE of the vector. The
CC vector comprises a high efficiency packaging vector nucleic acid encoding
CC a portion of an Human immunodeficiency virus type 1 (HIV-1) particle,
CC which has reverse transcriptase activity, is non-infectious, and, when
CC transduced into a cell, renders the cell competent to package HIV-
CC packagable RNA (comprising a HIV-1 packaging site) with a titre of at
CC least 104 transducing units/ml. Packaging vectors and cell lines enable
CC efficient transduction of target cells (e.g. CD4+ cells) with HIV-based
CC gene therapy vectors. The target cells can be rendered resistant to HIV
CC infection which will be useful in vitro to reduce the risk of handling
CC cells, e.g. in tissue culture techniques, and in ex vivo and in vivo gene
CC therapy procedures. The products can be used for the treatment of HIV
CC infection, T-cell lymphomas, HTLV-1 infection, Adult T cell leukaemia,
CC Myosis Fungusides and Segary's syndromes, CD4+ lymphoblastic lymphomas or
CC peripheral CD4+ T cell lymphomas. The packaging vectors can also be used
CC for the detection of HIV
XX SQ
SQ Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1817 TAGTTTGGAAAGTGCC 1834

703D4 antigen; hnRNP-A2; hnRNP-B1; lung cancer; liver cancer; renal cancer; prostate cancer; melanoma; head cancer; neck cancer; myeloma; marker; carcinogenesis; diagnosis; human; polymerase chain reaction; PCR; primer; ss.

Synthetic.

WO9712975-A1.

10-APR-1997.

02-OCT-1996; 96WO-US015825.

02-OCT-1995; 95US-00538711.

02-OCT-1996; 96US-00725027.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

(UYJO) UNIV JOHNS HOPKINS.

Mulshine JL, Tockman MS;

WPI; 1997-226219/20.

A new purified protein from epithelial cells - is expressed in high amounts in cancer and pre-cancer cells; used as a marker for diagnosis and treatment of cancer.

Example 1; Page 33; 171pp; English.

Specific PCR primers (AAT90338-42) are used to amplify the gene encoding an epithelial protein (see AAW26546-51) that is useful in early cancer detection. The primers may also be used to detect mRNA in a biological sample. The method is important in detecting and differentiating precancer and cancer cells and normal cells and in detecting subsets of epithelial cells destined to become cancer cells. Diagnostic screens are claimed for lung, renal, breast or prostate cancer, myeloma and melanoma

Sequence 20 BP; 1 A; 5 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 1.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1252 GACGAAGACGACCTGAC 1269

Db 20 GACGAAGACGACCTGAC 3

RESULT 1841

AAT75391

ID AAT75391 standard; cDNA; 20 BP.

XX AC AAT75391;

XX DT 24-DEC-1998 (first entry)

XX DE Sau3A1 semiadapter #1 primer 1.

XX ss; human; RAD50; DNA repair; tumour suppression; cancer; Septin-2; central nervous system; PCR; primer; amplification.

XX Synthetic.

XX WO9727284-A2.

XX 31-JUL-1997.

XX 24-JAN-1997; 97WO-US001299.

XX 26-JAN-1996; 96US-00592126.

XX 17-JUL-1996; 96US-00687080.

XX (GENE-) GENELABS TECHNOLOGIES INC.

PA

18 TAGCTGTGAAAGATACC 1

RESULT 1839

AAT45145

ID AAT45145 standard; DNA; 20 BP.

XX AC AAT45145;

XX DT 08-MAR-1997 (first entry)

XX Carotenoid biosynthesis gene cluster PCR primer 8.

XX Carotenoid; lycopene; beta-carotene; echinenone; canthaxanthin; zeaxanthin; adonixanthin; astaxanthin; crtE;

XX geranylgeranyl pyrophosphate synthase; GGPP synthase; crtB;

XX phytylene synthase; phytoene synthase; crtI; phytoene desaturase; crtY;

XX lycopene cyclase; crtZ; beta-carotene hydroxylase; Flavobacterium;

XX polymerase chain reaction; PCR; primer; ss.

XX Synthetic.

XX EP747483-A2.

XX 11-DEC-1996.

XX 29-MAY-1996; 96EP-00108556.

XX 09-JUN-1995; 95EP-00108888.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Hohmann H, Pasamontes L, Tessier M, Van Loon A;

XX WPI; 1997-023160/03.

XX P-PSDB; AAW06515, AAW06516, AAW00871, AAW06517, AAW06518, AAW06519.

XX Flavobacterium gene sequences encoding carotenoid biosynthesis enzymes - for the production of carotenoid(s), useful in foods and animal feeds.

XX Example 1; Page 8; 80pp; English.

XX Partial genomic libraries of Flavobacterium sp. R1534 WT DNA were used to transform E. coli XL-1 blue or JM109. Transformed cells were screened by PCR using primers No. 7 (AAT45144) and No. 8 (AAT45145). Partial clones were obtd. that showed homology to genes of the carotenoid biosynthetic pathway. These were used to identify a gene cluster (see also AAT45143) including open reading frames coding for carotenoid biosynthetic enzymes (see also AAW06515-18 and AAW00871)

XX Sequence 20 BP; 5 A; 7 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 1.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1647 CAAGGCCCGAGCTCAGG 1664

Db 1 CAAGGCCCGAGCTCAGG 18

RESULT 1840

AAT90338/c

ID AAT90338 standard; DNA; 20 BP.

XX AC AAT90338;

XX DT 16-JAN-1998 (first entry)

XX Epithelial protein (precancer marker) PCR primer.

XX Epithelial protein; heterogeneous nuclear ribonuclear protein;

XX PI Dolganov G;
 XX WPI; 1997-393672/36.
 XX Human tumour suppressor gene RAD50 - useful to detect predisposition to,
 PT decrease risk of and treat cancer, also Septin-2 homologues.
 XX Example 2; Page 72; 195pp; English.
 XX The primers AAT75379-T75392 and AAT75398-T75409 were used in examples of
 CC the above specification. Disclosed in the invention is human RAD50
 CC (hRAD50) which is involved in DNA repair and has tumour suppression
 CC activity, and can be used to detect predisposition to, decrease the risk
 CC of or treat cancers, e.g. acute myeloid leukaemia, myelodysplastic
 CC syndrome, therapy related myelodysplastic syndrome, therapy related acute
 CC myeloid leukaemia, refractory anaemia or refractory anaemia with excess
 CC blasts. Also disclosed in this invention are human Septin-2 homologues
 CC which may be used as targets for cancer therapies and central nervous
 CC system directed treatment methods, and to measure the proliferative
 CC potential of selected cell types
 XX Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1029 GGAGATCCCTAATGAGCT 1046
 Db 3 GGAGATCTCTTAAGAGCT 20
 RESULT 1842
 ID AAV66747/c
 XX AAV66747 standard; DNA; 20 BP.
 AC AAV66747;
 XX 17-DEC-1998 (first entry)
 DE PCR forward primer P152 from W09844151 Example 4.
 XX Nucleic acid amplification; immobilised primer; sequencing; screening;
 KW diagnosis; in situ nucleic acid synthesis; fingerprinting;
 KW gene expression; PCR primer; ss.
 OS Synthetic.
 XX WO9844151-A1.
 PN 08-OCT-1998.
 PD 01-APR-1998; 98WO-GB000961.
 PF 01-APR-1997; 97GB-00006528.
 ER 01-APR-1997; 97GB-00006529.
 PR 23-JUN-1997; 97GB-00013236.
 PR 23-JUN-1997; 97GB-00013238.
 XX (GLAX) GLAXO GROUP LTD.
 PA Kawashima E, Farinelli L, Mayer P;
 PI WPI; 1998-568282/48.
 XX New nucleic acid amplification - by extension of immobilised primers
 PT annealed to target, separation of strands, annealing extended primer to
 PT second primer and repeating extension.
 XX Example 4; Page 35; 108pp; English.
 PS A method has been developed for nucleic acid (NA) amplification. The

CC method comprises: (a) annealing single-stranded (ss) target NA to one of
 CC many primers (P), immobilised but having one end free for extension, and
 CC extending P using the target as template, producing an immobilised
 CC extension product (EP); (b) separating EP and target NA; (c) annealing EP
 CC to another P and extending this, using EP as template, to give a second
 CC extension product (EP2); and (d) optionally separating EP and EP2. The
 CC method is used to produce NA for sequencing, diagnosis and screening, as
 CC supports for other materials, for generating free NA (particularly in
 CC situ RNA synthesis), monitoring gene expression, identifying heterozygotes and in NA
 CC fingerprinting. A very high density of DNA-bearing areas can be randomly
 CC arrayed and amplified on the support. The present sequence represents a
 CC PCR primer used in an example from the present invention
 XX Sequence 20 BP; 4 A; 8 C; 3 G; 5 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 129 CTATTATGGACAGGCCA 146
 Db 19 CTGTTAGGATAGGCCA 2
 RESULT 1843
 ID AAV71146
 XX AAV71146 standard; DNA; 20 BP.
 AC AAV71146;
 XX 11-FEB-1999 (first entry)
 DE PCR primer PBR6 used to amplify a DNA fragment unique to Bos sp.
 XX Bovine; mitochondrial DNA; detection; bovine spongiform encephalopathy;
 KW PCR primer; ss.
 XX Synthetic.
 OS Bos sp.
 XX PR2762842-A1.
 XX 06-NOV-1998.
 PD 05-MAY-1997; 97FR-00005517.
 PF 05-MAY-1997; 97FR-00005517.
 PR 05-MAY-1997; 97FR-00005517.
 XX (INSP) INST PASTEUR LILLE.
 PA Lange M, Pasteau S, Grangette C, Hanni C, Laudet V;
 PI WPI; 1998-586147/50.
 DR Detecting material of bovine origin in foods, cosmetics, animal feeds
 XX etc. - particularly to identify possible contamination by bovine
 PT spongiform encephalopathy, by amplifying new mitochondrial DNA sequence
 PT specific for all species of Bovidae.
 XX Claim 6; Page 23; 30pp; French.
 XX PCR primers AAV71144-50 represent primers used to amplify a DNA fragment
 CC (AAV71151) that is unique to Bos species. Primers AAV71145-46 are derived
 CC from primer AAV71144, and primers AAV71148-49 are derived from primer
 CC AAV71147. The unique DNA sequence can be amplified from crude organic
 CC extracts, and then detected to identify the extract as being of bovine
 CC origin. The unique DNA sequence is a mitochondrial sequence, and so is
 CC more resistant to degradation than nuclear DNA and is also present at 100
 CC -1000 greater copy number. The amplification and detection method allows
 CC specific detection of material from any species of cattle at very low
 CC levels (typically less than 0.05% bovine material), in a wide variety of
 CC compositions, e.g. bovine materials such as cooked or raw meat, pellets


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AAV25945/c
ID  AAV25945 standard; DNA; 20 BP.
XX
AC  AAV25945;
XX
DT  15-JUL-1998 (first entry)
XX
DE  Oligonucleotide PCR primer ECO1.1 uida gene.
XX
KW  Sequence-specific; probe; enterohaemorrhagic; Escherichia coli;
KW  Salmonella; Campylobacter; Shigella; Yersinia; beta-globin;
KW  gastroenteritis; PCR primer; ss.
XX
OS  Synthetic.
OS  Escherichia coli.
XX
PN  US5753444-A.
XX
PD  19-MAY-1998.
XX
PF  07-AUG-1996; 96US-00689235.
XX
PR  16-JAN-1996; 96US-00587209.
XX
PA  (GULL-) GULL LAB INC.
XX
PI  Malmstrom SL, Glass MJ, Wu L, Coombs J;
XX  WPI; 1998-3111393/27.
XX
PT  Distinguishing between similar nucleic acid samples - using sequence-
PT  specific probes e.g. between enterohaemorrhagic and normal Escherichia
PT  coli.
XX
PS  Example 3; Col 17; 21pp; English.
XX
CC  The present sequence represents a PCR primer used in an example of the
CC  present invention. The present invention describes a method for detecting
CC  mismatches between first and second nucleic acid sequences having at
CC  least one base difference. The method comprises: (a) obtaining at least
CC  one labelled probe consisting of an oligonucleotide sequence spanning the
CC  location of at least one base difference between the first and second
CC  sequences, where the oligonucleotide sequence contains at least one
CC  neutral base molecule in a position other than the position of the base
CC  difference(s) but is otherwise exactly complementary to the first
CC  sequence, so that the probe hybridises more weakly with the second
CC  sequence than with the first sequence; (b) mixing the probe(s) with the
CC  first and second sequences under hybridisation conditions; (c)
CC  dissociating any probe/second sequence hybrids; and (d) detecting
CC  probe/first sequence hybrids. The method can be used to distinguish
CC  between similar DNA/RNA sequences in a sample, especially to distinguish
CC  enterohaemorrhagic E. coli O157:H7 from other E. coli strains e.g. in
CC  stool samples from people suffering from gastroenteritis, caused
CC  specifically by enterohaemorrhagic E.coli. Use of the method shortens the
CC  time between sample preparation to obtaining results, than has been
CC  possible with previous similar procedures
XX
SQ  Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

Query Match          0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1450 GAGAAACCAAGGAGGAG 1467
DB  ||||| ||||| ||||| |||||
    18 GAGAAACCAATGGAGAG 1

RESULT 1847
AAV36064/c
ID  AAV36064 standard; DNA; 20 BP.
XX
AC  AAV36064;
XX

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```

XX
DT  02-SEP-1998 (first entry)
XX
DE  PCR primer Mcbhl-C of the specification.
XX
KW  Regulatory sequence; cellulase cbhl gene; mass production;
KW  Humicola insolens; endo-glucanase NCE4; PCR primer; ss.
XX
OS  Synthetic.
OS  Trichoderma viride.
XX
PN  WO9811239-A1.
XX
PD  19-MAR-1998.
XX
PF  16-SEP-1997; 97WO-JP003268.
XX
PR  13-SEP-1996; 96JP-00243695.
XX
PA  (MEIJ ) MEIJ SEIKA KAISHA LTD.
XX
PI  Watanabe M, Moriya T, Aoyagi K, Sumida N, Murakami T;
XX  WPI; 1998-250959/22.
XX
PT  Regulatory sequence for Trichoderma viride derived cellulase cbhl gene -
PT  for producing Humicola insolens derived endo-glucanase.
XX
PS  Example 4; Page 22; 92pp; Japanese.
XX
CC  PCR primers AAV36063-64 are used in the course of the invention. The
CC  specification describes a new regulatory sequence for Trichoderma viride
CC  derived cellulase cbhl gene and the establishment of a system for mass
CC  producing cellulase in moulds such as T. viride. As the regulatory
CC  sequence of cbhl genes originating in T. viride can highly express
CC  objective proteins, proteins such as cellulase can be expressed. An
CC  expression vector containing the regulatory sequence and Humicola
CC  insolens derived endo-glucanase NCE4 DNA was produced, and used to
CC  produce endo-glucanase at 15 grams per litre
XX
SQ  Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

Query Match          0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  409 GGTCTGTGGCAAGTGCT 426
DB  ||| ||||| ||||| |||||
    20 GGTACTGTGGCAAAAGCT 3

RESULT 1848
AAV56302/c
ID  AAV56302 standard; cDNA; 20 BP.
XX
AC  AAV56302;
XX
DT  18-NOV-1998 (first entry)
XX
DE  Human BRCA1 exon 11C PCR primer 11CF1.
XX
KW  BRCA1; omi gene; human; breast and ovarian cancer predisposing gene;
KW  polymorphism; susceptibility; anti-oncogene; tumour suppressor;
KW  chromosome 17q; PCR primer; ss.
XX
OS  Synthetic.
OS  Homo sapiens.
XX
PN  US5750400-A.
XX
PD  12-MAY-1998.
XX
PF  12-FEB-1997; 97US-00798691.

```


CC found to reduce transformed properties of tumour cells. The antisense
CC oligonucleotides can be used for modulating tumour cell growth, or for
CC inhibiting tumour cell proliferation. They can also be used for
CC increasing the sensitivity of neoplastic cells to chemotherapeutic drugs
CC (especially to hydroxyurea, methotrexate (MTX), and PALA). The antisense
CC oligonucleotides may be used to treat proliferative disorders including
CC leukaemias, lymphomas, sarcomas, melanomas, various other forms of
CC cancer, papillomas, arthrosclerosis, psoriasis, polythemia, mastocytosis,
CC autoimmune diseases, angiogenesis, bacterial infections and viral
CC infections (including HIV hepatitis, or herpes infections)
XX Sequence 20 BP; 3 A; 6 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1908 TCAGCCATTTTTCATG 1925
Db 3 TCAGCCACTTTTCATG 20

RESULT 1851
AAV62239/c
ID AAV62239 standard; DNA; 20 BP.
XX AC AAV62239;
XX DT 11-FEB-1999 (first entry)
DE PCR primer 11CF for exon 11C of BRCA1 (omil) coding sequence.
XX BRCA1; mutation detection; disease screening; multiple allele variation;
XX breast cancer; ovarian cancer; cystic fibrosis; Li-Fraumeni syndrome;
XX Duchenne muscular dystrophy; Becker muscular dystrophy; PCR primer; ss.
OS Synthetic.
OS Homo sapiens.
XX WO9844157-A2.
XX 08-OCT-1998.
XX 26-MAR-1998; 98WO-US006002.
XX 28-MAR-1997; 97US-00825487.
XX (ONCO-) ONCORMED INC.
XX Murphy PD, White MB;
XX WPI; 1998-542713/46.

Identifying variations in polynucleotide sequences - using allele
specific hybridisation assay, sequence variation locating assay, and
direct sequencing, in a stepwise procedure.
Example 1; Page 36; 62pp; English.
This sequence is a PCR primer for a fragment of the DNA encoding the
human BRCA (omil) protein, and was used to test the method of the
invention. The method is for determining the presence or absence of a
sequence variation in a gene sample, and comprises: (a) performing an
allele specific hybridisation assay for one or more pre-determined
sequence variations; (b) if no pre-determined sequence variation found in
step (a) then performing a sequence variation location assay; (ci) if no
sequence variation found in step (b) then sequencing the gene sample;
(cii) if sequence variation is found in step (b) then targeted
confirmatory sequencing is performed; and (d) determining the presence of
a sequence variation by analysing the sequence(s) obtained in step (ci)
or step (cii) against a reference sample. Alternatively, step (a) or step
(b) is omitted from the method. The invention provides a stepwise and
integrated method for the efficient and accurate detection of variations

CC in polynucleotide sequences, being directed towards screening for
CC diseases associated with multiple allele variations, including breast and
CC ovarian cancer, cystic fibrosis, Duchenne and Becker muscular dystrophy,
CC and Li-Fraumeni syndrome
XX Sequence 20 BP; 6 A; 2 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 846 TGGCTCAGACTCCCTATC 863
Db 19 TGATTCAGACTCCCAATC 2

RESULT 1852
AAV40150
ID AAV40150 standard; DNA; 20 BP.
XX AC AAV40150;
XX DT 10-AUG-1999 (first entry)
DE DNA sequence of primer #8.
XX Carotenoid; pigment; canthaxanthin; R1534; crtB; prephytoene synthase;
XX crtI; phytoene desaturase; crtY; lycopene cyclase; crtW2396; PCR primer;
XX beta-carotene beta-oxygenase; food product; fermentation; ss.
OS Synthetic.
XX JP10155497-A.
XX 16-JUN-1998.
XX 02-DEC-1997; 97JP-00348653.
XX 02-DEC-1996; 96EP-00810839.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX WPI; 1998-391048/34.
Preparation of carotenoid - comprises fermentation with transformed cell.
Example 1; Page 8; 80pp; Japanese.

The invention describes the preparation of carotenoid pigments e.g.
canthaxanthins using a cell transformed by a vector having DNA sequences
(a) to (e) or substantially homologous sequences. (a) a DNA sequence
(crtE) coding GPP synthase of Flavobacterium sp. R1534; (b) a DNA
sequence (crtB) coding prephytoene synthase of Flavobacterium sp. R1534;
(c) a DNA sequence (crtI) coding phytoene desaturase of Flavobacterium
sp. R1534; (d) a DNA sequence (crtY) coding lycopene cyclase of
Flavobacterium sp. R1534; and (e) a DNA sequence (crtW2396) coding beta-
carotene beta-oxygenase of a microbe E-396 (FERM BP-4283). The carotenoid
or a carotenoid mixture can also be used in preparation of food products.
The method is an improved method of fermentation for carotenoid
production
XX Sequence 20 BP; 5 A; 7 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1647 CAAGGCCCGAGCTCAGG 1664
Db 1 CAAGGCCCGAGCTCAGG 18

RESULT 1853

AAV52748
D AAV52748 standard; DNA; 20 BP.
K AAV52748;
C C
X X
T T
E E
X Angiotensin-converting enzyme PCR 5'-primer SEQ ID NO:1.
X Angiotensin-converting enzyme ACE; human; heart; PCR primer; detection;
W screening; cardiovascular disease; ss.
X Synthetic.
S Homo sapiens.
S S
N US5800990-A.
N D
D 01-SEP-1998.
F 06-DEC-1995; 95US-00568271.
F F
X 06-DEC-1995; 95US-00568271.
R R
(COLS) UNIV COLORADO.
A Perryman MB, Raynolds MV;
A WPI; 1998-494763/42.
I
X Detecting mutation(s) in angiotensin-converting enzyme gene - to assess
X cardiovascular disease risk.
X Example 1; Col 9; 12pp; English.

The following methods have been developed for detecting small deletions,
insertions or point mutations in an angiotensin-converting enzyme (ACE)
gene of a human patient: (1) a method comprising: (a) isolating an ACE
genomic DNA sequence from the patient, where the sequence spans intron
25, using oligonucleotide primers in the 3' region of exon 25 and the 5'
region of exon 26; (b) hybridising the genomic sequence with a detectable
probe specific for the corresponding sequence with no mutations; and (c)
detecting mismatches between the genomic sequence and the probe; (2) a
method comprising: (a) isolating an ACE genomic DNA sequence as in (1);
(b) amplifying the sequence; (c) hybridising the amplification products
with a probe as in (1); and (d) detecting mismatches between the
amplification products and the probe; (3) a method comprising: (a)
isolating an ACE genomic DNA sequence as in (1); (b) denaturing the
genomic sequence to obtain single-stranded DNA; (c) hybridising the
single-stranded DNA with a probe as in (1); and (d) detecting mismatches
between the single-stranded DNA and the probe; (4) a method comprising:
(a) isolating an ACE genomic DNA sequence as in (1); (b) amplifying the
sequence; (c) denaturing the amplification products to obtain single-
stranded DNA; (d) hybridising the single-stranded DNA with a probe as in
(1); and (e) detecting mismatches between the single-stranded DNA and the
probe. The methods are used for assessing the patient's risk of
developing cardiovascular disease. The present sequence represents a PCR
primer for ACE

Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 940 CTGCCCTATGCTGATGCTG 957
||||| ||||| |||||
Db 2 CTGCCGCTGCTGTGTTGCTG 19

RESULT 1854
AAV26438/C
ID AAV26438 standard; DNA; 20 BP.


```

PF 07-AUG-1996; 96US-00689236.
XX
XX 16-JAN-1996; 96US-00587209.
XX
XX (GULL-) GULL LAB INC.
XX
XX Malmstrom SL, Glass MJ, Wu L, Coombs J;
XX WPI; 1998-260031/23.
XX
XX Probes for detecting Escherichia coli strain O157:H7 - useful for
XX diagnosis of enterohaemorrhagic Escherichia coli infection(s).
XX
XX Example 3; Col 17; 21pp; English.
XX
XX The present sequence represents a PCR primer used in an example of the
XX present invention. The present invention describes probes used in the
XX detection of Escherichia coli strain O157:H7 in a sample. The method of
XX detection comprises: (a) obtaining at least 1 probe specifically given in
XX the specification, labelled with a label that permits probe detection
XX when hybridised to a complementary nucleic acid sequence which is
XX specific for a nucleic acid sequence of the microorganism; (b)
XX hybridising the probes and the sample, and (c) detecting hybrids
XX comprising the probes and the nucleic acid sequences. The method and
XX probes may be used for diagnosis of enterohaemorrhagic E. coli
XX infections. The methods and the materials permit the detection and
XX discrimination of multiple analytes
XX
XX Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1450 GAGAAACCCAGGAGGAG 1467
XX 18 GAGAAACCCATGGAGAG 1
XX
XX RESULT 1856
XX AAV16973
XX ID AAV16973 standard; cDNA to mRNA; 20 BP.
XX AC
XX AAV16973;
XX
XX 06-JUL-1998 (first entry)
XX
XX Oligonucleotide sequence of the specification.
XX
XX Slit-like protein; human; diagnosis; treatment; brain-specific disease;
XX cancer; antibody; ss.
XX
XX Synthetic.
XX
XX JP10087699-A.
XX
XX 07-APR-1998.
XX
XX 15-JUL-1997; 97JP-00205351.
XX
XX 16-JUL-1996; 96JP-00186219.
XX
XX (ASAH ) ASAH KASEI KOGYO KK.
XX
XX WPI; 1998-267127/24.
XX
XX Human Slit-like protein - useful for diagnosis and treatment of brain-
XX specific diseases and cancers.
XX
XX Disclosure; Page 38; 45pp; Japanese.
XX
XX The present sequence appears in the specification. The specification
XX describes a novel human slit-like protein (the mature protein is claimed

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CC in Claim 1). The slit-like polypeptide is useful for diagnosis and
CC treatment of brain-specific diseases and cancers. Antibodies directed
CC against the protein, or its fragments can also be used for diagnosing
CC cancer
XX
XX Sequence 20 BP; 4 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 536 TGGCCATCCTCGAACTGC 553
XX 1 TGGCCATGCGGCACTGC 18
XX
XX RESULT 1857
XX AAV31449/c
XX ID AAV31449 standard; DNA; 20 BP.
XX XX
XX AAV31449;
XX AC
XX 11-AUG-1998 (first entry)
XX DT
XX Escherichia coli nucleic acid sequence amplifying primer ECO1.1.
XX DE
XX Salmonella; microorganism; detection; multiple analyte; PCR primer;
XX KW
XX Yersinia; Escherichia coli; ss.
XX XX
XX Synthetic.
XX OS
XX Escherichia coli.
XX OS
XX US5756701-A.
XX PN
XX 26-MAY-1998.
XX PD
XX 06-AUG-1996; 96US-00692725.
XX PF
XX 16-JAN-1996; 96US-00587209.
XX PR
XX (GULL-) GULL LAB INC.
XX PA
XX Malmstrom SL, Glass MJ, Coombs J, Wu L;
XX PI
XX WPI; 1998-321634/28.
XX DR
XX Nucleic acid probes and primers - for detecting Salmonella, Yersinia or
XX E. coli.
XX PT
XX Claim 4; Col 17; 21pp; English.
XX PS
XX
XX This primer is used for the PCR amplification of E. coli nucleic acid
XX sequences. The invention provides nucleic acid probes and primers for
XX detecting Salmonella, Yersinia or E. coli. It provides methods and
XX apparatus for detecting and discriminating multiple analytes within a
XX test sample. The methods are simple, user-friendly, cost effective and
XX fast. The methods and the probes and primer sequences are used for
XX detecting the corresponding microorganisms in clinical samples
XX
XX Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1450 GAGAAACCCAGGAGGAG 1467
XX 18 GAGAAACCCATGGAGAG 1
XX
XX RESULT 1858
XX AAX15267
XX ID AAX15267 standard; DNA; 20 BP.

```

XX AC AAX15267;
XX DR 29-APR-1999 (first entry)
XX DE PCR primer F2S4 for DNA encoding a DNA polymerase binding factor F2.
XX KW Thermostable polypeptide factor; DNA synthesis activity; DNA polymerase;
XX KW in vitro DNA synthesis; PCR primer; ss.
XX OS Synthetic.
XX OS Pyrococcus furiosus.
XX PN WO9900506-A1.
XX PD 07-JAN-1999.
XX PF 24-JUN-1998; 98WO-JP002845.
XX PR 26-JUN-1997; 97JP-00187496.
XX PR 21-JUN-1997; 97JP-00320692.
XX PA (TAKI) TAKARA SHUZO CO LTD.
XX PI Uemori T, Sato Y, Fujita T, Miyake K, Mukai H, Asada K, Kato I;
XX WPI; 1999-095751/08.
XX PT Thermostable polypeptide factors promoting the activity of DNA polymerase
PT - for improvement of DNA synthesis and amplification in vitro.
XX Example 6; Page 114; 177pp; Japanese.
XX PCR primers AAX15266-67 were used to amplify Pyrococcus furiosus DNA
CC encoding a thermostable polypeptide factor. This factor binds to, and
CC promotes the DNA synthesis activity of DNA polymerase. The polymerase
CC related factors can be used to provide more efficient in vitro DNA
CC synthesis and amplification systems (e.g. for polymerase chain reaction)
CC by using the factors in conjunction with a DNA polymerase
XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. NO. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1934 TTCGTACTTCCCACTGG 1951
Db 1 TTCGTACAGTCCCTCTGG 18
RESULT 1859
AAX76914
ID AAX76914 standard; DNA; 20 BP.
XX AC AAX76914;
XX DT 05-AUG-1999 (first entry)
XX DE Probe used to test nucleic acid detection method.
XX KW Nucleic acid detection; probe; ss.
XX OS Synthetic.
XX PN JP11127862-A.
XX PD 18-MAY-1999.
XX PF 31-OCT-1997; 97JP-00300943.
XX PR 31-OCT-1997; 97JP-00300943.
XX

PA (CANO) CANON KK.
XX WPI; 1999-350323/30.
XX Detection of a target nucleic acid - using a labelled unit with labels
PT capable of interactive action in a phenomenon of electron flow in double
PT helix structure.
XX Example 3; Page 5; 9pp; Japanese.
XX This sequence is a probe used to test the method of the invention. The
CC method is for the detection of a hybrid of a target nucleic acid and a
CC probe nucleic acid in a sample comprises: (1) preparation of a labelled
CC unit composed of 1st and 2nd labelled substances capable of interactive
CC action in a phenomenon of electron flow in double helix structure in the
CC presence of a hybrid via a linker; (2) addition of a probe nucleic acid
CC having a complementary base sequence to the base sequence of target
CC nucleic acid; (3) placing the sample under conditions capable of forming
CC the target nucleic acid and the probe nucleic acid to give a hybrid; (4)
CC mixing the sample capable of forming the hybrid and the labelled unit;
CC (5) detection of the change in the 1st and/or 2nd labelled substances
CC caused by their interaction; and (6) detection of the presence of a
CC hybrid in the sample. The method can be used for the detection of a
CC target nucleic acid having a specified base sequence. The method allows
CC for the simple and easily operable detection of labelled nucleic acids
CC without complicated synthesis of labelled probe nucleic acids for
CC respective base sequence
XX Sequence 20 BP; 11 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. NO. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1613 TTTTATTAAATATTAATAT 1630
Db 1 TATATAAAATATATATAT 18
RESULT 1860
AAX99208/c
ID AAX99208 standard; DNA; 20 BP.
XX AC AAX99208;
XX DT 09-MAR-1999 (first entry)
XX DE Antisense primer for intron boundary mapping of DNA Metase exons 33-34.
XX KW DNA methyltransferase; DNA Metase; antisense oligonucleotide; human;
XX KW cellular growth; tumour growth inhibition; silenced gene activation;
XX KW beta thalassemia; sickle cell anemia; PCR primer; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9854313-A2.
XX PD 03-DEC-1998.
XX PF 29-MAY-1998; 98WO-IB001107.
XX PR 30-MAY-1997; 97US-00866340.
XX PR 17-DEC-1997; 97US-0089865P.
XX PA (UYMC-) UNIV MCGILL.
XX PI Szyf M, Bigey P, Ramchandani S;
XX WPI; 1999-059833/05.
XX New DNA methyltransferase nucleotide sequences - used particularly to
PT develop antisense oligonucleotides for diagnostic and therapeutic

PT purposes, particularly for inhibiting tumour growth.
 XX
 PS Example 8; Page 31; 108pp; English.
 XX
 CC PCR primers AAV99163-220 were used to map the intron boundaries of the
 CC exons of DNA methyltransferase (DNA Mefase) genomic sequence. Antisense
 CC oligonucleotides which inhibit DNA Mefase expression can be
 CC derived from the genomic DNA Mefase sequence. The antisense
 CC oligonucleotides can be used in investigating the role of DNA Mefase in
 CC cellular growth. They can be administered at different points in the cell
 CC cycle, or in conjugation with promoters or inhibitors of cell growth to
 CC determine the role of DNA Mefase in the growth of the cell type of
 CC interest. The antisense oligonucleotides can also be used for inhibiting
 CC tumour growth in a mammal, or to activate silenced genes to provide a
 CC missing gene function. This ameliorates disease symptoms, e.g. in beta
 CC thalassemia and sickle cell anemia. The antisense oligonucleotides can
 CC also be used as analytical and diagnostic tools and a potentiators of
 CC transgenic plant and animal studies
 XX
 SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 839 TACAGTGTGGCTCAGACT 856
 Db 19 TACGGGTGGCCAGACT 2
 RESULT 1861
 AAX91410/C
 ID AAX91410 standard; DNA; 20 BP.
 XX
 AC AAX91410;
 XX
 DT 24-SEP-1999 (first entry)
 XX
 DE T. gondii MGIS4-4 DNA sequencing primer.
 XX
 KW Immunogenic protein; Toxoplasma gondii protein; oocyst shedding; cat;
 KW T. gondii infection; enteric apicomplexa oocyst; Cryptosporidium oocyst;
 KW Toxoplasma oocyst; PCR primer; ss.
 XX
 OS Synthetic.
 OS Toxoplasma gondii.
 XX
 PN WO9932633-A1.
 XX
 PD 01-JUL-1999.
 XX
 PF 18-DEC-1998; 98WO-US027137.
 XX
 PR 19-DEC-1997; 97US-00994825.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Milhausen WJ, Lutz SB, Ng RK;
 XX
 DR WPI; 1999-418930/35.
 XX
 PT New isolated Toxoplasma gondii nucleic acids used, e.g. to treat
 PT infection caused by this microorganism.
 XX
 PS Example 15; Page 328; 381pp; English.
 XX
 CC The invention provides isolated Toxoplasma gondii nucleic acids that
 CC encode immunogenic polypeptides. The T. gondii nucleic acid molecules,
 CC immunogenic proteins and antibodies to the proteins can be used to
 CC inhibit T. gondii oocyst shedding in a cat due to infection with T.
 CC gondii. They can be used for preventing T. gondii infection and for
 CC preventing the spread of T. gondii infection. They can also be used for
 CC detecting T. gondii infection. The detection method can be used to detect

CC parasite cysts or oocysts in feces, e.g. from enteric apicomplexa oocysts
 CC such as Cryptosporidium oocysts and Toxoplasma oocysts. The present
 CC sequence represents a primer used in PCR amplification of a DNA encoding
 CC immunogenic T. gondii protein
 XX
 SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 807 AATGGAGATGTTCCAGCC 824
 Db 19 AATGGTGATGTTCCGCC 2
 RESULT 1862
 AAZ41094/C
 ID AAZ41094 standard; DNA; 20 BP.
 XX
 AC AAZ41094;
 XX
 DT 26-JAN-2000 (first entry)
 XX
 DE Human G-alpha-11 PCR forward primer SEQ ID NO:246.
 XX
 KW Identification; genetic target; gene modulation; human; probe;
 KW antisense oligonucleotide; phosphorothioate; PCR primer;
 KW nucleotide sequence-based technology; antisense drug discovery;
 KW target validation; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9953101-A1.
 XX
 PD 21-OCT-1999.
 XX
 PF 13-APR-1999; 99WO-US008268.
 XX
 PR 13-APR-1998; 98US-0081483P.
 PR 28-APR-1998; 98US-00067638.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 XX Cowsett LM, Baker BF, Mcneil J, Freier SM, Sasnor HM, Brooks DG;
 PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;
 XX
 DR WPI; 1999-620446/53.
 XX
 PT Identifying compounds which modulate expression of nucleic acids, used to
 PT provide compounds having defined physical, chemical or bioactive
 PT properties, e.g. antisense activity.
 XX
 PS Example 26; Page 107; 264pp; English.
 XX
 CC A method has been developed of defining a set of compounds that modulate
 CC the expression of a target nucleic acid (tNA) sequence via binding of the
 CC compounds with the tNA sequence. The method comprises generating a
 CC library of virtual compounds in silico according to defined criteria, and
 CC evaluating in silico the binding of the virtual compounds with the tNA
 CC according to defined criteria. Also described are: (1) a method of
 CC defining a set of oligonucleotides (ONs) that modulate the expression of
 CC a tNA sequence via binding of the ONs with the tNA sequence comprising
 CC generating a library of virtual compounds in silico according to defined
 CC criteria, and evaluating in silico the binding of the virtual ONs with
 CC the tNA according to defined criteria; and (2) a method of defining a set
 CC of compounds that modulate the expression of a tNA sequence via binding
 CC of the compounds with the tNA. The methods can be used for the generation
 CC and identification of synthetic compounds having defined physical,
 CC chemical or bioactive properties. Information gathered from assays of
 CC such compounds is used to identify nucleic acid sequences that are
 CC tractable to a variety of nucleotide sequence-based technologies, e.g.

CC antisense drug discovery and target validation. AAZ40852 to AAZ41220, and
 CC AAY52701 to AAY52706, represent sequences used in the exemplification of
 CC the present invention

XX SQ Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 949 CTGATGCTGGAGCGGT 966

DB 20 CTGATGCTCGAAGTGGT 3

RESULT 1863

AAZ37707/c

ID AAZ37707 standard; DNA; 20 BP.

XX AC AAZ37707;

XX DT 07-JAN-2000 (first entry)

XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #237.

XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
 KW antisense; modulation; oligonucleotide; expression; inhibition;
 KW hyperproliferation; blood cancer; brain cancer; breast cancer;
 KW lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;
 KW restenosis; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9949065-A1.

XX PD 30-SEP-1999.

XX PF 26-MAR-1999; 99WO-US006702.

XX PR 26-MAR-1998; 98US-00048810.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowse LM;

XX DR WPI; 1999-610754/52.

XX PT New antisense compounds used to treat eg. hyperproliferative conditions.
 XX Example 9; Page 54; 157pp; English.

XX CC AAZ37473-237738 represent human mdm2 phosphorothioate oligonucleotides.
 CC AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the
 CC exemplification of the present invention. The present invention describes
 CC novel nucleotide antisense compounds, targeted to the 5' untranslated,
 CC translation termination codon, or 3' untranslated region of a nucleic
 CC acid encoding human mdm2, that modulates expression of human mdm2. The
 CC oligonucleotides mediate their effect by antisense inhibition of
 CC hyperproliferative gene expression. The antisense compound is used to
 CC treat an animal having a disease or condition associated with mdm2,
 CC particularly a hyperproliferative condition, more particularly cancer,
 CC especially of the blood, brain, breast, lung or soft tissue, or
 CC psoriasis, fibrosis, atherosclerosis or restenosis

XX SQ Sequence 20 BP; 11 A; 2 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 1.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1613 TTTATTAAATATATAT 1630

|||||

DB 19 TTTCTTAAATATGTATAT 2

RESULT 1864

AAZ37716

ID AAZ37716 standard; DNA; 20 BP.

XX AC AAZ37716;

XX DT 07-JAN-2000 (first entry)

XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #246.

XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
 KW antisense; modulation; oligonucleotide; expression; inhibition;
 KW hyperproliferation; blood cancer; brain cancer; breast cancer;
 KW lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;
 KW restenosis; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9949065-A1.

XX PD 30-SEP-1999.

XX PF 26-MAR-1999; 99WO-US006702.

XX PR 26-MAR-1998; 98US-00048810.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowse LM;

XX DR WPI; 1999-610754/52.

XX PT New antisense compounds used to treat eg. hyperproliferative conditions.

XX Claim 4; Page 54; 157pp; English.

XX CC AAZ37473-237738 represent human mdm2 phosphorothioate oligonucleotides.
 CC AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the
 CC exemplification of the present invention. The present invention describes
 CC novel nucleotide antisense compounds, targeted to the 5' untranslated,
 CC translation termination codon, or 3' untranslated region of a nucleic
 CC acid encoding human mdm2, that modulates expression of human mdm2. The
 CC oligonucleotides mediate their effect by antisense inhibition of
 CC hyperproliferative gene expression. The antisense compound is used to
 CC treat an animal having a disease or condition associated with mdm2,
 CC particularly a hyperproliferative condition, more particularly cancer,
 CC especially of the blood, brain, breast, lung or soft tissue, or
 CC psoriasis, fibrosis, atherosclerosis or restenosis

XX SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 1.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1951 GCCTCAAGTGAGCCAGA 1968

|||||

DB 3 GCTTGCAAGTGAGCCAGA 20

RESULT 1865

AAZ15777/c

ID AAZ15777 standard; cDNA to mRNA; 20 BP.

XX AC AAZ15777;

XX DT 07-MAY-1999 (first entry)

XX DE Antisense oligonucleotide targeted to upstream sequence of VEGF.

XX Vascular endothelial cell growth factor; VEGF; antisense oligonucleotide;
KW solid tumor growth; anticancer agent; rheumatic arthritis;
KW diabetic retinitis; ss.
XX Synthetic.
XX JP11042091-A.
XX 16-FEB-1999.
XX 25-JUL-1997; 97JP-00213838.
XX 25-JUL-1997; 97JP-00213838.
XX (TOAG) TOA GOSEI CHEM IND LTD.
XX WPI; 1999-197823/17.
XX An antisense nucleic acid compound against vascular endothelial cell
PT growth factor (VEGF) - useful as an anticancer agent, and for treatment
PT of rheumatic arthritis and diabetic retinitis.
XX Example 1; Page 7; 16pp; English.
XX AAX15764-81 represent antisense oligonucleotides targeted to the upstream
CC sequence of the coding region for vascular endothelial cell growth factor
CC (VEGF). Antisense oligonucleotides targeted to this region inhibit at
CC least 50 % of VEGF expression by the cell. The antisense oligonucleotides
CC can inhibit the growth of solid tumor and are useful as anticancer agents
CC and for treating rheumatic arthritis and diabetic retinitis
XX Sequence 20 BP; 0 A; 10 C; 0 G; 10 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1401 GGATGAAAAGAGAGAAGA 1418
DB 20 GGAGGAGAGAGAGAAGA 3
RESULT 1866
AAX15610
ID AAX15610 standard; cDNA to mRNA; 20 BP.
XX
AC AAX15610;
XX
DT 07-MAY-1999 (first entry)
XX
DE Fragment of upstream sequence of coding region for VEGF.
XX
KW Vascular endothelial cell growth factor; VEGF; antisense oligonucleotide;
KW solid tumor growth; anticancer agent; rheumatic arthritis;
KW diabetic retinitis; ss.
XX Unidentified.
XX JP11042091-A.
XX 16-FEB-1999.
XX 25-JUL-1997; 97JP-00213838.
XX 25-JUL-1997; 97JP-00213838.
XX (TOAG) TOA GOSEI CHEM IND LTD.
XX WPI; 1999-197823/17.
XX An antisense nucleic acid compound against vascular endothelial cell
PT growth factor (VEGF) - useful as an anticancer agent, and for treatment

PT of rheumatic arthritis and diabetic retinitis.
XX Example 2; Page 12; 16pp; English.
XX
CC The present sequence represents the a fragment of the upstream sequence
CC of the coding region for vascular endothelial cell growth factor (VEGF).
CC Antisense oligonucleotides targeted to this region inhibit at least 50 %
CC of VEGF expression by the cell. The antisense oligonucleotides can
CC inhibit the growth of solid tumor and are useful as anticancer agents and
CC for treating rheumatic arthritis and diabetic retinitis
XX Sequence 20 BP; 10 A; 0 C; 10 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1401 GGATGAAAAGAGAGAAGA 1418
DB 1 GGAGGAGAGAGAGAAGA 18
RESULT 1867
AAX31287/c
ID AAX31287 standard; DNA; 20 BP.
XX
AC AAX31287;
XX
DT 24-JAN-2000 (first entry)
XX
DE CCR5 gene inhibiting antisense oligo AS(s)-44.
XX HIV cofactor inhibitor; HIV infection; CXCR4 gene; CCR5 gene;
KW drug composition; antisense; ss.
XX Synthetic.
XX WO9951751-A1.
XX 14-OCT-1999.
XX 01-APR-1999; 99WO-JP001722.
XX 02-APR-1998; 98JP-00125452.
XX (MARI-) MARINE BIO CO LTD.
XX Takaku H, Yamamoto N, Kimura T, Takai K, Wada A;
XX WPI; 1999-620207/53.
XX Antisense oligonucleotide-based HIV cofactor inhibitors, as drug
PT compositions for treatment of HIV infection.
XX
PS Claim 6; Page 16; 59pp; Japanese.
XX
CC The invention provides HIV cofactor inhibitors that contain
CC oligonucleotides with a base sequence complementary to the CXCR4 or CCR5
CC genes. Such inhibitors can be formulated into drug compositions for
CC prevention or treatment of HIV infection, with inhibition of expression
CC of CXCR4 or/and CCR5 gene. Sequences AAX31244-306 represent antisense
CC oligonucleotides to the CCR5 gene
XX Sequence 20 BP; 13 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1573 GATTTCATATTTCTATT 1590
DB 20 GATTTCATATTTCTATT 3

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RESULT 1868
AAZ27507
ID AAZ27507 standard; DNA; 20 BP.
XX
AC AAZ27507;
XX
DT 13-DEC-1999 (first entry)
XX
DE PCR primer for P. mirabilis lpp gene.
XX
KW PCR primer; species determination; microorganism; diagnosis;
XX bacterial disease; viral disease; fungal disease; protozoan disease;
XX drug resistance; antibiotic resistance; lpp gene; ss.
XX
OS Synthetic.
OS Proteus mirabilis.
XX
PN WO9950441-A1.
XX
PD 07-OCT-1999.
XX
PF 25-MAR-1999; 99WO-US006610.
XX
PR 27-MAR-1998; 98US-0079684P.
XX
PA (SAIG-) SAIGENE CORP.
XX
PI Haydock PV, Uren JR;
XX
DR WPI; 1999-591330/50.
XX
PT Determination of the identity of live microorganisms in a mixed culture
PT useful for diagnosing microorganism infection.
XX
PS Example 5; Page 44; 62pp; English.
XX
CC This sequence is a PCR primer for the P. mirabilis lpp gene. The
CC invention relates to an assay for determining the identity of unknown
CC live microorganisms in a mixed culture. It comprises: (a) culturing the
CC microorganism in an aqueous medium which is able to culture one or more
CC microorganisms other than the unknown microorganism, and comprising a
CC nucleic acid analog which is recognized by an analog-specific binding
CC member and which is incorporated into nucleic acids of replicating cells
CC or virions of the unknown microorganism; (b) lysing the microorganisms;
CC (c) capturing nucleic acids incorporating the analog using the analog
CC specific binding member; (d) separating the captured nucleic acids from
CC any which have not been captured; (e) amplifying captured nucleic acids
CC originating from the unknown microorganism; and (f) determining the
CC identity of the microorganism from which the captured and amplified
CC nucleic acids originate. The method is expected to be useful in the
CC identification of microorganisms in clinical, research, industrial and
CC public health applications. Clinical uses include diagnosis of bacterial,
CC viral, fungal, and protozoan diseases, and for identification of strains
CC that are resistant to drugs and antibiotics. The method may also be used
CC for the screening of new chemical compounds, and to determine the
CC susceptibility of a particular strain of organism. Public health
CC applications include testing of water samples. The method may also be
CC used in food preparation and processing industries to determine the
CC presence and viability of organism in food samples
XX
SQ Sequence 20 BP; 8 A; 3 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 433 CTTAATAAGCGACGACG 450
| | | | | | | | | | | | | | | | | |
Db 3 CTTAATAAGCTGAAACG 20

RESULT 1869
AAZ27507
ID AAZ27507 standard; DNA; 20 BP.
XX
AC AAZ27507;
XX
DT 13-DEC-1999 (first entry)
XX
DE PCR primer for P. mirabilis lpp gene.
XX
KW PCR primer; species determination; microorganism; diagnosis;
XX bacterial disease; viral disease; fungal disease; protozoan disease;
XX drug resistance; antibiotic resistance; lpp gene; ss.
XX
OS Synthetic.
OS Proteus mirabilis.
XX
PN WO9950441-A1.
XX
PD 07-OCT-1999.
XX
PF 25-MAR-1999; 99WO-US006610.
XX
PR 27-MAR-1998; 98US-0079684P.
XX
PA (SAIG-) SAIGENE CORP.
XX
PI Haydock PV, Uren JR;
XX
DR WPI; 1999-591330/50.
XX
PT Determination of the identity of live microorganisms in a mixed culture
PT useful for diagnosing microorganism infection.
XX
PS Example 5; Page 44; 62pp; English.
XX
CC This sequence is a PCR primer for the P. mirabilis lpp gene. The
CC invention relates to an assay for determining the identity of unknown
CC live microorganisms in a mixed culture. It comprises: (a) culturing the
CC microorganism in an aqueous medium which is able to culture one or more
CC microorganisms other than the unknown microorganism, and comprising a
CC nucleic acid analog which is recognized by an analog-specific binding
CC member and which is incorporated into nucleic acids of replicating cells
CC or virions of the unknown microorganism; (b) lysing the microorganisms;
CC (c) capturing nucleic acids incorporating the analog using the analog
CC specific binding member; (d) separating the captured nucleic acids from
CC any which have not been captured; (e) amplifying captured nucleic acids
CC originating from the unknown microorganism; and (f) determining the
CC identity of the microorganism from which the captured and amplified
CC nucleic acids originate. The method is expected to be useful in the
CC identification of microorganisms in clinical, research, industrial and
CC public health applications. Clinical uses include diagnosis of bacterial,
CC viral, fungal, and protozoan diseases, and for identification of strains
CC that are resistant to drugs and antibiotics. The method may also be used
CC for the screening of new chemical compounds, and to determine the
CC susceptibility of a particular strain of organism. Public health
CC applications include testing of water samples. The method may also be
CC used in food preparation and processing industries to determine the
CC presence and viability of organism in food samples
XX
SQ Sequence 20 BP; 8 A; 3 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 433 CTTAATAAGCGACGACG 450
| | | | | | | | | | | | | | | | | |
Db 3 CTTAATAAGCTGAAACG 20

RESULT 1870
AAZ04185
ID AAZ04185 standard; DNA; 20 BP.
XX
AC AAZ04185;
XX
DT 07-OCT-1999 (first entry)
XX

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AAZ32095/C
ID AAZ32095 standard; DNA; 20 BP.
XX
AC AAZ32095;
XX
DT 14-JUN-1999 (first entry)
XX
DE BRCA1 gene specific primer.
XX
KW Allele profile; diagnosis; treatment; pharmacogenetic; breast cancer;
KW CTR; cystic fibrosis; dystrophin; Duchenne muscular dystrophy; p53;
KW Becker muscular dystrophy; Li-Fraumeni syndrome; neurofibromatosis;
KW colorectal cancer; MSH2 gene; MLH1 gene; BRCA1 gene; BRCA2 gene;
KW BAP1 gene; PCR primer; ss.
XX
OS Synthetic.
OS WO9906598-A2.
XX
PN 11-FEB-1999.
XX
PD 04-AUG-1998; 98WO-US016574.
XX
PF 04-AUG-1997; 97US-00905772.
XX
PR 22-MAY-1998; 98US-00084471.
XX
PA (ONCO-) ONCORMED INC.
XX
PI Murphy PD;
XX
DR WPI; 1999-153820/13.
XX
PT Determining common functional alleles in a population - useful in the
PT diagnosis of disease associated with allelic heterogeneity.
XX
PS Example 3; Page 31; 78pp; English.
XX
CC The invention relates to methods of determining a functional allele
CC profile of a gene in a population. Functional allele profiles comprise
CC the commonly occurring alleles in a population, and the relative
CC frequencies at which such alleles of a given gene occur. The methods are
CC used to identify and determine the frequency of the functional alleles of
CC genes which display extensive allelic heterogeneity, particularly those
CC implicated in disease or conditions, such as the BRCA1 gene associated
CC with breast cancer, CTR associated with cystic fibrosis, dystrophin
CC associated with Duchenne muscular dystrophy and Becker muscular
CC dystrophy, and p53 associated with Li-Fraumeni syndrome. The methods can
CC also be employed for diseases where allelic and genetic heterogeneity
CC exist, such as breast cancer, neurofibromatosis, and hereditary non-
CC polyposis colorectal cancer. Identification of functional alleles is
CC necessary for identification of mutations which may be implicated in the
CC disease. Sequences AAZ32001-172 represent primers for determining the
CC functional allele profiles of various genes. The primers are specific for
CC genes such as MSH2 gene, MLH1 gene, BRCA1 gene, BRCA2 gene and BAP1 gene
XX
SQ Sequence 20 BP; 6 A; 2 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 846 TGGCTCAGACTCCCTATC 863
| | | | | | | | | | | | | | | | | |
Db 19 TGATTCAGACTCCCTATC 2

RESULT 1870
AAZ04185
ID AAZ04185 standard; DNA; 20 BP.
XX
AC AAZ04185;
XX
DT 07-OCT-1999 (first entry)
XX

```

XX DE PCR primer used to amplify an ORF of Chlamydia trachomatis.

XX

KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; perihhepatitis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.

XX OS Synthetic.
 OS Chlamydia trachomatis.

XX PN WO9928475-A2.
 XX

XX PD 10-JUN-1999.
 XX

XX PF 27-NOV-1998; 98WO-IB001939.
 XX

XX PR 28-NOV-1997; 97FR-00015041.
 PR 17-DEC-1997; 97FR-00016034.
 PR 04-NOV-1998; 98US-0107077P.

XX (GEST) GENSET.
 XX

XX PI Griffais R;
 XX

XX DR WPI; 1999-371125/31.
 XX

XX PF 27-NOV-1998; 98WO-IB001939.
 XX

XX PR 28-NOV-1997; 97FR-00015041.
 PR 17-DEC-1997; 97FR-00016034.
 PR 04-NOV-1998; 98US-0107077P.

XX (GEST) GENSET.
 XX

XX PI Griffais R;
 XX

XX DR WPI; 1999-371125/31.
 XX

XX PF Genome sequence of Chlamydia trachomatis.
 XX

XX PS Disclosure; Page 1668; 1755pp; English.
 XX

XX CC PCR primers AAZ01426-206209 were used to amplify open reading frames
 CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
 CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
 CC be used to control growth of the microorganism. Chlamydia trachomatis is
 CC responsible for a large number of diseases, e.g. eye diseases such as
 CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
 CC conjunctivitis; genital diseases such as nongonococcal urethritis,
 CC epididymitis, cervicitis, salpingitis, perihhepatitis, bartholinitis;
 CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
 CC The polypeptides of the invention may be of use in treating these
 CC diseases

XX SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1300 CGAATTGCTGTGAGGAA 1317
 ||| ||||| |||||
 Db 2 CCAGAGCCTGTGAGGAA 19

RESULT 1871
 AAZ04447/c
 ID AAZ04447 standard; DNA; 20 BP.
 XX
 AC AAZ04447;
 XX

DT 07-OCT-1999 (first entry)
 XX
 DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
 XX

KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; perihhepatitis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.

XX OS Synthetic.
 OS Chlamydia trachomatis.

XX PN WO9928475-A2.
 XX

XX PD 10-JUN-1999.
 XX

XX PF 27-NOV-1998; 98WO-IB001939.
 XX

XX PR 28-NOV-1997; 97FR-00015041.
 PR 17-DEC-1997; 97FR-00016034.
 PR 04-NOV-1998; 98US-0107077P.

XX (GEST) GENSET.
 XX

PN WO9928475-A2.
 XX

XX PD 10-JUN-1999.
 XX

XX PF 27-NOV-1998; 98WO-IB001939.
 XX

XX PR 28-NOV-1997; 97FR-00015041.
 PR 17-DEC-1997; 97FR-00016034.
 PR 04-NOV-1998; 98US-0107077P.

XX (GEST) GENSET.
 XX

XX PI Griffais R;
 XX

XX DR WPI; 1999-371125/31.
 XX

XX PF Genome sequence of Chlamydia trachomatis.
 XX

XX PS Disclosure; Page 1689; 1755pp; English.
 XX

XX CC PCR primers AAZ01426-206209 were used to amplify open reading frames
 CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
 CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
 CC be used to control growth of the microorganism. Chlamydia trachomatis is
 CC responsible for a large number of diseases, e.g. eye diseases such as
 CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
 CC conjunctivitis; genital diseases such as nongonococcal urethritis,
 CC epididymitis, cervicitis, salpingitis, perihhepatitis, bartholinitis;
 CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
 CC The polypeptides of the invention may be of use in treating these
 CC diseases

XX SQ Sequence 20 BP; 8 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 930 GAGCTTTAACTGCTAT 947
 ||| ||||| |||||
 Db 19 GAGCCTTAACCTTCTAT 2

RESULT 1872
 AAZ03676
 ID AAZ03676 standard; DNA; 20 BP.
 XX
 AC AAZ03676;
 XX

DT 07-OCT-1999 (first entry)
 XX
 DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
 XX

KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; perihhepatitis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.

XX OS Synthetic.
 OS Chlamydia trachomatis.

XX PN WO9928475-A2.
 XX

XX PD 10-JUN-1999.
 XX

XX PF 27-NOV-1998; 98WO-IB001939.
 XX

XX PR 28-NOV-1997; 97FR-00015041.
 PR 17-DEC-1997; 97FR-00016034.
 PR 04-NOV-1998; 98US-0107077P.

XX (GEST) GENSET.
 XX

CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC be used to control growth of the microorganism. Chlamydia trachomatis is
CC responsible for a large number of diseases, e.g. eye diseases such as
CC conjunctivitis; genital diseases such as nongonococcal urethritis;
CC epididymitis, cervicitis, salpingitis, perihepatitis, bartholinitis;
CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
CC The polypeptides of the invention may be of use in treating these
CC diseases
CC
XX Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1819 GCTTTGGAAAGGTGCCCT 1836
||||| ||||| |||||
Db 3 GCTTTTAATAGGTGCCCT 20
RESULT 1874
AAZ03142
ID AAZ03142 standard; DNA; 20 BP.
XX
AC AAZ03142;
XX
DT 07-OCT-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
OS Synthetic.
OS Chlamydia trachomatis.
XX
FN WO9928475-A2.
XX
PD 10-JUN-1999.
XX
XX 27-NOV-1998; 98WO-IB001939.
PF
XX 28-NOV-1997; 97FR-00015041.
PR
XX 17-DEC-1997; 97FR-00016034.
PR
XX 04-NOV-1998; 98US-0107077P.
PR
XX (GEST) GENSET.
PA
XX Griffais R;
XX
XX WPI; 1999-371125/31.
XX
XX Genome sequence of Chlamydia trachomatis.
XX
XX Disclosure; Page 1582; 1755pp; English.
XX
XX PCR primers AAZ01426-Z06209 were used to amplify open reading frames
XX (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
XX encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
XX against Chlamydia trachomatis. Antisense and ribozyme sequences can also
XX be used to control growth of the microorganism. Chlamydia trachomatis is
XX responsible for a large number of diseases, e.g. eye diseases such as
XX conjunctivitis; genital diseases such as nongonococcal urethritis;
XX epididymitis, cervicitis, salpingitis, perihepatitis, bartholinitis;
XX pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
XX The polypeptides of the invention may be of use in treating these
XX diseases
XX

XX Griffais R;
XX
XX WPI; 1999-371125/31.
XX
XX Genome sequence of Chlamydia trachomatis.
XX
XX Disclosure; Page 1626; 1755pp; English.
XX
XX PCR primers AAZ01426-Z06209 were used to amplify open reading frames
XX (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
XX encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
XX against Chlamydia trachomatis. Antisense and ribozyme sequences can also
XX be used to control growth of the microorganism. Chlamydia trachomatis is
XX responsible for a large number of diseases, e.g. eye diseases such as
XX conjunctivitis; genital diseases such as nongonococcal urethritis;
XX epididymitis, cervicitis, salpingitis, perihepatitis, bartholinitis;
XX pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
XX The polypeptides of the invention may be of use in treating these
XX diseases
XX
XX Sequence 20 BP; 9 A; 9 C; 1 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1777 ACCATAGACAAACTCCT 1794
||||| ||||| |||||
Db 3 ACCACAAACAAACCCCT 20
RESULT 1873
AAZ04599
ID AAZ04599 standard; DNA; 20 BP.
XX
AC AAZ04599;
XX
DT 07-OCT-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
OS Synthetic.
OS Chlamydia trachomatis.
XX
FN WO9928475-A2.
XX
XX 10-JUN-1999.
XX
XX 27-NOV-1998; 98WO-IB001939.
PF
XX 28-NOV-1997; 97FR-00015041.
PR
XX 17-DEC-1997; 97FR-00016034.
PR
XX 04-NOV-1998; 98US-0107077P.
PR
XX (GEST) GENSET.
PA
XX Griffais R;
XX
XX WPI; 1999-371125/31.
XX
XX Genome sequence of Chlamydia trachomatis.
XX
XX Disclosure; Page 1702; 1755pp; English.
XX
XX PCR primers AAZ01426-Z06209 were used to amplify open reading frames
XX (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
XX


```

SQ Sequence 20 BP; 6 A; 2 C; 8 G; 4 T; 0 U; 0 Other;
  Query Match          0.6%; Score 13.2; DB 1; Length 20;
  Best Local Similarity 83.3%; Pred. No. 1.3e+03;
  Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1329 TTCTGAAGAGGAGGAGA 1346
    ||| ||||| |||||
Db 3 TTCATATGAGGAGGAGA 20

RESULT 1875
AAZ06040/c
ID AAZ06040 standard; DNA; 20 BP.
XX
AC AAZ06040;
XX
DT 07-OCT-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihhepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
OS Synthetic.
OS Chlamydia trachomatis.
PN WO9928475-A2.
XX
PD 10-JUN-1999.
XX
PF 27-NOV-1998; 98WO-IB001939.
XX
PR 28-NOV-1997; 97FR-00015041.
PR 17-DEC-1997; 97FR-00016034.
PR 04-NOV-1998; 98US-0107077P.
XX
PA (GEST ) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-371125/31.
XX
PT Genome sequence of Chlamydia trachomatis.
PS Disclosure; Page 1820; 1755pp; English.
XX
CC PCR primers AAZ01426-Z06209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC be used to control growth of the microorganism. Chlamydia trachomatis is
CC responsible for a large number of diseases, e.g. eye diseases such as
CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
CC conjunctivitis; genital diseases such as nongonococcal urethritis,
CC epididymitis, cervicitis, salpingitis, perihhepatitis, bartholinitis;
CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
CC The polypeptides of the invention may be of use in treating these
CC diseases
XX
SQ Sequence 20 BP; 10 A; 5 C; 4 G; 1 T; 0 U; 0 Other;
  Query Match          0.6%; Score 13.2; DB 1; Length 20;
  Best Local Similarity 83.3%; Pred. No. 1.3e+03;
  Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 398 TGCTACTGGTGGTCTG 415
    ||| ||||| |||||
Db 20 TGTGACTTTGGTCTG 3

RESULT 1876
AAZ03615
ID AAZ03615 standard; DNA; 20 BP.
XX
AC AAZ03615;
XX
DT 07-OCT-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihhepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
OS Synthetic.
OS Chlamydia trachomatis.
PN WO9928475-A2.
XX
PD 10-JUN-1999.
XX
PF 27-NOV-1998; 98WO-IB001939.
XX
PR 28-NOV-1997; 97FR-00015041.
PR 17-DEC-1997; 97FR-00016034.
PR 04-NOV-1998; 98US-0107077P.
XX
PA (GEST ) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-371125/31.
XX
PT Genome sequence of Chlamydia trachomatis.
PS Disclosure; Page 1621; 1755pp; English.
XX
CC PCR primers AAZ01426-Z06209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC be used to control growth of the microorganism. Chlamydia trachomatis is
CC responsible for a large number of diseases, e.g. eye diseases such as
CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
CC conjunctivitis; genital diseases such as nongonococcal urethritis,
CC epididymitis, cervicitis, salpingitis, perihhepatitis, bartholinitis;
CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
CC The polypeptides of the invention may be of use in treating these
CC diseases
XX
SQ Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 U; 0 Other;
  Query Match          0.6%; Score 13.2; DB 1; Length 20;
  Best Local Similarity 83.3%; Pred. No. 1.3e+03;
  Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 401 CTACTGGTGGTCTGCTG 418
    ||||| ||||| |||||
Db 2 CTACTGGGATTCTGCTG 19

RESULT 1877
AAV80052/c
ID AAV80052 standard; DNA; 20 BP.
XX
AC AAV80052;
XX
DT 16-MAR-1999 (first entry)
XX
DE Human PMM2 intron 6/exon 7 junction sequence.
XX
KW Phosphomannomutase-2; PMM2; mutation; human; transgenic; assay;

```

KW carbohydrate-deficient glycoprotein syndrome type 1; drug screening;
KW Jaeken disease; prenatal diagnosis; ss.
XX Homo sapiens.
XX WO9849324-A2.
XX PN
XX PD
XX PF
XX PF 30-APR-1998; 98WO-EP002593.
XX PR 30-APR-1997; 97GB-00008851.
XX PR 27-JAN-1998; 98GB-00001719.
XX XX
XX PA (GENZ) GENZYME UK LTD.
XX PI
XX PI Matthijs G;
XX DR WPI; 1999-024063/02.
XX DR
XX PT New DNA encoding human phosphomannomutase or its fragments - used to
XX PT detect mutations associated with carbohydrate-deficient glycoprotein
XX PT syndrome-1, particularly for prenatal diagnosis.
XX XX
XX PS Disclosure; Fig 3-6; 104pp; English.
XX CC The invention relates to a human phosphomannomutase-2 (PM2) protein and
XX CC the nucleotide sequence encoding the protein. The DNA or its fragments
XX CC are used to detect mutation in the PM2 genes that are associated with
XX CC the carbohydrate-deficient glycoprotein syndrome type 1 (CDG1). The
XX CC sequences can also be used to detect expression of PM2-related cDNA; to
XX CC express PM2 or its mutants; and to create transgenic animals for use in
XX CC drug screening and for studying expression pathways. The expressed
XX CC proteins are used to screen for agents that modulate activity of PM2,
XX CC for therapy and to raise specific antibodies (for detecting PM2 or its
XX CC mutants, in competitive or capture assays). Biochemical assays for
XX CC phosphomannomutase activity are used to identify possible carriers of CDG1
XX CC (Jaeken disease). Measuring enzymatic activity in foetal cells (or in
XX CC parental leucocytes if such cells are unavailable) and detecting
XX CC mutations in the PM2 gene makes possible a better prenatal diagnosis of
XX CC CDG1. Sequences AAV80046-60 represent PM2 exon/intron junction sequences
XX SQ Sequence 20 BP; 5 A; 7 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1528 TCTGGCTTCCTGCTGAGT 1545
DB 19 TCTGGCTTCCTGCTGAGT 2
RESULT 1878
AA89183
ID AA89183 standard; DNA; 20 BP.
XX XX
XX AC AA89183;
XX XX
XX DT 15-SEP-1999 (first entry)
XX XX
XX DE Seq ID No: 37 of JP11164690.
XX XX
XX KW Vertebrate-derived protein; slit protein; diagnosis; cancer; nerve;
XX KW muscle; endocrine system; ss.
XX OS Synthetic.
XX PN JP11164690-A.
XX XX
XX PD 22-JUN-1999.
XX XX
XX PF 05-DEC-1997; 97JP-00335435.
XX PR

XX 05-DEC-1997; 97JP-00335435.
XX PR (ASAH) ASahi KASEI KOGYO KK.
XX PA
XX XX
XX DR WPI; 1999-411830/35.
XX XX
XX PT New vertebrate slit protein - useful for diagnosis and treatment of
XX PT cancers in nerves, muscle and endocrine system.
XX PS Disclosure; Page 90; 102pp; Japanese.
XX XX
XX CC The invention relates to a vertebrate-derived protein containing an amino
XX CC acid sequence shown in AAY27137 and AAY27139. The vertebrate-derived
XX CC protein has at least 55 % homology to one of sequences shown in AAY27141-
XX CC Y27143, and has slit protein-like activity. The vertebrate slit proteins
XX CC encoding nucleic acid sequences have at least 60% homology to nucleic
XX CC acid sequences AAX89161-163. The vertebrate-derived proteins can be
XX CC produced recombinantly by transforming host cells with expression vectors
XX CC comprising the encoding nucleic acids. The proteins of the invention are
XX CC for diagnosing and treating cancer of the nerves, muscle and/or endocrine
XX CC system
XX XX
XX SQ Sequence 20 BP; 4 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 536 TGGCCATCTCTGGAACCTGC 553
DB 1 TGGCCATCTCTGGAACCTGC 18
RESULT 1879
AAZ19462/c
ID AAZ19462 standard; DNA; 20 BP.
XX XX
XX AC AAZ19462;
XX XX
XX DT 15-NOV-1999 (first entry)
XX XX
XX DE Human G-alpha-11 PCR primer SEQ ID NO:2.
XX XX
XX KW Human; G-alpha-11; antisense oligonucleotide; inhibition; expression;
XX KW phosphorothioate; PCR primer; probe; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN US5951455-A.
XX XX
XX PD 14-SEP-1999.
XX XX
XX PF 04-DEC-1998; 98US-00205922.
XX PR 04-DEC-1998; 98US-00205922.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX XX
XX PI Cowser LM;
XX XX
XX DR WPI; 1999-539140/45.
XX XX
XX PT Inhibitory antisense compounds useful for the treatment of diseases
XX PT associated with G-alpha-11.
XX XX
XX PS Example 13; Col 38; 38pp; English.
XX XX
XX CC The present invention describes inhibitory antisense compounds of 8-30
XX CC nucleotides, targeted to a nucleic acid molecule encoding human G-alpha-
XX CC 11. The present sequence encodes human G-alpha-11. AAZ19468 to AAZ19547
XX CC represent human G-alpha-11 phosphorothioate antisense oligonucleotides

CC given in the present invention. The oligonucleotides may be useful for
 CC the treatment of diseases associated with G-alpha-11. The present
 CC sequence represents an oligonucleotide used in the exemplification of the
 CC present invention

SQ Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 949 CTGATGCTGGGAGCGGT 966
 |||||
 Db 20 CTGATGCTGAAGTGGT 3

RESULT 1880
 AAX60572
 ID AAX60572 standard; DNA; 20 BP.
 XX
 AC AAX60572;
 XX
 DT 26-JUL-1999 (first entry)
 XX
 DE HSV-TK specific primer LMC11.
 XX
 KW Cell-specific expression vector; vector replication; tissue-specific;
 KW transcriptional regulatory sequence; therapeutic; cell proliferation;
 KW tumour; HSV-TK; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9925860-A1.
 XX
 PD 27-MAY-1999.
 XX
 PF 17-NOV-1998; 98WO-EP007380.
 XX
 PR 19-NOV-1997; 97US-00974391.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX
 PI Chang Y, Hallenbeck PL, Hay CM, Stewart DA;
 XX WPI; 1999-338012/28.
 PS Cell-specific adenovirus expression vectors.
 XX
 XX Example 2; Page 40; 76pp; English.

CC The invention relates to cell-specific expression vectors containing a
 CC gene essential for vector replication under the control of a heterologous
 CC tissue-specific transcriptional regulatory sequence and at least one
 CC additional coding sequence encoding a heterologous gene product, which is
 CC operably linked to the tissue-specific transcriptional regulatory
 CC sequence or is operably linked to a second transcriptional regulatory
 CC sequence that is activated by the gene product of the first coding
 CC sequence. The vectors are useful for the delivery of exogenous genes
 CC efficiently, with high distribution in tumours and in a controlled
 CC manner. The vectors can be introduced into tumour cells or abnormally
 CC proliferating cells. The vectors contain a gene having therapeutic value
 CC and are able to replicate conditionally. Adding a nucleoside analogue can
 CC modulate the replication of the vector. The nucleoside analogue, e.g.
 CC gancyclovir, acyclovir, 1,2-deoxy-2-fluoro- beta-arabinofuranosil-5-
 CC iodouracil and fencyclovir, also has anti-tumour activity or eliminates
 CC cell proliferation. The vectors target a specific cell type. Adding a
 CC compound to dampen replication if it were excessive can control the level
 CC of replication, e.g. where vector replication is interfering with
 CC treatment

SQ Sequence 20 BP; 8 A; 5 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1430 AGAAGAAGTCACCGAAG 1447
 |||||
 Db 1 AGCAAGAAGCCACGGAAG 18

RESULT 1881
 AAX94196/c
 ID AAX94196 standard; DNA; 20 BP.
 XX
 AC AAX94196;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
 XX
 KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 KW neutralising epitope; PCR primer; ss.
 XX
 OS Synthetic.
 OS Chlamydothila pneumoniae.
 XX
 PN WO9927105-A2.
 XX
 PD 03-JUN-1999.
 XX
 PF 20-NOV-1998; 98WO-IB001890.
 XX
 PR 21-NOV-1997; 97FR-00014673.
 PR 04-NOV-1998; 98US-0107078P.
 XX
 PA (GEST) GENSET.
 XX
 PI Griffais R;
 XX
 DR WPI; 1999-357842/30.
 XX
 PT Genome sequence of Chlamydia pneumoniae.
 XX
 PS Page 1651; Disclosure; 1912pp; English.

CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
 CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
 CC (see AAX91990). C. pneumoniae causes respiratory disease such as
 CC pneumonia and bronchitis and is thought to be a contributing factor in
 CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
 CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotide sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae

SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 776 AGGCCATTTTCAAGCCGG 793
 |||||
 Db 18 AGGTCAATTTTAAAGCCCG 1

RESULT 1882
 AAX94646
 ID AAX94646 standard; DNA; 20 BP.
 XX
 AC AAX94646;

XX 13-SEP-1999 (first entry)
 DT PCR primer used to amplify an ORF of Chlamydia pneumoniae.
 XX
 DE Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 XX sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 KW neutralising epitope; PCR primer; ss.
 KW
 XX Synthetic.
 OS Chlamydophila pneumoniae.
 OS
 XX WO9927105-A2.
 PN
 XX 03-JUN-1999.
 XX
 PD 20-NOV-1998; 98WO-IB001890.
 XX
 PF 21-NOV-1997; 97FR-00014673.
 XX
 PR 04-NOV-1998; 98US-0107078P.
 XX
 XX (GEST) GENSET.
 PA
 XX Griffais R;
 XX
 PI WPI; 1999-357842/30.
 XX
 DR Genome sequence of Chlamydia pneumoniae.
 XX
 XX Page 1686; Disclosure; 1912pp; English.
 PS
 XX AAX91991-X97517 represent PCR primers used to amplify open reading frames
 XX and other nucleic acid sequences from the genome of Chlamydia pneumoniae
 CC (see AAX91990). C. pneumoniae causes respiratory disease such as
 CC pneumonia and bronchitis and is thought to be a contributing factor in
 CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AAX34584- AAX35879) can be used
 CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotides sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae
 XX
 XX Sequence 20 BP; 3 A; 2 C; 7 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 911 AGTGTGGGAATTGCTCA 928
 DB |||||||
 2 ATTGTGGGATTGCCA 19
 RESULT 1883
 AAX97263/C
 ID AAX97263 standard; DNA; 20 BP.
 XX
 XX AAX97263;
 AC
 XX 13-SEP-1999 (first entry)
 DT
 XX Primer used to amplify Chlamydia pneumoniae polynucleotides.
 DE
 XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 KW neutralising epitope; PCR primer; ss.
 KW
 XX Synthetic.
 OS Chlamydophila pneumoniae.
 OS
 XX WO9927105-A2.
 PN
 XX

PD 03-JUN-1999.
 XX
 XX 20-NOV-1998; 98WO-IB001890.
 XX
 PR 21-NOV-1997; 97FR-00014673.
 PR
 PR 04-NOV-1998; 98US-0107078P.
 XX
 XX (GEST) GENSET.
 PA
 XX Griffais R;
 XX
 PI WPI; 1999-357842/30.
 XX
 DR Genome sequence of Chlamydia pneumoniae.
 XX
 XX Page 1890; Disclosure; 1912pp; English.
 PS
 XX AAX91991-X97517 represent PCR primers used to amplify open reading frames
 XX and other nucleic acid sequences from the genome of Chlamydia pneumoniae
 CC (see AAX91990). C. pneumoniae causes respiratory disease such as
 CC pneumonia and bronchitis and is thought to be a contributing factor in
 CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AAX34584- AAX35879) can be used
 CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotides sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae
 XX
 XX Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 101 ACTACTACGACGGGATG 118
 DB |||||||
 19 ACTACCCTACGAGGATG 2
 RESULT 1884
 AAX97266/C
 ID AAX97266 standard; DNA; 20 BP.
 XX
 XX AAX97266;
 AC
 XX 13-SEP-1999 (first entry)
 DT
 XX Primer used to amplify Chlamydia pneumoniae polynucleotides.
 DE
 XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 KW neutralising epitope; PCR primer; ss.
 KW
 XX Synthetic.
 OS Chlamydophila pneumoniae.
 OS
 XX WO9927105-A2.
 PN
 XX 03-JUN-1999.
 XX
 PD 20-NOV-1998; 98WO-IB001890.
 XX
 PF 21-NOV-1997; 97FR-00014673.
 XX
 PR 04-NOV-1998; 98US-0107078P.
 XX
 XX (GEST) GENSET.
 PA
 XX Griffais R;
 XX
 PI WPI; 1999-357842/30.
 XX
 DR Genome sequence of Chlamydia pneumoniae.
 XX
 XX

```

XX PS Page 1890; Disclosure; 1912pp; English.
XX CC
XX CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
XX CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
XX CC (see AAX91990). C. pneumoniae causes respiratory disease such as
XX CC pneumonia and bronchitis and is thought to be a contributing factor in
XX CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
XX CC nodosum or pharyngitis. The polypeptides encoded by the open reading
XX CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
XX CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
XX CC nucleotides sequences can also be used as immunogenic compositions,
XX CC especially where the vector directs the expression of a neutralising
XX CC epitope of C. pneumoniae
XX SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 101 ACTACTACGACGGGGATG 118
Db 20 ACTACCACTACGAGGATG 3

RESULT 1885
AAX93611
ID AAX93611 standard; DNA; 20 BP.
XX AC AAX93611;
XX DT 13-SEP-1999 (first entry)
XX DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
XX KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
XX KW neutralising epitope; PCR primer; ss.
XX OS Synthetic.
XX OS Chlamydophila pneumoniae.
XX PN WO9927105-A2.
XX PD 03-JUN-1999.
XX PF 20-NOV-1998; 98WO-IB001890.
XX PR 21-NOV-1997; 97FR-00014673.
XX PR 04-NOV-1998; 98US-0107078P.
XX PA (GEST ) GENSET.
XX PI Griffais R;
XX DR WPI; 1999-357842/30.
XX PT Genome sequence of Chlamydia pneumoniae.
XX PS Page 1855; Disclosure; 1912pp; English.
XX CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
XX CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
XX CC (see AAX91990). C. pneumoniae causes respiratory disease such as
XX CC pneumonia and bronchitis and is thought to be a contributing factor in
XX CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
XX CC nodosum or pharyngitis. The polypeptides encoded by the open reading
XX CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
XX CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
XX CC nucleotides sequences can also be used as immunogenic compositions,
XX CC especially where the vector directs the expression of a neutralising
XX CC epitope of C. pneumoniae
XX SQ Sequence 20 BP; 3 A; 4 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1467 GAAGCAGAGCAAGG 1484
Db 1 GAAGCAAGAGCAAGG 18

RESULT 1887
AAX92258

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ID AAX92258 standard; DNA; 20 BP.
XX AC AAX92258;
XX DT 13-SEP-1999 (first entry)
XX DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
XX KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
XX KW neutralising epitope; PCR primer; ss.
XX OS Synthetic.
XX OS Chlamydia pneumoniae.
XX PN WO9927105-A2.
XX PD 03-JUN-1999.
XX PF 20-NOV-1998; 98WO-IB001890.
XX PR 21-NOV-1997; 97FR-00014673.
XX PR 04-NOV-1998; 98US-0107078P.
XX PA (GEST ) GENSET.
XX PI Griffais R;
XX PI Griffais R;
XX DR WPI; 1999-357842/30.
XX PT Genome sequence of Chlamydia pneumoniae.
XX PS Page 1497; Disclosure; 1912pp; English.
XX CC AAX9191-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX9190). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAX34584- AAX35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotide sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX SQ Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1746 CAGGTCGGTGAAAGGG 1763
Db | ||||| ||||| |||||
2 CTGGTCGGTAAAGCG 19

RESULT 1888
AAX95676
ID AAX95676 standard; DNA; 20 BP.
XX AC AAX95676;
XX DT 13-SEP-1999 (first entry)
XX DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
XX KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
XX KW neutralising epitope; PCR primer; ss.
XX OS Synthetic.
XX OS Chlamydia pneumoniae.

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XX WO9927105-A2.
XX PN 03-JUN-1999.
XX PD 20-NOV-1998; 98WO-IB001890.
XX PF 21-NOV-1997; 97FR-00014673.
XX PR 04-NOV-1998; 98US-0107078P.
XX PA (GEST ) GENSET.
XX PI Griffais R;
XX PI WPI; 1999-357842/30.
XX DR Genome sequence of Chlamydia pneumoniae.
XX PT Page 1766; Disclosure; 1912pp; English.
XX PS AAX9191-X97517 represent PCR primers used to amplify open reading frames
XX and other nucleic acid sequences from the genome of Chlamydia pneumoniae
XX (see AAX9190). C. pneumoniae causes respiratory disease such as
XX pneumonia and bronchitis and is thought to be a contributing factor in
XX heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
XX nodosum or pharyngitis. The polypeptides encoded by the open reading
XX frames of the C. pneumoniae genome (see AAX34584- AAX35879) can be used
XX in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
XX nucleotide sequences can also be used as immunogenic compositions,
XX especially where the vector directs the expression of a neutralising
XX epitope of C. pneumoniae
XX SQ Sequence 20 BP; 2 A; 6 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 940 CTGCTATGCTGATGCTG 957
Db | ||||| ||||| |||||
2 CTGCCGATGATGCTGCTG 19

RESULT 1889
AAX96526/C
ID AAX96526 standard; DNA; 20 BP.
XX AC AAX96526;
XX DT 13-SEP-1999 (first entry)
XX DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
XX KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
XX KW neutralising epitope; PCR primer; ss.
XX OS Synthetic.
XX OS Chlamydia pneumoniae.
XX PN WO9927105-A2.
XX PD 03-JUN-1999.
XX PF 20-NOV-1998; 98WO-IB001890.
XX PR 21-NOV-1997; 97FR-00014673.
XX PR 04-NOV-1998; 98US-0107078P.
XX PA (GEST ) GENSET.
XX PI Griffais R;
XX PI Griffais R;

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DR WPI; 1999-357842/30.
XX Genome sequence of Chlamydia pneumoniae.
XX Page 1833; Disclosure; 1912pp; English.
XX
CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX
SQ Sequence 20 BP; 7 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1549 TCACGTTTCTTCCCAAC 1566
Db 18 TGACGTTTCTTCTCCAGC 1
RESULT 1890
AAX92394
ID AAX92394 standard; DNA; 20 BP.
XX
AC AAX92394;
XX
DT 13-SEP-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX
OS Synthetic.
OS Chlamydophila pneumoniae.
XX
PN WO9927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98WO-IB001890.
XX
PR 21-NOV-1997; 97FR-00014673.
XX
PR 04-NOV-1998; 98US-0107078P.
XX
PA (GEST ) GENSET.
XX
PI Griffais R;
XX
OS Chlamydophila pneumoniae.
XX
PN WO9927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98WO-IB001890.
XX
PR 21-NOV-1997; 97FR-00014673.
XX
PR 04-NOV-1998; 98US-0107078P.
XX
PA (GEST ) GENSET.
XX
PI Griffais R;
XX
WPI; 1999-357842/30.
XX
Genome sequence of Chlamydia pneumoniae.
XX
Page 1508; Disclosure; 1912pp; English.
XX
CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX
SQ Sequence 20 BP; 7 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1549 TCACGTTTCTTCCCAAC 1566
Db 18 TGACGTTTCTTCTCCAGC 1
RESULT 1890
AAX92394
ID AAX92394 standard; DNA; 20 BP.
XX
AC AAX92394;
XX
DT 13-SEP-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX
OS Synthetic.
OS Chlamydophila pneumoniae.
XX
PN WO9927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98WO-IB001890.
XX
PR 21-NOV-1997; 97FR-00014673.
XX
PR 04-NOV-1998; 98US-0107078P.
XX
PA (GEST ) GENSET.
XX
PI Griffais R;
XX
WPI; 1999-357842/30.
XX
Genome sequence of Chlamydia pneumoniae.
XX
Page 1508; Disclosure; 1912pp; English.
XX
CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX
SQ Sequence 20 BP; 7 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1549 TCACGTTTCTTCCCAAC 1566
Db 18 TGACGTTTCTTCTCCAGC 1

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CC nucleotides sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae

SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 614 AAGAGGCTTCTTACACCA 631
 |||||
 Db 2 AAGAGGCTTCTTACACCA 19
 |||||

RESULT 1891

AAX95611

ID AAX95611 standard; DNA; 20 BP.

XX AC AAX95611;

XX DT 13-SEP-1999 (first entry)

XX DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.

XX KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 KW neutralising epitope; PCR primer; ss.

XX OS Synthetic.

OS Chlamydophila pneumoniae.

XX PN WO9927105-A2.

XX PD 03-JUN-1999.

XX PF 20-NOV-1998; 98WO-IB001890.

XX PR 21-NOV-1997; 97FR-00014673.

XX PR 04-NOV-1998; 98US-0107078P.

XX PA (GEST) GENSET.

XX PI Griffais R;

XX DR WPI; 1999-357842/30.

XX Genome sequence of Chlamydia pneumoniae.

XX Page 1761; Disclosure; 1912pp; English.

XX CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
 CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
 CC (see AAX91990). C. pneumoniae causes respiratory disease such as
 CC pneumonia and bronchitis and is thought to be a contributing factor in
 CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
 CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotides sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae

SQ Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 1.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1021 CTGGATTCGAAATCCCT 1038
 |||||

Db 1 CTGGATTCGAAATCCCT 18

XX	Synthetic.	
OS	Chlamydophila pneumoniae.	
XX		
XX	WO9927105-A2.	
XX		
XX	03-JUN-1999.	
PD		
XX		
XX	20-NOV-1998; 98WO-IB001890.	
PF		
XX		
XX	21-NOV-1997; 97FR-00014673.	
PR		
PR	04-NOV-1998; 98US-0107078P.	
XX		
XX	(GEST) GENSET.	
PA		
XX		
XX	Griffais R;	
PI		
XX		
XX	WPI; 1999-357842/30.	
DR		
XX		
XX	Genome sequence of Chlamydia pneumoniae.	
PT		
XX		
XX	Page 1677; Disclosure; 1912pp; English.	
PS		
XX		
XX	AAx91991-X97517 represent PCR primers used to amplify open reading frames	
CC	and other nucleic acid sequences from the genome of Chlamydia pneumoniae	
CC	(see AAx91990). C. pneumoniae causes respiratory disease such as	
CC	pneumonia and bronchitis and is thought to be a contributing factor in	
CC	heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema	
CC	nodosum or pharyngitis. The polypeptides encoded by the open reading	
CC	frames of the C. pneumoniae genome (see AAx34594- AAx35879) can be used	
CC	in immunogenic compositions as vaccines. Vectors containing C. pneumoniae	
CC	nucleotides sequences can also be used as immunogenic compositions,	
CC	especially where the vector directs the expression of a neutralising	
CC	epitope of C. pneumoniae	
XX		
SQ	Sequence 20 BP; 3 A; 6 C; 3 G; 8 T; 0 U; 0 Other;	
	Query Match 0.6%; Score 13.2; DB 1; Length 20;	
	Best Local Similarity 83.3%; Pred. NO. 1.3e+03;	
	Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0	
QY	658 CATRAGTATGGAGAGTAC 675	
Db	19 CATATCATGGAGAGAC 2	
	RESULT 1894	
	AAx96356	
ID	AAx96356 standard; DNA; 20 BP.	
XX		
AC	AAx96356;	
XX		
DT	13-SEP-1999 (first entry)	
XX		
DE	PCR primer used to amplify an ORF of Chlamydia pneumoniae.	
XX		
KW	Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;	
KW	sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;	
KW	neutralising epitope; PCR primer; ss.	
XX		
OS	Synthetic.	
OS	Chlamydophila pneumoniae.	
XX		
PN	WO9927105-A2.	
XX		
PD	03-JUN-1999.	
XX		
PF	20-NOV-1998; 98WO-IB001890.	
XX		
XX	21-NOV-1997; 97FR-00014673.	
PR		
PR	04-NOV-1998; 98US-0107078P.	
XX		
PA	(GEST) GENSET.	


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XX PI Griffais R;
XX XX
DR WPI; 1999-357842/30.
XX XX
XX Genome sequence of Chlamydia pneumoniae.
XX XX
PS Page 1819; Disclosure; 1912pp; English.
XX XX
CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX XX
SQ Sequence 20 BP; 8 A; 7 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 294 CTCCTCGTCCGATGAA 311
Db 1 CTCACACGTCAGAAAA 18

RESULT 1895
AAX95482
ID AAX95482 standard; DNA; 20 BP.
XX AC AAX95482;
XX XX
DT 13-SEP-1999 (first entry)
XX XX
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX XX
OS Synthetic.
OS Chlamydophila pneumoniae.
XX PN WO927105-A2.
XX XX
DT 13-SEP-1999 (first entry)
XX XX
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX XX
OS Synthetic.
OS Chlamydophila pneumoniae.
XX PN WO927105-A2.
XX XX
DT 03-JUN-1999.
XX XX
PF 20-NOV-1998; 98WO-IB001890.
XX XX
PR 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.
XX XX
PA (GEST ) GENSET.
XX XX
PI Griffais R;
XX XX
DR WPI; 1999-357842/30.
XX XX
PT Genome sequence of Chlamydia pneumoniae.
XX XX
PS Page 1751; Disclosure; 1912pp; English.
XX XX
CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX XX
SQ Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 311 ACATGTCGGAGTACAGCA 328
Db 1 AAATGTTGGAGTACCGCA 18

RESULT 1896
AAX92671/C
ID AAX92671 standard; DNA; 20 BP.
XX AC AAX92671;
XX XX
DT 13-SEP-1999 (first entry)
XX XX
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX XX
OS Synthetic.
OS Chlamydophila pneumoniae.
XX PN WO927105-A2.
XX XX
DT 03-JUN-1999.
XX XX
PF 20-NOV-1998; 98WO-IB001890.
XX XX
PR 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.
XX XX
PA (GEST ) GENSET.
XX XX
PI Griffais R;
XX XX
DR WPI; 1999-357842/30.
XX XX
PT Genome sequence of Chlamydia pneumoniae.
XX XX
PS Page 1530; Disclosure; 1912pp; English.
XX XX
CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX XX
SQ Sequence 20 BP; 7 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1980 CCTCTGTCGTCTCTC 1997

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Db 18 CCCTCTATCGTCTGCTC 1

RESULT 1897
AAAX96748
ID AAX96748 standard; DNA; 20 BP.
XX AC
XX AC
XX AAX96748;
DT 13-SEP-1999 (first entry)
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX XX
OS Synthetic.
OS Chlamydophila pneumoniae.
XX WO9927105-A2.
XX PD
XX 03-JUN-1999.
XX PF 20-NOV-1998; 98WO-IB001890.
XX ER 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.
XX PA (GEST) GENSET.
XX PI Griffais R;
XX DR WPI; 1999-357842/30.
XX PT Genome sequence of Chlamydia pneumoniae.
XX PS Page 1499; Disclosure; 1912pp; English.
XX CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAX34584-AAX35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX SQ Sequence 20 BP; 8 A; 1 C; 9 G; 2 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 601 GGTGACGCGTGGAGAG 618
Db 1 GGTGAAGGCATGGAAG 18
||||| ||| ||||| |||
RESULT 1899
AAAX94291/c
ID AAX94291 standard; DNA; 20 BP.
XX AC
XX AAX94291;
DT 13-SEP-1999 (first entry)
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX XX
OS Synthetic.
OS Chlamydophila pneumoniae.
XX WO9927105-A2.
XX PD 03-JUN-1999.
XX PF 20-NOV-1998; 98WO-IB001890.
XX PR 21-NOV-1997; 97FR-00014673.

Db 18 CCCTCTATCGTCTGCTC 1

RESULT 1897
AAAX96748
ID AAX96748 standard; DNA; 20 BP.
XX AC
XX AC
XX AAX96748;
DT 13-SEP-1999 (first entry)
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX XX
OS Synthetic.
OS Chlamydophila pneumoniae.
XX WO9927105-A2.
XX PD 03-JUN-1999.
XX PF 20-NOV-1998; 98WO-IB001890.
XX PR 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.
XX PA (GEST) GENSET.
XX PI Griffais R;
XX DR WPI; 1999-357842/30.
XX PT Genome sequence of Chlamydia pneumoniae.
XX PS Page 1850; Disclosure; 1912pp; English.
XX CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAX34584-AAX35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX SQ Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 928 AAGAGCTTTAACTGCCT 945
Db 2 ACGAGCTTTAACTGCAT 19
||||| ||| ||||| |||
RESULT 1898
AAAX92285
ID AAX92285 standard; DNA; 20 BP.
XX AC
XX AAX92285;
DT 13-SEP-1999 (first entry)
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX XX

```
PR 04-NOV-1998; 98US-0107078P.
XX (GEST ) GENSET.
XX
XX Griffais R;
XX
XX WPI; 1999-357842/30.
XX
XX Genome sequence of Chlamydia pneumoniae.
XX
XX Page 1658; Disclosure; 1912pp; English.
XX
XX AAX91991-X97517 represent PCR primers used to amplify open reading frames
XX and other nucleic acid sequences from the genome of Chlamydia pneumoniae
XX (see AAX91990). C. pneumoniae causes respiratory disease such as
XX pneumonia and bronchitis and is thought to be a contributing factor in
XX heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
XX nodosum or pharyngitis. The polypeptides encoded by the open reading
XX frames of the C. pneumoniae genome (see AAX34584- AAX35879) can be used
XX in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
XX nucleotide sequences can also be used as immunogenic compositions,
XX especially where the vector directs the expression of a neutralising
XX epitope of C. pneumoniae
XX
XX Sequence 20 BP; 2 A; 1 C; 12 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1560 CCCCAACCCCTCAGATT 1577
Db 18 CCCCAACCCACAGCTCT 1

RESULT 1900
AAX15180/c
ID AAX15180 standard; DNA; 20 BP.
XX
XX AAX15180;
XX
XX 28-APR-1999 (first entry)
XX
XX Oligonucleotide of the invention.
XX
XX Artificial nuclease function; cleavage; nucleic acid;
XX dioxyporphorus(V) tetraphenylporphyrin group; ss.
XX
XX Synthetic.
XX
XX JP11029591-A.
XX
XX 02-FEB-1999.
XX
XX 08-JUL-1997; 97JP-00199390.
XX
XX 08-JUL-1997; 97JP-00199390.
XX
XX (KANS-) KANSAI SHINGIJUTSU KENKYUSHO KK.
XX
XX WPI; 1999-175663/15.
XX
XX New oligodeoxyribonucleotide - having artificial nuclease function.
XX
XX Disclosure; Page 9; 9pp; Japanese.
XX
XX The specification describes an oligodeoxyribonucleotide that has
XX artificial nuclease function. The oligodeoxyribonucleotide has a chemical
XX structure in which at least one phosphate diester group combining the
XX saccharide groups of two thymidines is replaced by a dioxyporphorus(V)
XX tetraphenylporphyrin group. The oligodeoxyribonucleotide is used for
XX cleavage of nucleic acid. The present sequence appears in the
XX specification
XX
XX JP11029591-A.
XX
XX 02-FEB-1999.
XX
XX 08-JUL-1997; 97JP-00199390.
XX
XX 08-JUL-1997; 97JP-00199390.
XX
XX (KANS-) KANSAI SHINGIJUTSU KENKYUSHO KK.
XX
XX WPI; 1999-175663/15.
XX
XX New oligodeoxyribonucleotide - having artificial nuclease function.
XX
XX Disclosure; Page 9; 9pp; Japanese.
XX
XX The specification describes an oligodeoxyribonucleotide that has
XX artificial nuclease function. The oligodeoxyribonucleotide has a chemical
XX structure in which at least one phosphate diester group combining the
XX saccharide groups of two thymidines is replaced by a dioxyporphorus(V)
XX tetraphenylporphyrin group. The oligodeoxyribonucleotide is used for
XX cleavage of nucleic acid. The present sequence appears in the
XX specification
XX
XX
```

```
XX
XX Sequence 20 BP; 10 A; 0 C; 2 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1607 TAAAAATTTTAAATAT 1624
Db 19 TATAAATTCCTTAAATAT 2

RESULT 1901
AAX15179/c
ID AAX15179 standard; DNA; 20 BP.
XX
XX AAX15179;
XX
XX 28-APR-1999 (first entry)
XX
XX Oligonucleotide of the invention.
XX
XX Artificial nuclease function; cleavage; nucleic acid;
XX dioxyporphorus(V) tetraphenylporphyrin group; ss.
XX
XX Synthetic.
XX
XX JP11029591-A.
XX
XX 02-FEB-1999.
XX
XX 08-JUL-1997; 97JP-00199390.
XX
XX 08-JUL-1997; 97JP-00199390.
XX
XX (KANS-) KANSAI SHINGIJUTSU KENKYUSHO KK.
XX
XX WPI; 1999-175663/15.
XX
XX New oligodeoxyribonucleotide - having artificial nuclease function.
XX
XX Disclosure; Page 9; 9pp; Japanese.
XX
XX The specification describes an oligodeoxyribonucleotide that has
XX artificial nuclease function. The oligodeoxyribonucleotide has a chemical
XX structure in which at least one phosphate diester group combining the
XX saccharide groups of two thymidines is replaced by a dioxyporphorus(V)
XX tetraphenylporphyrin group. The oligodeoxyribonucleotide is used for
XX cleavage of nucleic acid. The present sequence appears in the
XX specification
XX
XX Sequence 20 BP; 11 A; 0 C; 1 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1607 TAAAAATTTTAAATAT 1624
Db 19 TATAAATTCCTTAAATAT 2

RESULT 1902
AAX19575
ID AAX19575 standard; DNA; 20 BP.
XX
XX AAX19575;
XX
XX 02-JUN-1999 (first entry)
XX
XX PCR primer SEQ ID NO:16 from US5888983.
XX
XX Genome; genetic lesion; haematopoietic stem cell; hepatocyte; RNase;
```

KW human wild-type allele; mutation; sickle cell anaemia; thalassaemia;
 KW Gaucher's disease; glucocerebrosidase gene; hypercholesterolaemia;
 KW emphysema; haemophilia; Christmas disease; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN US5888983-A.
 XX
 PD 30-MAR-1999.
 XX
 XX 05-AUG-1997; 97US-00906265.
 XX
 XX 01-MAY-1996; 96US-00640517.
 PR 17-JUN-1996; 96US-00664487.
 XX
 XX (UJVE-) UNIV JEFFERSON THOMAS.
 PA
 XX Cole-Strauss AD, Kmiec EB;
 PI
 XX WPI; 1999-243264/20.
 DR
 XX Double-stranded oligonucleotides with containing a human wild-type allele
 PT - useful for repairing mutations in human cells, particularly those
 PT causing sickle cell anemia or thalassemia.
 XX
 XX Example 3; Col 20; 40pp; English.
 PS
 XX The present invention describes double-stranded oligonucleotides (I)
 CC containing fragments of wild-type human alleles. (I) are used to repair
 CC disease associated mutations in human cells. (I) are preferably used to
 CC treat sickle cell anaemia or thalassemia (mutations in the beta-globin
 CC gene, including the promoter region), or Gaucher's disease (mutations in
 CC the glucocerebrosidase gene), in haematopoietic cells. (I) may also be
 CC used to treat familial hypercholesterolaemia (mutations in the low-
 CC density lipoprotein receptor gene), emphysema (the alpha 1-anti-trypsin
 CC gene), haemophilia (the factor VIII gene) or Christmas disease (the
 CC factor IX gene), in hepatocytic cells. (I) provides repair of small
 CC genetic mutations. The present sequence represents an oligonucleotide
 CC from the present invention
 XX
 SQ Sequence 20 BP; 9 A; 5 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1625 AATATATCCCGAGGACAG 1642
 |||||
 Db 3 AACAGCCCCAGGGACAG 20
 RESULT 1903
 AAX19571
 ID AAX19571 standard; DNA; 20 BP.
 AC AAX19571;
 XX
 XX 02-JUN-1999 (first entry)
 DT
 XX PCR primer SEQ ID NO:12 from US5888983.
 DE
 XX Genome; genetic lesion; haematopoietic stem cell; hepatocyte; RNase;
 KW human wild-type allele; mutation; sickle cell anaemia; thalassaemia;
 KW Gaucher's disease; glucocerebrosidase gene; hypercholesterolaemia;
 KW emphysema; haemophilia; Christmas disease; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 XX US5888983-A.
 PN
 XX 30-MAR-1999.
 PD
 XX 05-AUG-1997; 97US-00906265.
 PF

XX 01-MAY-1996; 96US-00640517.
 PR 17-JUN-1996; 96US-00664487.
 XX
 XX (UJVE-) UNIV JEFFERSON THOMAS.
 PA
 XX Cole-Strauss AD, Kmiec EB;
 PI
 XX WPI; 1999-243264/20.
 DR
 XX Double-stranded oligonucleotides with containing a human wild-type allele
 PT - useful for repairing mutations in human cells, particularly those
 PT causing sickle cell anemia or thalassemia.
 XX
 XX Example 2; Col 18; 40pp; English.
 PS
 XX The present invention describes double-stranded oligonucleotides (I)
 CC containing fragments of wild-type human alleles. (I) are used to repair
 CC disease associated mutations in human cells. (I) are preferably used to
 CC treat sickle cell anaemia or thalassemia (mutations in the beta-globin
 CC gene, including the promoter region), or Gaucher's disease (mutations in
 CC the glucocerebrosidase gene), in haematopoietic cells. (I) may also be
 CC used to treat familial hypercholesterolaemia (mutations in the low-
 CC density lipoprotein receptor gene), emphysema (the alpha 1-anti-trypsin
 CC gene), haemophilia (the factor VIII gene) or Christmas disease (the
 CC factor IX gene), in hepatocytic cells. (I) provides repair of small
 CC genetic mutations. The present sequence represents an oligonucleotide
 CC from the present invention
 XX
 SQ Sequence 20 BP; 9 A; 5 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1625 AATATATCCCGAGGACAG 1642
 |||||
 Db 3 AACAGCCCCAGGGACAG 20
 RESULT 1904
 AAZ37159/C
 ID AAZ37159 standard; DNA; 20 BP.
 XX
 XX AAZ37159;
 AC
 XX 01-FEB-2000 (first entry)
 DT
 XX Rx specific primer X26 used to sequence the potato Rx gene.
 DE
 XX Potato; Rx gene; resistance gene; potato virus X; PVX; transgenic plant;
 KW broad spectrum extreme resistance; Narcissus mosaic virus; NMV; NVX; VMV;
 KW Nandina virus X; Viola mosaic virus; Cymbidium mosaic virus; PopMV;
 KW Poplar mosaic virus; White clover mosaic virus; WCLMV; PCR primer; ss.
 XX
 OS Synthetic.
 OS Solanum tuberosum.
 XX
 XX WO9954490-A2.
 PN
 XX 28-OCT-1999.
 PD
 XX 16-APR-1999; 99WO-GB001182.
 PF
 XX 16-APR-1999; 98GB-00008083.
 PR
 XX (PLAN-) PLANT BIOSCIENCE LTD.
 PA
 XX Bendahmane A, Baulcombe DC, Kanyuka KV;
 PI
 XX WPI; 1999-634006/54.
 DR
 XX New isolated plant virus resistance gene, used to produce transgenic
 XX

PT plants with resistance to virus infection.
 PS Claim 19; Page 97; 124pp; English.
 XX
 CC Primers AAZ37155-237175 are used in the sequencing of the potato Rx gene (AAZ37153). The Rx gene is a resistance gene which confers extreme resistance against potato virus X (PVX). Sequence AAZ37154 is the Rx coding sequence free from introns. The Rx gene can be used to create a recombinant vector which encodes the Rx resistance polypeptide AAY52152, this vector can be used to transform plant cells to produce a transgenic plant with resistance to PVX. The Rx gene can be used to engineer resistance traits, preferably broad spectrum extreme resistance, into plants. The Rx gene can also be activated by non-PVX viruses, e.g. Narcissus mosaic virus (NMV), Nandina virus X (NVX), Viola mosaic virus (WV), Cymbidium mosaic virus (CyMV), Poplar mosaic virus (PopMV) and White clover mosaic virus (WCLMV). Rx can be used to offer specific protection against this group. The Rx gene sequence can be used to create antibodies specific for Rx. The antibodies can be used to down-regulate Rx activity and also for the detection, identification or isolation of Rx or homologues
 XX
 SQ Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 114 GGATGTTGGAATTACTA 131
 Db 19 GAAAGTTGGAATTACTA 2
 RESULT 1905
 AAX80838/c
 ID AAX80838 standard; DNA; 20 BP.
 XX
 AC AAX80838;
 DT 04-NOV-1999 (first entry)
 XX
 DE Probe for isolating yc20_1 clone.
 XX
 KW Oligonucleotide probe; yc20_1 clone; biotinylated residue; labelled; Gamma-32 Phosphorus ATP; T4 polynucleotide kinase; secreted protein; transmembrane protein; biological activity; ameliorating; preventing; treating; gene therapy; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9941284-A1.
 XX
 PD 19-AUG-1999.
 XX
 PF 11-FEB-1999; 99WO-US002898.
 XX
 PR 11-FEB-1998; 98US-0075118P.
 PR 10-FEB-1999; 99US-00075118.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Wong GG, Clark HF, Fechtel K, Agostino MJ;
 DR WPI; 1999-508625/42.
 XX
 PT New polynucleotides encoding human secreted proteins used for therapeutic, diagnostic and research purposes.
 XX
 PS Disclosure; Page 83; 88pp; English.
 XX
 CC The present sequence is of an oligonucleotide probe designed to an area of the yc20_1 clone sequence having the least number of ambiguous bases. The probe was designed to have a Tm of approximately 80 degrees Celsius.

CC In preferred probes the nucleotide at position 2 is occupied by a biotinylated residue. The oligonucleotide probe should preferably be labelled with Gamma-32 Phosphorus ATP and T4 polynucleotide kinase. This probe was used to isolate and sequence the yc20_1 clone which encodes the yc20_1 secreted or transmembrane protein. The yc20_1 polynucleotide and its encoded protein exhibit various biological activities. These biological activities make them suitable for ameliorating, preventing or treating medical conditions in humans and animals. The polynucleotide can also be used for gene therapy
 XX
 SQ Sequence 20 BP; 8 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1979 GCCTCTGTCTGTCTTCT 1996
 Db 20 GCCCTATGGCTTCTTCT 3
 RESULT 1906
 AAC69242
 ID AAC69242 standard; DNA; 20 BP.
 XX
 AC AAC69242;
 DT 29-JAN-2001 (first entry)
 XX
 DE Human ABC1 gene exon 36 3' PCR primer, SEQ ID NO:141.
 XX
 KW Human ABC1 cholesterol transporter; chromosome 9q31; ATP-binding cassette; HDL deficiency disorder; high density lipoprotein; Tangier disease; ID; familial HDL deficiency; FHA; polymorphism; cardiovascular disease; coronary artery disease; coronary restenosis; cerebrovascular disease; peripheral vascular disease; Alzheimer's disease; Niemann-Pick disease; Huntington's disease; X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis; prognosis; prophylaxis; drug screening; transgenic animal; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200055318-A2.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-IB000532.
 XX
 PR 15-MAR-1999; 99US-0124702P.
 PR 08-JUN-1999; 99US-0138048P.
 PR 17-JUN-1999; 99US-0139600P.
 PR 01-SEP-1999; 99US-0151977P.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (XENO-) XENON BIORESEARCH INC.
 XX
 PI Hayden MR, Wilson AR, Pimstone SN;
 DR WPI; 2000-587528/55.
 XX
 PT New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's disease and cancer.
 PT
 PS Disclosure; Fig 10; 229pp; English.
 XX
 CC The invention relates to the human ABC1 cholesterol transporter protein (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is a member of the ATP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly intracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol efflux from the cell. The gene encoding ABC1 is

CC located on chromosome 9q31, and mutations in this gene are associated
 CC with two genetic HDL (high density lipoprotein) deficiency disorders,
 CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
 CC are distinguishable in that TD is an autosomal recessive disorder, while
 CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
 CC cholesterol") in the blood correlate with a high risk of cardiovascular
 CC disease, particularly coronary artery disease, but also cerebrovascular
 CC disease, coronary restenosis, and peripheral vascular disease.
 CC Conversely, a high level of HDL has protective effects against
 CC cardiovascular disease. The invention provides genetic constructs and
 CC transgenic cells and non-human animals comprising human ABC1 nucleic
 CC acids, and methods of gene therapy for the treatment or prevention of
 CC cardiovascular disease comprising the administration of an expression
 CC vector encoding ABC1 or an active fragment thereof. The invention also
 CC encompasses compounds which mimic ABC1 activity, compounds which
 CC stimulate ABC1 expression and methods of screening for such compounds. It
 CC further relates to methods for determining whether a patient has an
 CC increased risk for cardiovascular disease due to polymorphisms in the
 CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or
 CC prevent cardiovascular disease, especially coronary artery disease,
 CC cerebrovascular disease, coronary restenosis or peripheral vascular
 CC disease. They may also be used in the treatment of diseases associated
 CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
 CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
 CC The invention specifically excludes proteins with the exact amino acid
 CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
 CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The
 CC present sequence represents a human ABC1 gene PCR primer which may be
 CC used to amplify an exon of the human ABC1 gene

XX SQ Sequence 20 BP; 1 A; 10 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1514 TGGACCTCTCCAGCTCTG 1531
 |||||
 Db 3 TGCACCTCTCTCTCTG 20

RESULT 1907
 AAZ46543/c
 ID AAZ46543 standard; DNA; 20 BP.

AC AAZ46543;

XX 13-MAR-2000 (first entry)

DE Human CACNA1F DNA amplifying forward primer.

XX Retinal calcium channel; RCC gene; alpha1F-subunit; retinal disorder;
 KW myopia; nystagmus; strabismus; calcium-regulated development pathway;
 KW eye disorder; human; CACNA1F; CSNB; PCR primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9963078-A2.

XX 09-DEC-1999.

XX 02-JUN-1999; 99WO-CA000514.

XX 02-JUN-1998; 98US-0087635P.

XX (UYTE-) UNIV TECHNOLOGIES INT INC.

XX Bech-Hansen T, Naylor MJ;

XX WPI; 2000-097327/08.

XX New isolated mammalian retinal calcium channel gene, used to develop

PT products for the diagnosis and treatment of incomplete congenital
 PT stationary night blindness and related disorders.

XX Disclosure; Fig 2; 55pp; English.

XX The invention provides a DNA molecule comprising a sequence of
 CC nucleotides encoding an alpha1F-subunit of a mammalian retinal calcium
 CC channel (RCC), including a human alpha1F-subunit, a murine alpha1F-
 CC subunit and orthologs of the human and murine alpha1F-subunits. The RCC
 CC gene may be used to develop products for diagnostic tests, for incomplete
 CC CSNB and risk assessment in affected families. The RCC gene can provide
 CC information as to the basic defect in this retinal conditions, which
 CC could lead to effective methods for treatment or cure of the disorder. As
 CC the associated features of myopia, nystagmus and strabismus frequently
 CC observed in patients with incomplete CSNB may be caused by calcium-
 CC regulated development pathways, identification of the RCC gene may help
 CC to elucidate the molecular details of eye development and which may lead
 CC to treatment for related eye disorders or diseases. Sequences AAZ46541-62
 CC represent primers used to determine the nucleotide sequence of human
 CC CACNA1F (alpha1F-subunit of RCC gene), by amplifying retina cDNA and
 CC sequencing it

XX SQ Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1246 GATGAGGACGAGACGAC 1263

|||||

Db 20 GATGATGACGAGAGAC 3

RESULT 1908

AAZ46583/c

ID AAZ46583 standard; DNA; 20 BP.

XX AAZ46583;

XX 13-MAR-2000 (first entry)

XX Forward primer specific for human CACNA1F exon 21.

XX Retinal calcium channel; RCC gene; alpha1F-subunit; retinal disorder;
 KW myopia; nystagmus; strabismus; calcium-regulated development pathway;
 KW eye disorder; human; CACNA1F; CSNB; mutational analysis; PCR primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9963078-A2.

XX 09-DEC-1999.

XX 02-JUN-1999; 99WO-CA000514.

XX 02-JUN-1998; 98US-0087635P.

XX (UYTE-) UNIV TECHNOLOGIES INT INC.

XX Bech-Hansen T, Naylor MJ;

XX WPI; 2000-097327/08.

XX New isolated mammalian retinal calcium channel gene, used to develop
 PT products for the diagnosis and treatment of incomplete congenital
 PT stationary night blindness and related disorders.

XX Disclosure; Fig 6; 55pp; English.

XX The invention provides a DNA molecule comprising a sequence of
 CC nucleotides encoding an alpha1F-subunit of a mammalian retinal calcium
 CC channel (RCC), including a human alpha1F-subunit, a murine alpha1F-

CC subunit and orthologs of the human and murine alpha1F-subunits. The RCC
 CC gene may be used to develop products for diagnostic tests, for incomplete
 CC CSMB and risk assessment in affected families. The RCC gene can provide
 CC information as to the basic defect in this retinal conditions, which
 CC could lead to effective methods for treatment or cure of the disorder. As
 CC the associated features of myopia, nystagmus and strabismus frequently
 CC observed in patients with incomplete CSNB may be caused by calcium-
 CC regulated development pathways, identification of the RCC gene may help
 CC to elucidate the molecular details of eye development and which may lead
 CC to treatment for related eye disorders or diseases. Sequences AAZ46532-
 CC 650 represent human CACNA1F (alpha1F-subunit of RCC gene) exon-specific
 CC PCR primers, used for mutational analysis in humans
 XX
 SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1006 GAGACAGCTGTGGCCCTG 1023
 Db ||||| |||||
 19 GATACAGTCTGTGGCCCTG 2
 RESULT 1909
 AAZ46532
 ID AAZ46532 standard; DNA; 20 BP.
 AC AAZ46532;
 XX
 DT 13-MAR-2000 (first entry)
 DE Mouse CACNA1F gene specific primer.
 XX
 DE Retinal calcium channel; RCC gene; alpha1F-subunit; retinal disorder;
 KW myopia; nystagmus; strabismus; calcium-regulated development pathway;
 KW eye disorder; mouse; CACNA1F; CSNB; PCR primer; ss.
 XX
 OS Synthetic.
 OS Mus sp.
 OS
 PN WO9963078-A2.
 XX
 PD 09-DEC-1999.
 PF 02-JUN-1999; 99WO-CA000514.
 XX
 PR 02-JUN-1998; 98US-0087635P.
 XX
 PA (UYTE-) UNIV TECHNOLOGIES INT INC.
 XX
 PI Bech-Hansen T, Naylor MJ;
 XX
 DR WPI; 2000-097327/08.
 XX
 PT New isolated mammalian retinal calcium channel gene, used to develop
 PT products for the diagnosis and treatment of incomplete congenital
 PT stationary night blindness and related disorders.
 XX
 PS Example 4; Page 27; 55pp; English.
 XX
 CC The invention provides a DNA molecule comprising a sequence of
 CC nucleotides encoding an alpha1F-subunit of a mammalian retinal calcium
 CC channel (RCC), including a human alpha1F-subunit, a murine alpha1F-
 CC subunit and orthologs of the human and murine alpha1F-subunits. The RCC
 CC gene may be used to develop products for diagnostic tests, for incomplete
 CC CSMB and risk assessment in affected families. The RCC gene can provide
 CC information as to the basic defect in this retinal conditions, which
 CC could lead to effective methods for treatment or cure of the disorder. As
 CC the associated features of myopia, nystagmus and strabismus frequently
 CC observed in patients with incomplete CSNB may be caused by calcium-
 CC regulated development pathways, identification of the RCC gene may help
 CC to elucidate the molecular details of eye development and which may lead

CC to treatment for related eye disorders or diseases. Sequences AAZ46522-
 CC 540 represent PCR primers used for the isolation of murine CACNA1F
 CC (alpha1F- subunit of RCC gene) ortholog
 XX
 SQ Sequence 20 BP; 6 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1729 TGAACCATAAAGGTGTC 1746
 Db ||||| |||||
 3 TGAACCATACCGAGTGCC 20
 RESULT 1910
 AAZ95095/C
 ID AAZ95095 standard; DNA; 20 BP.
 AC AAZ95095;
 XX
 DT 05-JUN-2000 (first entry)
 DE Human UGT2B15 exon 1 polymorphism 2a nucleotide sequence.
 XX
 DE UDP-glucuronosyltransferase 2B15; UGT2B15; polymorphism; metabolism;
 KW drug interaction; detect; human; single nucleotide polymorphism; SNPs;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT variation replace(11,G)
 FT /*tag= a
 PN WO200006776-A1.
 XX
 PD 10-FEB-2000.
 XX
 PF 22-JUL-1999; 99WO-US016675.
 XX
 PR 28-JUL-1998; 98US-0094391P.
 XX
 PA (AXYS-) AXYS PHARM INC.
 XX
 PI Galvin M, Miller A, Penny L, Riedy M;
 XX
 DR WPI; 2000-195321/17.
 XX
 PT Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
 PT genotyping individuals to predict rate of metabolism of substrates and
 PT for identifying potential drug interactions.
 XX
 PS Claim 1; Page 26; 72pp; English.
 XX
 CC This sequence represents a polymorphic fragment of exon 1 of the human
 CC UDP-glucuronosyltransferase 2B15 (UGT2B15) gene. UDP-
 CC glucuronosyltransferase (UGTs) are a family of enzymes that catalyze the
 CC glucuronic acid conjugation of a wide range of endogenous and exogenous
 CC substrates. The UGT2B gene subfamily encode steroid metabolizing isoforms
 CC in the liver. Alteration of the expression or function of UGTs may effect
 CC drug metabolism. The invention relates to non-chromosomal nucleic acid
 CC molecules, which comprise human UGT2B sequence polymorphisms. Probes
 CC which detect the UGT2B locus polymorphisms can be used to detect altered
 CC UGT2B metabolism of a substrate in an individual. The nucleic acid
 CC molecules comprising a human UGT2B sequence polymorphism can be used in
 CC screening assays for genotyping individuals, also to predict their rate
 CC of metabolism of UGT2B substrate, potential drug-drug interactions and
 CC adverse side effects. The polymorphisms can be used as single nucleotide
 CC polymorphisms (SNPs) for detecting genetic linkage related to phenotypic
 CC variation in activity or expression of UGT2B protein. The polymorphism
 CC containing nucleic acid molecules may also be used for generating
 CC genetically modified non-human animals and for obtaining site specific

CC gene modification in cell lines
XX
SQ Sequence 20 BP; 3 A; 6 C; 2 G; 9 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1585 TCTATTCTCTGTGTATT 1602
DB 2 TCCATTCATCTGTGTATT 19
RESULT 1912
AAA41078/c
ID AAA41078 standard; DNA; 20 BP.
XX
AC AAA41078;
XX
DT 16-AUG-2000 (first entry)
XX
DE Human TNFalpha antisense oligonucleotide ISIS# 104719.
XX
KW Antisense oligonucleotide; phosphorothioate; TNFalpha; cytokine; inhibit;
KW tumour necrosis factor alpha; inflammatory bowel disease; diabetes;
KW rheumatoid arthritis; infectious disease; multiple sclerosis; hepatitis;
KW pancreatitis; atopic dermatitis; allograft rejection; autoimmune disease;
KW inflammatory disease; ss.
XX
OS Synthetic.
XX
PN WO200020645-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US023205.
XX
PR 05-OCT-1998; 98US-00166186.
XX
PR 18-MAY-1999; 99US-00313932.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Bennett CF, Butler MM, Shanahan WJ;
XX
DR WPI; 2000-303808/26.
XX
PT Oligonucleotide for treating diseases associated with human tumor
PT necrosis factor-alpha (TNF-alpha) such as, diabetes and rheumatoid
PT arthritis, comprises nucleotide sequence complementary to intron of
PT nucleic acid encoding TNF-alpha.
XX
PS Example 22; Page 101; 283pp; English.
XX
This sequence represents an antisense oligonucleotide sequence which
targets a region of the human tumour necrosis factor alpha (TNFalpha)
nucleotide sequence. TNFalpha is an important cytokine that plays a role
in host defence. It is produced mainly in macrophages and monocytes in
response to infection, invasion, injury or inflammation. Overexpression
of TNFalpha can result in disease states, particularly in infectious,
inflammatory and autoimmune diseases. The invention relates to antisense
oligonucleotides, such as that represented by the present sequence which
are capable of modulating the TNFalpha gene expression. The
oligonucleotides optionally have a phosphorothioate backbone, and may
also optionally contain at least one 2'-O-methoxyethyl modification. The
oligonucleotides are useful for modulating the expression of human
TNFalpha in cells and tissues, reducing a human cell inflammatory
response, reducing the blood glucose level in a human and treating a
human having a disease or condition associated with TNFalpha. Examples of
diseases associated with TNFalpha include diabetes, inflammatory bowel
disease, multiple sclerosis, pancreatitis, rheumatoid arthritis,
infectious disease, hepatitis, atopic dermatitis or allograft rejection.
The antisense oligonucleotides are also useful for modulating the
function of a selected nucleic acid sequence in adipose tissue

CC
XX
SQ Sequence 20 BP; 2 A; 5 C; 4 G; 9 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1473 AGAAGCCAAAGGGGTCAA 1490
DB 20 AGAAGCCGAGATGTCAA 3
RESULT 1911
AAA40831
ID AAA40831 standard; DNA; 20 BP.
XX
AC AAA40831;
XX
DT 16-AUG-2000 (first entry)
XX
DE Human TNFalpha antisense oligonucleotide ISIS# 21691.
XX
KW Antisense oligonucleotide; phosphorothioate; TNFalpha; cytokine; inhibit;
KW tumour necrosis factor alpha; inflammatory bowel disease; diabetes;
KW rheumatoid arthritis; infectious disease; multiple sclerosis; hepatitis;
KW pancreatitis; atopic dermatitis; allograft rejection; autoimmune disease;
KW inflammatory disease; ss.
XX
OS Synthetic.
XX
PN WO200020645-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US023205.
XX
PR 05-OCT-1998; 98US-00166186.
XX
PR 18-MAY-1999; 99US-00313932.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Bennett CF, Butler MM, Shanahan WJ;
XX
DR WPI; 2000-303808/26.
XX
PT Oligonucleotide for treating diseases associated with human tumor
PT necrosis factor-alpha (TNF-alpha) such as, diabetes and rheumatoid
PT arthritis, comprises nucleotide sequence complementary to intron of
PT nucleic acid encoding TNF-alpha.
XX
PS Example 6; Page 57; 283pp; English.
XX
This sequence represents an antisense oligonucleotide sequence which
targets a region of the human tumour necrosis factor alpha (TNFalpha)
nucleotide sequence. TNFalpha is an important cytokine that plays a role
in host defence. It is produced mainly in macrophages and monocytes in
response to infection, invasion, injury or inflammation. Overexpression
of TNFalpha can result in disease states, particularly in infectious,
inflammatory and autoimmune diseases. The invention relates to antisense
oligonucleotides, such as that represented by the present sequence which
are capable of modulating the TNFalpha gene expression. The
oligonucleotides optionally have a phosphorothioate backbone, and may
also optionally contain at least one 2'-O-methoxyethyl modification. The
oligonucleotides are useful for modulating the expression of human
TNFalpha in cells and tissues, reducing a human cell inflammatory
response, reducing the blood glucose level in a human and treating a
human having a disease or condition associated with TNFalpha. Examples of
diseases associated with TNFalpha include diabetes, inflammatory bowel
disease, multiple sclerosis, pancreatitis, rheumatoid arthritis,
infectious disease, hepatitis, atopic dermatitis or allograft rejection.
The antisense oligonucleotides are also useful for modulating the
function of a selected nucleic acid sequence in adipose tissue

SQ Sequence 20 BP; 5 A; 8 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1674 CTGGGTGAGCTCTCCAG 1691
|||||
Db 20 CTGGGAGGGGTCTCCAG 3

RESULT 1913

AAA40842

ID AAA40842 standard; DNA; 20 BP.

XX AC AAA40842;

XX DT 16-AUG-2000 (first entry)

XX DE Human TNFalpha antisense oligonucleotide ISIS# 21702.

XX KW Antisense oligonucleotide; phosphorothioate; TNFalpha; cytokine; inhibit;
KW tumour necrosis factor alpha; inflammatory bowel disease; diabetes;
KW rheumatoid arthritis; infectious disease; multiple sclerosis; hepatitis;
KW pancreatitis; atopic dermatitis; allograft rejection; autoimmune disease;
KW inflammatory disease; ss.

XX OS Synthetic.

XX PN WO200020645-A1.

XX PD 13-APR-2000.

XX PF 05-OCT-1999; 99WO-US0232305.

XX PR 05-OCT-1998; 98US-0016186.

XX PR 18-MAY-1999; 99US-00313932.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Baker BF, Bennett CF, Butler MM, Shanahan WJ;

XX DR WPI; 2000-303808/26.

XX OL Oligonucleotide for treating diseases associated with human tumor
PT necrosis factor-alpha (TNF-alpha) such as, diabetes and rheumatoid
PT arthritis, comprises nucleotide sequence complementary to intron of
PT nucleic acid encoding TNF-alpha.

PS Example 6; Page 58; 283pp; English.

XX CC This sequence represents an antisense oligonucleotide sequence which
CC targets a region of the human tumour necrosis factor alpha (TNFalpha)
CC nucleotide sequence. TNFalpha is an important cytokine that plays a role
CC in host defence. It is produced mainly in macrophages and monocytes in
CC response to infection, invasion, injury or inflammation. Overexpression
CC of TNFalpha can result in disease states, particularly in infectious,
CC inflammatory and autoimmune diseases. The invention relates to antisense
CC oligonucleotides, such as that represented by the present sequence which
CC are capable of modulating the TNFalpha gene expression. The
CC oligonucleotides optionally have a phosphorothioate backbone, and may
CC also optionally contain at least one 2'-O-methoxyethyl modification. The
CC oligonucleotides are useful for modulating the expression of human
CC TNFalpha in cells and tissues, reducing a human cell inflammatory
CC response, reducing the blood glucose level in a human and treating a
CC human having a disease or condition associated with TNFalpha. Examples of
CC diseases associated with TNFalpha include diabetes, inflammatory bowel
CC disease, multiple sclerosis, pancreatitis, rheumatoid arthritis,
CC infectious disease, hepatitis, atopic dermatitis or allograft rejection.
CC The antisense oligonucleotides are also useful for modulating the
CC function of a selected nucleic acid sequence in adipose tissue

XX SQ Sequence 20 BP; 1 A; 8 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1978 TGCCCTCTGTCTGTCTTC 1995
|||||
Db 2 TCCTCTCTGTCTGTCTTC 19

RESULT 1914

AAA40705/c

ID AAA40705 standard; DNA; 20 BP.

XX AC AAA40705;

XX DT 15-AUG-2000 (first entry)

XX DE Rat ILG6 primer ILG6F SEQ ID NO:93.

XX KW Human; rat; CD36; SHR; spontaneous hypertensive rat; diagnosis; therapy;
KW screening; polymorphism; variant; detection; mutant; blood; mutation;
KW insulin; glucose metabolism; fatty acid metabolism; catecholamine;
KW malaria; infection; parasite; antiparasitic; antidiabetic; primer; ss.

XX OS Rattus sp.

XX PN WO200019883-A2.

XX PD 13-APR-2000.

XX PF 07-OCT-1999; 99WO-US023418.

XX PR 07-OCT-1998; 98US-00167750.

XX PR 28-DEC-1998; 98US-00221222.

XX PR 17-MAR-1999; 99US-00270542.

XX PA (MEDI-) MEDICAL RES COUNCIL.

XX PA (SCIO-) SCIOS INC.

XX PA (AITM/) AITMAN T J.

XX PA (SCOT/) SCOTT J.

XX PA (STAN/) STANTON L W.

XX PI Aitman TJ, Scott J, Stanton LW;

XX DR WPI; 2000-303596/26.

XX PT Nucleic acids encoding mutant CD36 proteins useful for preventing,
PT diagnosing and treating parasitic infections, especially malaria.

PS Example 1; Page 110; 167pp; English.

XX CC The present invention describes isolated nucleic acid molecules (A)
CC encoding mutant CD36 proteins (B). Parasites such as Plasmodium
CC falciparum (the major cause of malaria) are unable to utilise the mutated
CC proteins to gain entry to, and infect cells. The mutant CD36 proteins do
CC not function correctly preventing parasites utilising them to infect
CC cells. The nucleic acids may be used for the recombinant production of
CC mutant CD36 proteins according to standard methodologies. They may be
CC used in this way to prevent and treat parasitic infections that utilise
CC the CD36 protein to infect cells, such as P. falciparum, the major cause
CC of malaria. For example, the protein may be used to identify modulators
CC of CD36 expression and activity or a patient's CD36 DNA may be screened
CC to determine whether there are any mutations present that may confer
CC resistance to parasitic infections. The proteins and nucleic acids may
CC also be used to prevent, diagnose and treat diseases associated with
CC defects in insulin action and/or glucose metabolism and/or fatty acid
CC metabolism and/or catecholamine action in subjects possessing mutations
CC in the CD36 genes. AAA40606 to AAA40759, and AAA02515 to AAB02564,
CC represent nucleotide and amino acid sequences respectively which are used
CC in the exemplification of the present invention

XX SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match		0.6%;	Score 13.2;	DB 1;	Length 20;
Best Local Similarity		83.3%;	Pred. No. 1.3e+03;		
Matches		15;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
QY	534	CTTGGCCATCTCTGGAAC	551		
	20	CCTGGGTATCTCTGGAAC	3		
Db					
RESULT 1915					
AAZ57079/c					
ID AAZ57079 standard; DNA; 20 BP.					
XX AC AAZ57079;					
XX DT 19-MAY-2000 (first entry)					
XX DE Murine melanocortin receptor MC5-R amplifying primer.					
XX KW Medicament; agonist; melanocortin receptor type 3; ACTH; PMN; MC3-R;					
XX KW adrenocorticotrophic hormone; neutrophil chemoattractant; antitoxin;					
XX KW polymorphonuclear cell; septic shock; skin disorder; antiarthritic;					
XX KW melanocortin receptor; anti-inflammatory; antiasmatic; PCR primer; ss.					
XX OS Mus sp.					
XX PN WO200005263-A2.					
XX PD 03-FEB-2000.					
XX PF 22-JUL-1999; 99WO-GB002392.					
XX PR 24-JUL-1998; 96GB-00016234.					
XX PA (HARV-) HARVEY RES LTD WILLIAM.					
XX PI Perretti M, Getting S, Flower R;					
XX WPI; 2000-182651/16.					
XX PT Inhibition of neutrophil chemoattractant production, inhibition of					
XX PT polymorphonuclear cell accumulation or reduction/treatment of					
XX PT inflammation using compounds comprising the peptide sequence HFRW.					
XX PS Disclosure; Page 8; 20pp; English.					
XX CC The invention relates to the use of a compound comprising an amino acid					
XX CC sequence His-Phe-Arg-Tip (HFRW) in the manufacture of a medicament and/or					
XX CC an agonist of melanocortin receptor type 3 (MC3-R) where the compound is					
XX CC not adrenocorticotrophic hormone (ACTH)1-39. The compounds are used to					
XX CC inhibit neutrophil chemoattractant production, polymorphonuclear cell					
XX CC (PMN) accumulation or reduction/treatment of inflammation. Especially,					
XX CC these compounds are agonists of the MC3-R. The inflammatory response/					
XX CC disease is selected from gout, gouty arthritis, rheumatoid arthritis,					
XX CC asthma, reperfusion injury or damage, stroke, myocardial infarction,					
XX CC septic shock, or a skin disorder. Sequences AAZ57073-80 represent PCR					
XX CC primers used for amplifying murine melanocortin receptors					
XX SQ Sequence 20 BP; 4 A; 10 C; 1 G; 5 T; 0 U; 0 Other;					
Query Match		0.6%;	Score 13.2;	DB 1;	Length 20;
Best Local Similarity		83.3%;	Pred. No. 1.3e+03;		
Matches		15;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
QY	1484	GGGTCAAGGAGGAGGTCA	1501		
	19	GGGTGGAGGAGGAGGTCA	2		
Db					
RESULT 1916					
AAZ52587/c					
ID AAZ52587 standard; DNA; 20 BP.					
XX AC AAZ52587;					
XX DT 29-FEB-2000 (first entry)					
XX DE Human secreted protein clone yc20_1 probe SEQ ID NO:220.					
XX KW Human; secreted protein; immunostimulatory; haemostatic; cytokine;					
XX KW proliferative; differentiative; chemotactic; chemokinetic; vaccine;					
XX KW thrombolytic; antiinflammatory; cytostatic; immunosuppressive;					
XX KW gene therapy; hybridisation; probe; ss.					
XX OS Synthetic.					
XX OS Homo sapiens.					
XX PN WO9958642-A2.					
XX PD 18-NOV-1999.					
XX PF 14-MAY-1999; 99WO-US010843.					
XX PR 14-MAY-1998; 98US-0085472P.					
XX PR 17-AUG-1998; 98US-0096824P.					
XX PR 11-SEP-1998; 98US-0099843P.					
XX PR 11-SEP-1998; 98US-0099950P.					
XX PR 15-SEP-1998; 98US-0100424P.					
XX PR 29-SEP-1998; 98US-0102329P.					
XX PR 09-OCT-1998; 98US-0103615P.					
XX PR 11-DEC-1998; 98US-0111799P.					
XX PR 14-DEC-1998; 98US-0112159P.					
XX PR 31-DEC-1998; 98US-0114415P.					
XX PR 10-FEB-1999; 99US-00248059.					
XX PR 06-APR-1999; 99US-00287150.					
XX PR 13-MAY-1999; 99US-00311021.					
XX PA (GEMY) GENETICS INST INC.					
XX PI Wong GG, Clark HF, Fechtel K, Agostino MJ;					
XX WPI; 2000-053095/04.					
XX PT Novel polynucleotides and proteins having biological activities which					
XX PT make them suitable for treating, preventing or ameliorating medical					
XX PT conditions in humans or animals.					
XX PS Disclosure; Page 720; 730pp; English.					
XX CC The present invention describes human secreted proteins encoded by					
XX CC polynucleotides obtained from adult testes, foetal brain, adult brain,					
XX CC brain (foetal and adult), foetal kidney, adult spleen, and adult thymus					
XX CC cDNA libraries. The polynucleotides and proteins are predicted to have					
XX CC biological activities which would make them suitable for treating,					
XX CC preventing or ameliorating medical conditions in humans and animals.					
XX CC Suggested activities include nutritional activity, cytokine and cell					
XX CC proliferation/differentiation activity, immune stimulating (e.g. as					
XX CC vaccines) or suppressing activity, haematopoiesis regulating activity,					
XX CC tissue growth activity, activin/inhibin activity, chemotactic/					
XX CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/					
XX CC ligand activity, anti-inflammatory activity, cadherin/tumour invasion					
XX CC suppressor activity, and tumour inhibition activity. The polynucleotides					
XX CC are also stated to be useful for gene therapy. Therapeutic compositions					
XX CC are also presently valuable for veterinary applications. AAZ52475 to					
XX CC AAZ52581 encode human secreted proteins, and AAY73390 to AAY73500					
XX CC represent human secreted proteins, given in the present invention.					
XX CC AAZ52582 to AAZ52631 represent probes for human secreted protein clones,					
XX CC used in the exemplification from the present invention					
XX SQ Sequence 20 BP; 8 A; 4 C; 6 G; 2 T; 0 U; 0 Other;					
Query Match		0.6%;	Score 13.2;	DB 1;	Length 20;
Best Local Similarity		83.3%;	Pred. No. 1.3e+03;		
Matches		15;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;

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QY 1979 GCCCTGTGTCTGTCTTCT 1996
Db 20 GCCCTATGGCTTCTTCT 3

RESULT 1917
AAZ76637/c
ID AAZ76637 standard; DNA; 20 BP.
XX
AC AAZ76637;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:10993.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-TB000822.
XX
PR 21-APR-1998; 98US-0082614P.
XX
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST ) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 9; Page 2574; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 20 BP; 5 A; 2 C; 9 G; 4 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1697 ACCTGCCACCCATCTCT 1714
Db 18 ATCTGCCACCCATCTT 1

RESULT 1918
AAZ72728/c
ID AAZ72728 standard; DNA; 20 BP.
XX
AC AAZ72728;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:7064.
XX
KW Human genome; biallelic marker; high density disequilibrium map;

```

KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.
 XX Homo sapiens.
 XX WO9954500-A2.
 XX PN
 XX PD 28-OCT-1999.
 XX PF 21-APR-1999; 99WO-IB000822.
 XX PR 21-APR-1998; 98US-0082614P.
 XX PR 23-NOV-1998; 98US-0109732P.
 XX PA (GEST) GENSET.
 XX PI Cohen D, Blumenfeld M, Chumakov I;
 XX DR WPI; 2000-013267/01.
 XX PT Novel biallelic markers used to construct a high density disequilibrium
 XX map of the human genome.
 XX PS Claim 9; Page 1737; 2745pp; English.
 XX CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 353 GTGAGGACTGTCAGTAT 370
 Db 18 GTAGGAGTGCCAGTAT 1
 RESULT 1920
 ID AAZ70211 standard; DNA; 20 BP.
 XX AC AAZ70211;
 XX DT 10-SEP-2001 (first entry)
 XX DE Human biallelic marker upstream amplification primer SEQ ID NO:4567.
 KW Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.
 XX Homo sapiens.
 XX WO9954500-A2.
 XX PN

XX 28-OCT-1999.
 XX PF 21-APR-1999; 99WO-IB000822.
 XX PR 21-APR-1998; 98US-0082614P.
 XX PR 23-NOV-1998; 98US-0109732P.
 XX PA (GEST) GENSET.
 XX PI Cohen D, Blumenfeld M, Chumakov I;
 XX DR WPI; 2000-013267/01.
 XX PT Novel biallelic markers used to construct a high density disequilibrium
 XX map of the human genome.
 XX PS Claim 8; Page 1204; 2745pp; English.
 XX CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX Sequence 20 BP; 13 A; 5 C; 2 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1405 GAAAAAGAGAAAGACCCA 1422
 Db 1 GAAAAACAGAAACACACA 18
 RESULT 1921
 ID AAA80157 standard; DNA; 20 BP.
 XX AC AAA80157;
 XX DT 20-NOV-2000 (first entry)
 XX DE Hepatitis B virus related oligonucleotide probe #420.
 XX KW Hepatitis B virus; HBV; Hepatitis A virus; HAV; probe; detection;
 XX mutation; high-density gene chip; ss.
 XX OS Hepatitis B virus.
 XX PN CN1252452-A.
 XX PD 10-MAY-2000.
 XX PF 24-SEP-1999; 99CN-00114460.
 XX PR 24-SEP-1999; 99CN-00114460.
 XX PA (UYDO-) UNIV DONGNAN.
 XX PI Sun X, Lu Z, Wang Y;
 XX

DR WPI; 2000-443233/39.
 XX High-density gene chip making process.
 PT Example 1; Fig 15; 19pp; Chinese.
 PS
 XX
 CC The present invention describes a method which comprises making a high-
 CC density gene chip, specifically for making high-density micro-array of
 CC oligonucleotide probes. An oligonucleotide probe selecting process to
 CC seek preferentially length variable and coverage variable probes is
 CC provided to ensure identical cross melting temperature of probes to the
 CC maximum limit, and this can make the cross control of gene chip
 CC relatively simple and raise the reliability of the gene chip detecting
 CC results. The process proposes a specific probe selection method for
 CC detecting target sequence directly, detecting mutation in both specific
 CC and non-specific sites and a probe overall arrangement scheme. AA79738
 CC to AAA80201 represent oligonucleotide probe sequences which are used in
 CC examples from the present invention
 XX
 SQ Sequence 20 BP; 9 A; 4 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 487 GCAAAGAGTCCGAGGCA 504
 DB 1 GCAAAGAGGACCGAGTCA 18
 RESULT 1922
 AAZ45057/c
 ID AAZ45057 standard; DNA; 20 BP.
 XX
 AC AAZ45057;
 XX
 DT 28-FEB-2000 (first entry)
 XX
 DE Reverse PCR primer used in the primary amplification of UGT1 exon 1J.
 XX
 KW Uridine diphosphate-glucuronosyltransferase 1; UGT1; polymorphism; probe;
 KW glucuronic acid; Crigler-Najjar syndrome; Gilbert syndrome; jaundice;
 KW unconjugated hyperbilirubinaemia; drug metabolism; transgenic animal;
 KW pharmacogenetic screening; diagnosis; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9957322-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 04-MAY-1999; 99WO-US009702.
 XX
 PR 07-MAY-1998; 98US-0084807P.
 XX
 PA (AXYS-) AXYS PHARM INC.
 XX
 PI Penny L, Galvin M;
 XX
 DR WPI; 2000-052981/04.
 XX
 XX New nucleic acid representing polymorphisms in the human uridine
 PT diphosphate glucuronosyltransferase gene, used for diagnosis and evaluation
 PT of drug metabolism.
 XX
 PS Example; Page 16; 63pp; English.
 XX
 CC PCR primers AAZ45042-245073 are used to amplify human uridine diphosphate
 CC -glucuronosyltransferase 1 (UGT1) exon sequences. The UGTs are a family
 CC of enzymes that catalyse the glucuronic acid conjugation of a wide range
 CC of endogenous and exogenous substrates including phenols, alcohols,
 CC amines and fatty acids. Many of the reactions catalysed by UGTs result in

CC toxic substances being converted to compounds which are more water
 CC soluble and are excreted. The invention relates to and identifies UGT1
 CC polymorphisms (AAZ45004-245041). The polymorphism sequences are useful as
 CC probes for detecting UGT1 locus polymorphisms, indicative of altered UGT1
 CC expression or activity. These polymorphisms are associated with Crigler-
 CC Najjar and Gilbert syndromes (unconjugated hyperbilirubinaemia) and drug
 CC metabolism. The genotyping of the UGT1 gene is used to predict the rate
 CC of metabolism of UGT1 substrates, possible drug-drug interactions and
 CC adverse side effects (i.e. to optimize drug dosage), and to screen for
 CC diseases caused by exposure to toxins and to study the effects of
 CC polymorphisms on enzymatic activity. The UGT1 sequences, including
 CC its fragments, can also be used to produce the corresponding protein (or
 CC for pharmacogenetic screening
 XX
 SQ Sequence 20 BP; 6 A; 2 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1826 AAAGTCCCTTATTGAA 1843
 DB 18 AAAACTGCCCTTCTTGAA 1
 RESULT 1923
 AAZ44550
 ID AAZ44550 standard; DNA; 20 BP.
 XX
 AC AAZ44550;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Newcastle disease virus LaSota primer P7110+(L).
 XX
 KW Avian-paramyxovirus; infection; lentogenic; F protein; vaccine;
 KW respiratory disease; gastrointestinal disease; poultry pathogen;
 KW local immunity; primer; ss.
 XX
 OS Newcastle disease virus.
 XX
 PN WO9966045-A1.
 XX
 PD 23-DEC-1999.
 XX
 PF 17-JUN-1999; 99WO-NL000377.
 XX
 PR 19-JUN-1998; 98EP-00202054.
 XX
 PA (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.
 XX
 PI Peeters BPH, De Leeuw OS, Koch G, Gielkens ALJ;
 XX
 DR WPI; 2000-106102/09.
 XX
 PT New avian paramyxovirus cDNA, useful for production of vaccine against
 PT Newcastle disease virus.
 XX
 PS Disclosure; Page 76; 115pp; English.
 XX
 CC This invention describes a novel avian-paramyxovirus cDNA (I) which
 CC comprises a nucleic acid sequence corresponding to the 5' terminal end of
 CC the genome of avian-paramyxovirus allowing the generation of an
 CC infectious copy of avian-paramyxovirus. The cell line is useful for the
 CC production of infectious lentogenic NDV (Newcastle Disease virus) without
 CC the addition of exogenous proteolytic activity. Also it is possible to
 CC generate a stable transfected cell line that expresses the wild-type F
 CC protein in the virus envelope therefore providing infectious particles,
 CC useful in the form of a vaccine, especially against respiratory and/or
 CC gastrointestinal diseases. NDV can be easily cultured to very high titers
 CC in embryonated eggs. Mass culture of embryonated eggs is relatively
 CC cheap. NDV vaccines are relatively stable and can be simply administered

CC by mass application methods e.g. drinking water or by spraying or by
CC aerosol formation. The natural route of infection is by the respiratory
CC and/or gastrointestinal tract which are also the major routes of
CC infection of many other poultry pathogens. NDV can induce local immunity
CC despite the presence of circulating maternal antibody. AAZ44527-244609
CC and AAZ44618-244650 represent primers used in the isolation of the NDV
CC strain LaSota genome
XX Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 830 CGGTGGTCTTACAGTGTG 847
Db 3 CGGAAGCTTCAGTGTG 20

RESULT 1924
AAC60815/C
ID AAC60816 standard; DNA; 20 BP.
XX AC AAC60816;
XX 07-FEB-2001 (first entry)
XX Human BRCA1 PCR primer SEQ ID NO:27.
XX Human; BRCA1; chromosome 17; 17q21; breast cancer; ovarian cancer;
KW gene therapy; diagnosis; cytostatic; genetic susceptibility; mutation;
KW polymorphism; identification; PCR primer; ss.
XX Homo sapiens.
OS US6130322-A.
XX 10-OCT-2000.
XX 06-MAY-1998; 98US-00074476.
XX 12-FEB-1996; 96US-00598591.
PR 12-DEC-1997; 97US-00798691.
XX (GENE-) GENE LOGIC INC.
XX Zeng B, Thurber D, Olson SJ, Alvares CP, Allen ACP, Murphy PD;
PI Critz BS;
XX WPI; 2000-646756/62.
XX New coding sequence of the human BRCA1 gene, i.e. BRCA1 (om12), useful in
PT gene therapy, especially for preventing or treating breast or ovarian
PT cancer, as well as for diagnosing or monitoring breast or ovarian cancer.
XX Example 1; Col 17-18; 56pp; English.

XX AAC60793 to AAC60795 encode the human BRCA1 (om11-3) proteins given in
CC AAB24217 to AAB24219 respectively. BRCA1 is found on chromosome 17
CC mapping to position 17q21. The BRCA1 (om12) coding sequence is
CC specifically claimed in the present invention. The BRCA1 (om12) coding
CC sequence is useful in gene therapy, especially for preventing or treating
CC breast or ovarian cancer. It is also useful for diagnosing or monitoring
CC breast or ovarian cancer. Furthermore, the BRCA1 (om12) coding sequence
CC is useful for: (a) identifying individuals having BRCA1 gene mutations
CC and having an increased genetic susceptibility to breast or ovarian
CC cancer, or identifying a mutation that increases the genetic
CC susceptibility to breast or ovarian cancer; (b) avoiding
CC misinterpretation of polymorphisms found in the BRCA1 gene; (c)
CC determining the presence of a previously unknown mutation in the BRCA1
CC gene; (d) probing a human sample of the BRCA1 gene by allele to determine
CC the presence of either polymorphic alleles or mutations; and (e)
CC performing diagnosis with a reagent derived from the BRCA1 (om1) cDNA

CC sequence. AAC60796 to AAC60861 represent PCR primers for the BRCA1 gene,
CC which are used in an example from the present invention
XX Sequence 20 BP; 6 A; 2 C; 7 G; 5 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 846 TGGCTCAGACTCCCTATC 863
Db 19 TGATTCAGACTCCCATC 2

RESULT 1925
AAC60539/C
ID AAC60539 standard; DNA; 20 BP.
XX AC AAC60539;
XX 31-JAN-2001 (first entry)
XX Human fra-1 mRNA antisense oligonucleotide ISIS 109030.
XX Human; fra-1; antisense oligonucleotide; phosphorothioate; cytostatic;
KW antinflammatory; 2'-methoxyethyl wing; 2'-MOE wing; infection; cancer;
KW ss.
XX Homo sapiens.
OS Synthetic.
XX US6124133-A.
XX 26-SEP-2000.
XX 15-OCT-1999; 99US-00418641.
XX 15-OCT-1999; 99US-00418641.
XX (ISIS-) ISIS PHARM INC.
XX Taylor JK, Cowsett LM;
XX WPI; 2000-601552/57.
XX Novel antisense compound 8-30 nucleobases in length targeted to human fra
PT -1 and which specifically hybridizes with and inhibits the expression of
PT human fra-1, useful for modulating the expression of fra-1 in cells.
XX Claim 3; Col 41; 38pp; English.

XX The present sequence is one of a large number of antisense
CC oligonucleotides which are targeted to nucleic acids encoding fra-1. The
CC sequences may be oligodeoxyribonucleotides or chimeric oligonucleotides,
CC containing a central gap region consisting of ten 2'-deoxynucleotides,
CC which is flanked on both sides by 2'-methoxyethyl (2'-MOE) wings. The
CC oligonucleotides have a phosphorothioate backbone and the cytidine
CC residues in the 2'-MOE wings are 5-methylcytidines. The fra-1 antisense
CC oligonucleotides are useful for inhibiting the expression of fra-1 in
CC human cells or tissues. They can be used for diagnostics, therapeutics,
CC prophylaxis and as research reagents and in kits. Use of the antisense
CC compounds may also be useful prophylactically, e.g. to prevent or delay
CC infection, inflammation or tumour formation
XX Sequence 20 BP; 0 A; 10 C; 5 G; 5 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1338 GGAGGGAGAGGGGGCGC 1355
Db 18 GGAGGGAAGAGGAGCGCG 1

RESULT 1926
 AAA90778
 ID AAA90778 standard; DNA; 20 BP.
 XX
 AC AAA90778;
 XX
 DT 20-DEC-2000 (first entry)
 XX
 DE Ribonucleotide reductase R1 message antisense oligo AS-I-658-20.
 XX
 KW Antisense oligonucleotide; ribonucleotide reductase; R1 protein;
 KW R2 protein; tumour cell proliferation inhibition; cancer; cytostatic; ss.
 XX
 OS Synthetic.
 XX
 XX WO200047733-A1.
 PN
 XX 17-AUG-2000.
 XX
 XX 09-FEB-2000; 2000WO-CA000120.
 PF
 XX
 XX 11-FEB-1999; 99US-00249730.
 PR
 XX (GENE-) GENESENSE TECHNOLOGIES INC.
 PA
 XX Wright JA, Young AH;
 PI
 PI WPI; 2000-558216/51.
 DR
 XX
 XX New antisense oligonucleotide, AS-I-618-20, is useful for inhibiting
 PT tumor cell growth.
 PT
 XX
 XX Example 3; Page 30; 137pp; English.
 PS
 XX
 CC The present sequence is an antisense oligonucleotide directed against the
 CC mRNA encoding the R1 component of mammalian ribonucleotide reductase.
 CC Ribonucleotide reductase catalyses the conversion of ribonucleotides to
 CC their corresponding deoxyribonucleotides and thus plays an important role
 CC in DNA synthesis and cell proliferation. Regulation of ribonucleotide
 CC reductase is altered in cultured malignant cells and increased levels of
 CC R2 protein and R2 mRNA have been found in pre-malignant and malignant
 CC tissues as compared to normal control tissue samples. The present
 CC antisense sequence is therefore useful for inhibiting tumorigenicity of
 CC neoplastic cells and inhibiting metastasis of tumour cells. It is also
 CC useful for increasing sensitivity of neoplastic cells to chemotherapeutic
 CC drugs, thus allowing chemotherapeutic treatments to be used in patients
 CC who have become resistant or less sensitive to chemotherapy. The sequence
 CC may be RNA or DNA and may comprise a modified backbone and/or nucleotide
 CC analogues
 XX
 SQ Sequence 20 BP; 3 A; 6 C; 2 G; 9 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1908 TCAGCCATTTTAGATTG 1925
 DB 3 TCAGCCATTTTCCATTG 20
 |||||
 RESULT 1927
 AAA90280
 ID AAA90280 standard; DNA; 20 BP.
 XX
 AC AAA90280;
 XX
 DT 19-DEC-2000 (first entry)
 XX
 DE Human GDF-8 antisense oligonucleotide 12.
 XX

KW GDF-8; growth differentiation factor-8; myostatin;
 KW human antisense oligonucleotide; expression inhibitor; cancer;
 KW muscle-associated disorder; muscular dystrophy; traumatic injury;
 KW spinal cord injury; congestive obstructive pulmonary disease; AIDS;
 KW cachexia; adipocyte proliferative disorder; obesity;
 KW glucose transport modulation; diabetes; ss.
 XX
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT misc_binding 1..20
 FT /*tag= a
 FT /bound_moiety= "Bases 523-542 of human GDF-8 cDNA
 FT (AAA90292)"
 XX
 PN WO200043781-A2.
 XX
 XX 27-JUL-2000.
 XX
 XX 21-JAN-2000; 2000WO-US001552.
 PF
 XX
 XX 21-JAN-1999; 99US-0116639P.
 PR
 XX 10-JUN-1999; 99US-0138363P.
 PR
 XX (META-) METAMORPHIX INC.
 PA
 XX Topouzis S, Wright JF, Ratovitski T, Liang L, Brady JL, Sinha D;
 PI Yaswen-Corkery L;
 PI
 XX WPI; 2000-505849/45.
 DR
 XX
 XX Novel method for identifying inhibitors of growth differentiation factor
 PT (GDF) proteins which used to treat a variety of diseases.
 PT
 XX
 PS Claim 46; Fig 22; 122pp; English.
 XX
 CC Sequences AAA90269-A90288 represent antisense oligonucleotides targeted
 CC to the human GDF-8 gene (cDNA shown in AAA90292), thus inhibiting GDF-8
 CC expression. The invention relates to inhibitors of GDFs, and methods of
 CC identifying such inhibitors. The GDF inhibitors of the invention
 CC encompass GDF-specific ribozymes (AAA90265- AAA90268 and AAA90294-
 CC A90297), GDF-8 antisense oligonucleotides (AAA90269-A90288), and GDF
 CC protein fragments or variants (AAB21078, AAB21082-B21083 and AAB21085-
 CC B21086). The methods are used to identify inhibitors of GDF proteins,
 CC especially GDF-8 (also known as myostatin) and GDF-11. The inhibitors can
 CC be used to modulate GDF-8 or GDF-11 activity or expression. They can be
 CC used to treat diseases or disorders characterised by aberrant expression
 CC of GDF-8 or GDF-11, such as muscle-associated disorders including cancer,
 CC muscular dystrophy, spinal cord injury, traumatic injury, congestive
 CC obstructive pulmonary disease, AIDS and cachexia, and may also be used to
 CC treat obesity and other disorders related to abnormal proliferation of
 CC adipocytes. They may also be used to treat diabetes via the modulation of
 CC glucose transport (e.g., by increasing the activity of the GLUT4 glucose
 CC transporter)
 XX
 SQ Sequence 20 BP; 4 A; 2 C; 5 G; 9 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1056 TCAGTACTTTGAATCTT 1073
 DB 3 TCAGTAGTTTGGATCTT 20
 |||||
 RESULT 1928
 AAA95328
 ID AAA95328 standard; DNA; 20 BP.
 XX
 AC AAA95328;
 XX
 XX 12-FEB-2001 (first entry)
 DT

XX DE B. cereus zwittermicin A coding sequence sequencing primer #12.
 XX KW Zwittermicin A; aminopolylol antibiotic; crop protection; phytopathogen;
 XX KW biocontrol agent; infectious disease; PCR primer; ss.
 XX OS Bacillus cereus.
 XX PN WO200058351-A2.
 XX XD 05-OCT-2000.
 XX XX 22-MAR-2000; 2000WO-US007570.
 XX PF 23-MAR-1999; 99US-0125769P.
 XX XX (WISC) WISCONSIN ALUMNI RES FOUND.
 XX PA Handelsman J, Milner JL, Stohl EA, Emmert EA;
 XX PI WPI; 2000-647222/62.
 XX DR Novel Bacillus cereus nucleic acid molecule useful for synthesis of
 XX XX zwittermicin A for protecting crops against phytopathogens.
 XX PT Example 1; Page 22; 80pp; English.
 XX PS The present invention describes the coding sequence for the enzymes from
 XX CC Bacillus cereus which form the zwittermicin A aminopolylol antibiotic.
 XX CC These enzymes are known as Orf1, Orf2, Orf3 and ZnaR. The antibiotic is
 XX CC useful in plants as a biocontrol agent as it help protect them from
 XX CC phytopathogens, which destroy crops. In addition, the coding sequence and
 XX CC proteins are useful for the treatment of human infectious diseases. The
 XX CC present sequence is a primer used to sequence the zwittermicin A genes
 XX SQ Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1123 AACACGATGAGTACCTG 1140
 |||||
 Db 3 AACACGGCATTAGTACCTG 20
 RESULT 1929
 AAC93193
 ID AAC93193 standard; DNA; 20 BP.
 XX AC AAC93193;
 XX XX 15-FEB-2001 (first entry)
 XX DE Human STAT3 phosphorothioate antisense oligonucleotide SEQ ID NO:44.
 XX KW Human; mouse; STAT3; phosphorothioate; antisense oligonucleotide;
 XX KW modulation; signal transducer and activator of transcription;
 XX KW DNA-binding protein; signal transduction; inhibition; apoptosis;
 XX KW inflammatory disease; cancer; antiinflammatory; antirheumatic;
 XX KW cytostatic; immunostimulatory; rheumatoid arthritis; leukaemia; myeloma;
 XX KW melanoma; lymphoma; diagnosis; ss.
 XX OS Homo sapiens.
 XX PN WO200061602-A1.
 XX XX 19-OCT-2000.
 XX PD 06-APR-2000; 2000WO-US009054.
 XX PF 08-APR-1999; 99US-00288461.
 XX PR (CNRS) CNRS CENT NAT RECH SCI.

PA (ISIS-) ISIS PHARM INC.
 XX Karas JG;
 XX PI WPI; 2000-619223/59.
 XX DR New antisense compound for inhibiting the expression of signal transducer
 XX PT and activator of transcription 3 (STAT3) in cells or tissues and treating
 XX PT diseases or condition associated with STAT3, such as rheumatoid arthritis
 XX PT and cancer.
 XX XX Example 2; Page 47; 104pp; English.
 XX PS The present invention describes an antisense compound (I), 8 to 30
 XX CC nucleobases in length, that is targeted to a nucleic acid molecule
 XX CC encoding STAT3 (Signal Transducer and Activator of Transcription) and
 XX CC which inhibits the expression of it. (I) has antiinflammatory,
 XX CC antirheumatic, cytostatic and immunostimulatory activities. (I) is used
 XX CC for inhibiting the expression of STAT3 in cells or tissues, treating an
 XX CC animal having a disease or condition associated with STAT3 or a human
 XX CC having a disease or condition characterised by a reduction in apoptosis,
 XX CC and inducing apoptosis in a cell. Diseases or conditions that are treated
 XX CC are rheumatoid arthritis, cancer of the breast, prostate, brain, head
 XX CC and/or neck, leukaemia, myeloma, melanoma or lymphoma. (I) can also be
 XX CC used for diagnostic methods in detecting and determining the role of
 XX CC STAT3 in various cell functions, physiological processes and conditions
 XX CC and for diagnosing the conditions associated with expression of STAT3.
 XX CC (I) can be used alone or with other drugs as an immunostimulator. (I) is
 XX CC used in sandwich and colourimetric assays, involving enzyme conjugation
 XX CC and radiolabeling and is used in diagnostic kits. AAC93150 encodes human
 XX CC STAT3 and AAC93231 encodes mouse STAT3 as given in the exemplification of
 XX CC the present invention. AAC93151 to AAC93230 and AAC93232 to AAC93299
 XX CC represent STAT3 phosphorothioate antisense oligonucleotides, and AAC93300
 XX CC represents a mismatch control oligonucleotide which are used in example
 XX CC from the present invention
 XX XX Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 497 CCGAGGCATCTGGCTTCT 514
 |||||
 Db 3 CCGAGGCATTGGCATCT 20
 RESULT 1930
 AAA66300
 ID AAA66300 standard; DNA; 20 BP.
 XX AC AAA66300;
 XX XX 09-OCT-2000 (first entry)
 XX DE Dog genomic marker oligonucleotide sequence SEQ ID NO:162.
 XX XX Dog; genome; genomic marker; radiation hybrid map; identification;
 XX KW chromosome location; gene marker; polymorphic microsatellite marker;
 XX KW phenotype; behaviour; pedigree; ss.
 XX OS Canis familiaris.
 XX PN WO200029615-A2.
 XX XX 25-MAY-2000.
 XX PD 15-NOV-1999; 99WO-IB001907.
 XX PF 13-NOV-1998; 98US-0108193P.
 XX PR (CNRS) CNRS CENT NAT RECH SCI.


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PI Galibert F, Andre C;
XX WPI; 2000-387821/33.
XX
XX New radiation hybrid map of the dog, Canine familiaris, genome, useful
XX for e.g. identifying genes implicated in phenotypic and behavioral traits
XX or in genetic diseases and for studying dog pedigrees.
XX
XX Claim 1; Page 60; 87pp; English.
XX
XX The present invention describes a radiation hybrid map of the dog (Canine
XX familiaris) genome comprising the genome location of a marker selected
XX from AAA66139 to AAA66942. The radiation hybrid map is useful for
XX identifying and localising dog genes, since it covers approximately 80 %
XX of the dog genome and provides a dense map integrating different types
XX (i.e. Type I and Type II) of markers. The map and the dog genome markers
XX (or complementary sequences) are especially useful to identify genes
XX responsible for phenotypic and behavioural traits in dogs, to identify
XX morbid genes, to analyse diseases and identify implicated genes in such
XX diseases and their alleles, and to study dog pedigrees. They may also be
XX useful for isolating corresponding human gene sequences e.g. genes
XX involved in genetic diseases
XX
XX Sequence 20 BP; 4 A; 3 C; 9 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1236 GGAGAGTGGCGATGAGGA 1253
DB ||||||| |||||
2 GGTGAGTGGCGATGATGA 19
RESULT 1931
AAA66357/C
ID AAA66357 standard; DNA; 20 BP.
XX
XX AAA66357;
XX
XX 09-OCT-2000 (first entry)
XX
XX Dog genomic marker oligonucleotide sequence SEQ ID NO:219.
XX
XX Dog; genome; Genomic marker; radiation hybrid map; identification;
XX chromosome location; gene marker; polymorphic microsatellite marker;
XX phenotype; behaviour; pedigree; ss.
XX
XX Canis familiaris.
XX
XX WO200029615-A2.
XX
XX 25-MAY-2000.
XX
XX 15-NOV-1999; 99WO-IB001907.
XX
XX 13-NOV-1998; 98US-0108193P.
XX
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Galibert F, Andre C;
XX
XX WPI; 2000-387821/33.
XX
XX New radiation hybrid map of the dog, Canine familiaris, genome, useful
XX for e.g. identifying genes implicated in phenotypic and behavioral traits
XX or in genetic diseases and for studying dog pedigrees.
XX
XX Claim 1; Page 62; 87pp; English.
XX
XX The present invention describes a radiation hybrid map of the dog (Canine
XX familiaris) genome comprising the genome location of a marker selected
XX from AAA66139 to AAA66942. The radiation hybrid map is useful for
XX identifying and localising dog genes, since it covers approximately 80 %
XX of the dog genome and provides a dense map integrating different types
XX (i.e. Type I and Type II) of markers. The map and the dog genome markers
XX (or complementary sequences) are especially useful to identify genes
XX responsible for phenotypic and behavioural traits in dogs, to identify
XX morbid genes, to analyse diseases and identify implicated genes in such
XX diseases and their alleles, and to study dog pedigrees. They may also be
XX useful for isolating corresponding human gene sequences e.g. genes
XX involved in genetic diseases
XX
XX Sequence 20 BP; 4 A; 3 C; 9 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1236 GGAGAGTGGCGATGAGGA 1253
DB ||||||| |||||
2 GGTGAGTGGCGATGATGA 19
RESULT 1931
AAA66357/C
ID AAA66357 standard; DNA; 20 BP.
XX
XX AAA66357;
XX
XX 09-OCT-2000 (first entry)
XX
XX Dog genomic marker oligonucleotide sequence SEQ ID NO:219.
XX
XX Dog; genome; Genomic marker; radiation hybrid map; identification;
XX chromosome location; gene marker; polymorphic microsatellite marker;
XX phenotype; behaviour; pedigree; ss.
XX
XX Canis familiaris.
XX
XX WO200029615-A2.
XX
XX 25-MAY-2000.
XX
XX 15-NOV-1999; 99WO-IB001907.
XX
XX 13-NOV-1998; 98US-0108193P.
XX
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Galibert F, Andre C;
XX
XX WPI; 2000-387821/33.
XX
XX New radiation hybrid map of the dog, Canine familiaris, genome, useful
XX for e.g. identifying genes implicated in phenotypic and behavioral traits
XX or in genetic diseases and for studying dog pedigrees.
XX
XX Claim 1; Page 60; 87pp; English.
XX
XX The present invention describes a radiation hybrid map of the dog (Canine
XX familiaris) genome comprising the genome location of a marker selected
XX from AAA66139 to AAA66942. The radiation hybrid map is useful for
XX identifying and localising dog genes, since it covers approximately 80 %
XX of the dog genome and provides a dense map integrating different types
XX (i.e. Type I and Type II) of markers. The map and the dog genome markers
XX (or complementary sequences) are especially useful to identify genes
XX responsible for phenotypic and behavioural traits in dogs, to identify
XX morbid genes, to analyse diseases and identify implicated genes in such
XX diseases and their alleles, and to study dog pedigrees. They may also be
XX useful for isolating corresponding human gene sequences e.g. genes
XX involved in genetic diseases
XX
XX Sequence 20 BP; 4 A; 3 C; 9 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1793 CTGAATGCCCAAGTGCT 1810
DB ||||||| |||||
18 CAGAACTCCCAAGTGCT 1
RESULT 1932
AAA74169
ID AAA74169 standard; DNA; 20 BP.
XX
XX AAA74169;
XX
XX 29-NOV-2000 (first entry)
XX
XX Forward PCR primer for loblolly pine locus RIPPT1013.
XX
XX PCR primer; loblolly pine; Simple Sequence Repeat; SSR;
XX microsatellite DNA repeat; genetic marker; mapping; inheritance study;
XX population genetics study; plant breeding programme; ss.
XX
XX Pinus taeda.
XX
XX WO200042210-A2.
XX
XX 20-JUL-2000.
XX
XX 06-JAN-2000; 2000WO-US000325.
XX
XX 15-JAN-1999; 99US-00232884.
XX
XX 13-JAN-1999; 99US-00232785.
XX
XX (INTO ) INT PAPER CO.
XX (ECHT/) ECHT C S.
XX (NELS/) NELSON C D.
XX (USDA ) US SEC OF AGRIC.
XX
XX Echt CS, Nelson CD;
XX
XX WPI; 2000-482836/42.
XX
XX Polynucleotide having simple sequence repeat useful as markers in plants
XX for genetic characterization e.g. genetic mapping study, an inheritance
XX study of a commercially important trait in a plant breeding program.
XX
XX Claim 6; Page 24; 57pp; English.
XX
XX The present invention relates to loblolly pine polynucleotides with one
XX or more Simple Sequence Repeats (SSRs) (see AAA74205-A74322). SSRs are
XX also known as microsatellite DNA repeats. The SSRs are useful as genetic
XX markers for genetic mapping, population genetics studies and inheritance
XX studies in various plant breeding programmes. The present sequence is a
XX PCR primer used for detecting the presence of a SSR locus in a pine
XX genomic DNA sample
XX
XX Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX
QY 1793 CTGAATGCCCAAGTGCT 1810
DB ||||||| |||||
18 CAGAACTCCCAAGTGCT 1
RESULT 1932
AAA74169
ID AAA74169 standard; DNA; 20 BP.
XX
XX AAA74169;
XX
XX 29-NOV-2000 (first entry)
XX
XX Forward PCR primer for loblolly pine locus RIPPT1013.
XX
XX PCR primer; loblolly pine; Simple Sequence Repeat; SSR;
XX microsatellite DNA repeat; genetic marker; mapping; inheritance study;
XX population genetics study; plant breeding programme; ss.
XX
XX Pinus taeda.
XX
XX WO200042210-A2.
XX
XX 20-JUL-2000.
XX
XX 06-JAN-2000; 2000WO-US000325.
XX
XX 15-JAN-1999; 99US-00232884.
XX
XX 13-JAN-1999; 99US-00232785.
XX
XX (INTO ) INT PAPER CO.
XX (ECHT/) ECHT C S.
XX (NELS/) NELSON C D.
XX (USDA ) US SEC OF AGRIC.
XX
XX Echt CS, Nelson CD;
XX
XX WPI; 2000-482836/42.
XX
XX Polynucleotide having simple sequence repeat useful as markers in plants
XX for genetic characterization e.g. genetic mapping study, an inheritance
XX study of a commercially important trait in a plant breeding program.
XX
XX Claim 6; Page 24; 57pp; English.
XX
XX The present invention relates to loblolly pine polynucleotides with one
XX or more Simple Sequence Repeats (SSRs) (see AAA74205-A74322). SSRs are
XX also known as microsatellite DNA repeats. The SSRs are useful as genetic
XX markers for genetic mapping, population genetics studies and inheritance
XX studies in various plant breeding programmes. The present sequence is a
XX PCR primer used for detecting the presence of a SSR locus in a pine
XX genomic DNA sample
XX
XX Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX
QY 1793 CTGAATGCCCAAGTGCT 1810
DB ||||||| |||||
18 CAGAACTCCCAAGTGCT 1

```

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1305 TGCTGTGAGGAGAGTT 1322
| | | | | | | | | |
Db 2 TCCTGTGGGATGAGTT 19

RESULT 1933
AAA74106/c
ID AAA74106 standard; DNA; 20 BP.
XX
AC AAA74106;
XX
DT 29-NOV-2000 (first entry)
XX
DE Reverse PCR primer for loblolly pine locus RIPPT649.
XX
KW PCR primer; loblolly pine; Simple Sequence Repeat; SSR;
KW microsatellite DNA repeat; genetic marker; mapping; inheritance study;
KW population genetics study; plant breeding programme; ss.
XX
OS Pinus taeda.
XX
PN WO200042210-A2.
XX
PD 20-JUL-2000.
XX
PF 06-JAN-2000; 2000WO-US000325.
XX
PR 15-JAN-1999; 99US-00232884.
PR 19-JAN-1999; 99US-00232785.
XX
PA (INTO) INT PAPER CO.
PA (ECHT/) ECHT C S.
PA (NELS/) NELSON C D.
PA (USDA) US SEC OF AGRIC.
XX
PI Echt CS, Nelson CD;
XX
DR WPI; 2000-482836/42.
XX
PT Polynucleotide having simple sequence repeat useful as markers in plants
PT for genetic characterization e.g. genetic mapping study, an inheritance
PT study of a commercially important trait in a plant breeding program.
XX
PS Claim 6; Page 23; 57pp; English.
XX
CC The present invention relates to loblolly pine polynucleotides with one
CC or more Simple Sequence Repeats (SSRs) (see AAA74205-A74322). SSRs are
CC also known as microsatellite DNA repeats. The SSRs are useful as genetic
CC markers for genetic mapping, population genetics studies and inheritance
CC studies in various plant breeding programmes. The present sequence is a
CC PCR primer used for detecting the presence of a SSR locus in a pine
CC genomic DNA sample
XX
SQ Sequence 20 BP; 1 A; 7 C; 3 G; 9 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1413 GAAGACCCAGAGGAGAA 1430
| | | | | | | | | |
Db 19 GAAGGACACAGAGGAGCA 2

RESULT 1934
AAC80262
ID AAC80262 standard; DNA; 20 BP.
XX
AC AAC80262;
XX
DT 03-MAY-2001 (first entry)

XX DE Reverse primer #90 used for amplification of HLA-A exon 3.
XX
KW HLA-A; HLA-B; HLA-C; typing; primer; human; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200061795-A2.
XX
PD 19-OCT-2000.
XX
PF 05-APR-2000; 2000WO-EP002998.
XX
PR 09-APR-1999; 99EP-00870068.
PR 11-JUN-1999; 99US-0138614P.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Canck I, Rombout A, Rossau R;
XX
DR WPI; 2000-647426/62.
XX
PT Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4
PT of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using defined
PT primer sets, useful for subtyping or typing of HLA Class I alleles.
XX
PS Claim 4; Page 40; 128pp; English.
XX
CC The present invention relates to a method for the locus-specific,
CC separate amplification of exon 2, exon 3, and/or exon 4 of human
CC leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful
CC for subtyping or typing of HLA class I alleles. The present sequence is
CC an amplification primer used in the method
XX
SQ Sequence 20 BP; 4 A; 1 C; 8 G; 6 T; 0 U; 1 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2012 GGAGTGTCTAGTCTAGTT 2031
| | | | | | | | | |
Db 1 GGAGGCGATATTTCTAGTGT 20

RESULT 1935
AAF33179/c
ID AAF33179 standard; DNA; 20 BP.
XX
AC AAF33179;
XX
DT 23-MAR-2001 (first entry)
XX
DE Human B7-2 antisense oligonucleotide SEQ ID NO: 262.
XX
KW Human; mouse; B7-1; B7-2; antisense; PCR primer; inflammation;
KW autoimmune disorder; phosphorothioate backbone; ss.
XX
OS Homo sapiens.
XX
PN WO200074687-A1.
XX
PD 14-DEC-2000.
XX
PF 25-MAY-2000; 2000WO-US014471.
XX
PR 04-JUN-1999; 99US-00326186.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Vickers TA, Karras JG;
XX

CC nitric oxide synthase and which specifically hybridise to and modulate
CC expression of inducible nitric oxide synthase. The antisense compounds
CC have immunomodulator, antidiabetic, cardiovascular, cardiac,
CC neuroprotective, disorder and vasotrophic activity. The antisense
CC oligonucleotides are useful for inhibiting the expression of inducible
CC nitric oxide synthase in cells or tissues. In particular, the antisense
CC oligonucleotides are useful for treating diseases or disorders associated
CC with inducible nitric oxide synthase, e.g. diabetes, immunological
CC disorder, cardiovascular disorder, neurological disorder or
CC ischaemia/reperfusion injury. The antisense oligonucleotides are also
CC useful for research and diagnostics. The present sequence is that of an
CC antisense 2'-O-methoxyethyl gapper oligonucleotide with a
CC phosphorothioate backbone, a central "gap" region of ten nucleotides
CC flanked by five nucleotide 2'-MOE (2'-methoxyethyl) wings and 5-
CC methylcytidine residues throughout the oligonucleotide. The antisense
CC oligonucleotide is targeted to mouse inducible nitric oxide synthase (NOS)
CC mRNA (AAH47974)
XX
XX
SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 817 TTCCAGCCTAGTGGGTG 834
Db 2 TTCCAGCCTAGTGGATG 19
|||||
|||||

RESULT 1938
AAH73455
ID AAH73455 standard; DNA; 20 BP.
XX
AC AAH73455;
XX
DT 09-OCT-2001 (first entry)
XX
DE Brevibacillus borstelensis BCS-1 16S rDNA PCR primer #2.
XX
KW Brevibacillus borstelensis BCS-1; 16S rDNA; D-amino acid production;
KW thermophile; amidase; PCR primer; 88.
XX
OS Brevibacillus borstelensis.
XX
PN WO200157197-A1.
XX
PD 09-AUG-2001.
XX
PF 27-JUN-2000; 2000WO-KR000673.
XX
PR 03-FEB-2000; 2000KR-00005514.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Sung M, Lee S, Baek D, Kwon S, Hong S, Kwak M, Yoon K;
XX
DR WPI; 2001-483432/52.
XX
PT Thermophile Brevibacillus borstelensis BCS-1 or producing D-amino-acids
PT from amides containing D,L-amino acids.
XX
PS Example 1; Page 28; 30pp; English.
XX
CC The present invention provides the thermophilic bacterium Brevibacillus
CC borstelensis BCS-1. The organism can be used to produce D-amino acids,
CC using the D-stereospecific amino acid amidase. The present sequence is a
CC PCR primer used to amplify the 16S rDNA from the bacterium
XX
XX
SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 817 TTCCAGCCTAGTGGGTG 834
Db 2 TTCCAGCCTAGTGGATG 19
|||||
|||||

RESULT 1938
AAH73455
ID AAH73455 standard; DNA; 20 BP.
XX
AC AAH73455;
XX
DT 09-OCT-2001 (first entry)
XX
DE Brevibacillus borstelensis BCS-1 16S rDNA PCR primer #2.
XX
KW Brevibacillus borstelensis BCS-1; 16S rDNA; D-amino acid production;
KW thermophile; amidase; PCR primer; 88.
XX
OS Brevibacillus borstelensis.
XX
PN WO200157197-A1.
XX
PD 09-AUG-2001.
XX
PF 27-JUN-2000; 2000WO-KR000673.
XX
PR 03-FEB-2000; 2000KR-00005514.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Sung M, Lee S, Baek D, Kwon S, Hong S, Kwak M, Yoon K;
XX
DR WPI; 2001-483432/52.
XX
PT Thermophile Brevibacillus borstelensis BCS-1 or producing D-amino-acids
PT from amides containing D,L-amino acids.
XX
PS Example 1; Page 28; 30pp; English.
XX
CC The present invention provides the thermophilic bacterium Brevibacillus
CC borstelensis BCS-1. The organism can be used to produce D-amino acids,
CC using the D-stereospecific amino acid amidase. The present sequence is a
CC PCR primer used to amplify the 16S rDNA from the bacterium
XX
XX
SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 807 AATGGAGATGTTCCAGCC 824
Db 3 AAAGGAGGTGATCCAGCC 20
|||||
|||||

RESULT 1939
AAK95034/c
ID AAK95034 standard; DNA; 20 BP.
XX
AC AAK95034;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human cDNA clone-specific primer, SEQ ID NO: 4279.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-00114089.
XX
PR 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX
PS Example 18; Page 129; 1380pp + Sequence Listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesising the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a primer used to amplify a human cDNA
CC clone provided in the invention
XX
SQ Sequence 20 BP; 7 A; 1 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1519 CTCTCCAGCTCTGGCTTC 1536
Db 18 CTCTCAAGCTCTACCTTC 1
|||||
|||||

RESULT 1940
AAK95207/c
ID AAK95207 standard; DNA; 20 BP.
XX
AC AAK95207;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human cDNA clone-specific primer, SEQ ID NO: 4452.
XX
KW Human cDNA clone-specific primer, SEQ ID NO: 4452.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-00114089.
XX
PR 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX
PS Example 18; Page 129; 1380pp + Sequence Listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesising the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a primer used to amplify a human cDNA
CC clone provided in the invention
XX
SQ Sequence 20 BP; 7 A; 1 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

XX Human; full length cDNA; cDNA synthesis; oligo-capping; PCR primer; ss.
XX Homo sapiens.
XX PF1130094-A2.
XX 05-SEP-2001.
XX 07-JUL-2000; 2000EP-00114089.
XX 08-JUL-1999; 99JP-00194486.
XX 11-JAN-2000; 2000JP-00118774.
XX 02-MAY-2000; 2000JP-00183765.
XX (HELI-) HELIX RES INST.
XX Oka T, Nishikawa T, Isoqai T, Hayashi K, Ishii S, Kawai Y;
XX Makamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2001-524255/58.
XX DR
XX PT 830 Primers useful for synthesizing full length cDNA clones and their use
XX in genetic manipulation.
XX PS Example 18; Page 133; 1380pp + Sequence Listing; English.
XX CC The invention relates to primers for synthesising full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been isolated
XX and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
XX been determined. Primers for synthesising the full length cDNA are useful
XX for clarifying the function of the protein encoded by the cDNA. The full
XX length clones were obtained by construction of full length enriched cDNA
XX libraries that were synthesised by the oligo-capping method. The primers
XX enable the production of the full length cDNA easily without any special
XX methods. The present sequence is a primer used to amplify a human cDNA
XX clone provided in the invention
XX SQ Sequence 20 BP; 2 A; 4 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1456 ACCAAGGAGGAGGACCA 1473
DB 20 ACCAAGGAGGAGGACCA 3

RESULT 1941
AAAF73060
ID AAFA73060 standard; DNA; 20 BP.
XX
XX AAFA73060;
AC
XX
XX 24-APR-2001 (first entry)
XX
XX Human daxx inhibitory antisense phosphorothioate oligonucleotide SEQ.161.
XX Antisense oligonucleotide; daxx; inhibition; phosphorothioate;
XX Fas binding protein; CENP-C binding protein; dap6; BAP; cytosstatic;
XX antiinflammatory; death associated protein 6; Ets-1 associated protein;
XX infection; inflammation; tumour formation; ss.
XX Homo sapiens.
XX US6180353-B1.
XX 30-JAN-2001.
XX 24-JAN-2000; 2000US-00490692.
XX 24-JAN-2000; 2000US-00490692.
XX PR

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XX PA (ISIS-) ISIS PHARM INC.
XX FI Dean NM, Cowsert LM;
XX DR WPI; 2001-217744/22.
XX PT Novel antisense compounds capable of modulating expression of daxx useful
XX for diagnosis, prophylaxis and treatment of diseases associated with
XX expression of daxx.
XX Claim 1; Col 49; 59pp; English.
XX CC The present invention describes an antisense compound (I) up to 30
XX nucleobases in length, where (I) inhibits expression of daxx (also known
XX as Fas binding protein, CENP-C binding protein, dap6 for death associated
XX protein 6 and BAP for Ets-1 associated protein). (I) has cytosstatic and
XX antiinflammatory activity, and can be used in antisense therapy and as a
XX modulator of daxx. (I) is useful for inhibiting the expression of daxx in
XX cells or tissues in vitro. (I) can be utilised for diagnostics,
XX therapeutics for the treatment of diseases associated with the expression
XX of daxx, prophylaxis e.g. to prevent or delay infection, inflammation or
XX tumour formation and as research reagent. The present sequence represents
XX an inhibitory human daxx antisense phosphorothioate oligonucleotide which
XX is used in the exemplification of the present invention
XX SQ Sequence 20 BP; 1 A; 7 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1982 CTCTGTCGTCCTCTCTCT 1999
DB 3 CTCTGTCGTCCTCTCTCT 20

RESULT 1942
AAS45816/c
ID AAS45816 standard; DNA; 20 BP.
XX
XX AAS45816;
AC
XX 18-DEC-2001 (first entry)
XX
XX Mouse PARP-2 antisense inhibitor ISIS #110282.
XX Mouse; ss; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide;
XX cytosstatic; neurotropic; neuroprotective; antiinflammatory; antidiabetic;
XX immunosuppressant; hyperproliferative disorder; cancer; cellular injury;
XX oxidative stress; neurological disorder; parkinsonism; apoptosis;
XX meningitis-associated intracranial complication; ischaemia; probe;
XX inflammatory disorder; autoimmune disorder; arthritis; diabetes.
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone"
XX modified_base 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "All cytidine residues are 5-methyl cytidine"
XX modified_base 1..5
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl nucleotides"
XX modified_base 16..20
XX /tag= d
XX /mod_base= OTHER
XX /note= "2' methoxyethyl nucleotides"
XX FT

```

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XX WO200164955-A1.
XX
XX PD
XX
XX 07-SEP-2001.
XX
XX 01-MAR-2001; 2001WO-US006572.
XX
XX 02-MAR-2000; 2000US-00517467.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Popoff I, Cowsert LM;
XX
XX WPI; 2001-602570/68.
XX
XX Antisense compound useful for treating hyperproliferative, neurological,
XX inflammatory and autoimmune disorders and diabetes inhibits human PARP.
XX
XX Example 17; Page 89; 168pp; English.
XX
XX The invention relates to antisense oligonucleotides targeted to human
XX PARP nucleic acid and inhibiting expression of human PARP. PARP (Poly
XX (ADP-ribose) polymerase plays an important role in chromatin
XX decondensation, DNA replication, DNA repair, gene expression, malignant
XX transformation, cellular differentiation and apoptosis. The antisense
XX oligonucleotide inhibitors are useful for inhibiting the expression of
XX PARP in human cells or tissues. They are also useful for treating a human
XX with a disease associated with PARP especially hyperproliferative
XX disorders (e.g. cancer), cellular injury resulting from oxidative stress,
XX neurological (e.g. parkinsonism, meningitis-associated intracranial
XX complications and ischaemia), inflammatory and autoimmune disorders (e.g
XX arthritis) and diabetes. The present sequence is an antisense
XX oligonucleotide of the invention
XX
XX Sequence 20 BP; 2 A; 8 C; 3 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 607 GCGTGGAGAGGCTTC 624
XX ||| ||| ||| ||| ||| ||| |||
XX Db 19 GGGGAGAAAGAGGCTTC 2
XX
XX RESULT 1943
XX AAC81346/C
XX ID AAC81346 standard; DNA; 20 BP.
XX
XX AC AAC81346;
XX
XX 23-FEB-2001 (first entry)
XX
XX Human Y-box binding protein 1 antisense oligonucleotide, SEQ ID NO:30.
XX
XX Human Y-box binding protein 1; YB-1; DNA binding protein B; dbpB;
XX transcription factor; nucleic acid binding; DNA repair;
XX cell sensitisation; genotoxic stress; immune regulation; MHC expression;
XX viral gene expression; extracellular matrix degradation regulator;
XX redox signalling; expression inhibition; tumour formation;
XX cancer multidrug resistance; inflammation; immune disorder; infection;
XX phosphorothioate; antisense oligonucleotide; ss.
XX
XX Homo sapiens.
XX
XX OS
XX US6140126-A.
XX
XX PN
XX
XX 31-OCT-2000.
XX
XX PD
XX
XX 26-OCT-1999; 99US-00429323.
XX
XX PF
XX
XX 26-OCT-1999; 99US-00429323.
XX
XX PR
XX

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PA (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Cowsert LM;
XX
XX WPI; 2001-023284/03.
XX
XX Antisense oligonucleotides, useful for modulating the expression of Y-box
XX binding protein 1, as well as for treating or preventing diseases
XX associated with Y-box binding protein 1 expression, e.g. inflammation or
XX tumor formation.
XX
XX Example 15; Col 43-44; 40pp; English.
XX
XX Sequences AAC81326-C81405 represent antisense oligonucleotides targeted
XX to the human Y-box binding protein 1 gene, which inhibit its expression.
XX The antisense oligonucleotides were designed to target different regions
XX of the human Y-box binding protein 1 mRNA, and were analysed for their
XX effect on Y-box binding protein 1 mRNA levels by quantitative real-time
XX PCR. Human Y-box binding protein 1 (also known as YB-1, DNA binding
XX protein B and dbpB) is a member of the Y-box binding protein family of
XX transcription factors, a highly conserved family of nucleic acid binding
XX proteins which bind to the Y-box, an inverted CCAAT sequence found in the
XX promoters of many genes. Y box binding proteins have a broad specificity
XX for nucleic acids, being able to bind double- stranded DNA, damaged DNA,
XX and single-stranded DNA and RNA. Y-box binding protein 1 plays a role in
XX DNA repair and the sensitisation of cells from a diverse array of
XX genotoxic stresses, including DNA cross- linking agents and ultraviolet
XX irradiation. Y-box binding protein 1 is also involved in immune
XX regulation, being a negative regulator of MHC (major histocompatibility
XX complex) gene expression, and additionally modulates viral gene
XX expression. It also participates in the regulation of extracellular
XX matrix degradation, and is thought to be involved in redox signalling.
XX The oligonucleotides of the invention are useful for diagnosis,
XX prevention and treatment of conditions associated with Y-box binding
XX protein 1 expression, such as tumour formation, cancer multidrug
XX resistance, inflammation, immune disorders and certain infections
XX
XX Sequence 20 BP; 1 A; 13 C; 5 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 GAGCGGAGCCCGGCGG 18
XX ||||| ||| ||| ||| |||
XX Db 18 GAGCGGTGGCCCGGCGG 1
XX
XX RESULT 1944
XX AAC92790
XX ID AAC92790 standard; DNA; 20 BP.
XX
XX AC AAC92790;
XX
XX 27-MAR-2001 (first entry)
XX
XX Human hnRNP A1 phosphorothioate antisense oligonucleotide, SEQ ID NO:62.
XX
XX Human hnRNP A1; heterogeneous nuclear ribonucleoprotein A1;
XX heterogeneous nuclear ribonucleoprotein core protein A1; p40CRS;
XX mRNA processing; transport; stabilisation; alternative splicing;
XX donor splice site selection; telomere biogenesis; oncogenesis;
XX apoptosis-associated protein; cancer; tumour formation;
XX expression inhibition; phosphorothioate; antisense oligonucleotide; ss.
XX
XX OS
XX Homo sapiens.
XX
XX PN
XX
XX US6165789-A.
XX
XX PD
XX
XX 26-DEC-2000.
XX
XX PF
XX
XX 27-OCT-1999; 99US-00428696.
XX
XX

```


CC product associated with endometriosis. The method comprises comparing the
 CC pattern of gene expression in a diseased endometrium tissue from a
 CC patient suffering from endometriosis to the pattern of gene expression in
 CC healthy endometrium tissue from the same patient, and selecting a gene
 CC whose level of expression differs between healthy and diseased tissues.
 CC the gene, gene product and their antagonists and agonists are useful in
 CC the manufacture of a medicament for diagnosing or treating endometriosis.
 CC The method is useful for screening genes or gene products that are
 CC implicated in endometriosis. It is particularly useful in diagnosing
 CC endometriosis, as well as for screening for agents for treating
 CC endometriosis. Prior methods of diagnosing endometriosis are more
 CC difficult to perform and are more expensive, normally involving surgery.
 CC The present method allows the disease to be diagnosed and treated at
 CC earlier stage. The present sequence is a primer used in a reverse
 CC transcription polymerase chain reaction (RT-PCR) procedure to validate
 CC the results of differential gene expression studies. It was used to
 CC amplify human endometrium cDNA encoding immunoglobulin lambda
 CC
 XX Sequence 20 BP; 9 A; 8 C; 1 G; 2 T; 0 U; 0 Other;
 SQ

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 376 GGCTGTTGAGTTCTGT 393
 ||| ||| ||| ||| ||| |||
 Db 18 GGCATGTGTGAGTTTGT 1

RESULT 1947
 AAH56775
 ID AAH56775 standard; DNA; 20 BP.
 AC AAH56775;
 DT 06-SEP-2001 (first entry)
 DE S. aureus groE operon antisense oligonucleotide SEQ ID NO:423.
 KW Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth;
 KW microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;
 KW Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;
 KW antibacterial; antiviral; antiproliferative; antisense therapy;
 KW microbial infection; ss.
 OS Staphylococcus aureus.
 PN WO200136625-A2.
 XX 25-MAY-2001.
 XX 20-NOV-2000; 2000WO-CA001347.
 PF 18-NOV-1999; 99US-0166249P.
 PR (GENE-) GENESENSE TECHNOLOGIES INC.
 PA Wright JA, Young AH, Dugourd D;
 PI WPI; 2001-355633/37.
 DR Novel antisense compounds targeting nucleic acid encoding groEL or groES
 XX gene of microorganism, which hybridize with and inhibit expression of the
 PT genes, useful to inhibit growth of microorganism having the genes.
 PS Claim 3; Page 52; 110pp; English.
 CC The present invention specifically claims AAH56368 to AAH56832 which are
 CC antisense oligonucleotides to nucleotide sequences encoding groE. More
 CC generally, antisense compounds (I) comprising antisense oligonucleotides
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat
 CC shock protein (HSP60) (GL) and groES (HSP10) (GS) gene from a
 CC microorganism, where the antisense compound is complementary to GL or GS

CC of a microorganism and specifically hybridizes with and inhibits the
 CC expression of GL or GS, is claimed (I) have antibacterial, antiviral and
 CC antiproliferative activities, and can be used in antisense therapy and
 CC for inhibition of expression of groES or groEL. (I) are useful for
 CC inhibiting expression of GL or GS in cells or tissues in vitro. (I) are
 CC also useful for inhibiting the growth of a microorganism, or inhibiting
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or a
 CC virus) having a GL or GS gene which involves administering to the
 CC microorganism or to a cell infected with the microorganism, (I). (I) are
 CC also useful for treating a mammalian pathological condition mediated by
 CC the microorganisms which involves identifying a eukaryotic organism
 CC having a pathological condition mediated by microorganisms having a GL or
 CC GS gene and administering (I) such that the growth of microorganism is
 CC inhibited. The antisense compounds are utilized for diagnostics,
 CC therapeutics, prophylaxis and as research reagents and kits, e.g., to
 CC prevent or delay microbial infections in humans. They are also useful as
 CC molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854
 CC represent PCR primers for groE sequences which are used in the
 CC exemplification of the present invention. AAH56855 to AAH56870 represent
 CC groE nucleotide sequence given in the present invention
 CC
 XX Sequence 20 BP; 5 A; 2 C; 2 G; 11 T; 0 U; 0 Other;
 SQ

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2046 TATTTTCATTTTGTGAG 2063
 ||| ||| ||| ||| ||| |||
 Db 2 TATTTTCACCTTTTGTGAG 19

RESULT 1948
 AAH56774
 ID AAH56774 standard; DNA; 20 BP.
 AC AAH56774;
 XX 06-SEP-2001 (first entry)
 DE S. aureus groE operon antisense oligonucleotide SEQ ID NO:422.
 KW Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth;
 KW microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;
 KW Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;
 KW antibacterial; antiviral; antiproliferative; antisense therapy;
 KW microbial infection; ss.
 OS Staphylococcus aureus.
 PN WO200136625-A2.
 XX 25-MAY-2001.
 XX 20-NOV-2000; 2000WO-CA001347.
 PF 18-NOV-1999; 99US-0166249P.
 PR (GENE-) GENESENSE TECHNOLOGIES INC.
 PA Wright JA, Young AH, Dugourd D;
 PI WPI; 2001-355633/37.
 DR Novel antisense compounds targeting nucleic acid encoding groEL or groES
 XX gene of microorganism, which hybridize with and inhibit expression of the
 PT genes, useful to inhibit growth of microorganism having the genes.
 PS Claim 3; Page 52; 110pp; English.
 CC The present invention specifically claims AAH56368 to AAH56832 which are
 CC antisense oligonucleotides to nucleotide sequences encoding groE. More
 CC generally, antisense compounds (I) comprising antisense oligonucleotides
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat
 CC shock protein (HSP60) (GL) and groES (HSP10) (GS) gene from a
 CC microorganism, where the antisense compound is complementary to GL or GS

CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat
 CC shock protein (HSP)60) (GL) and groES (HSP)10) (GS) gene from a
 CC microorganism, where the antisense compound is complementary to GL or GS
 CC of a microorganism and specifically hybridises with and inhibits the
 CC expression of GL or GS, is claimed. (I) have antibacterial, antiviral and
 CC antiproliferative activities, and can be used in antisense therapy and
 CC for inhibition of expression of groES or groEL. (I) are useful for
 CC inhibiting expression of GL or GS in cells or tissues in vitro. (I) are
 CC also useful for inhibiting the growth of a microorganism, or inhibiting
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or a
 CC virus) having a GL or GS gene which involves administering to the
 CC microorganism or to a cell infected with the microorganism, (I). (I) are
 CC also useful for treating a mammalian pathological condition mediated by
 CC the microorganisms which involves identifying a eukaryotic organism
 CC having a pathological condition mediated by microorganisms having a GL or
 CC GS gene and administering (I) such that the growth of microorganism is
 CC inhibited. The antisense compounds are utilised for diagnostics,
 CC therapeutics, prophylaxis and as research reagents and kits, e.g., to
 CC prevent or delay microbial infections in humans. They are also useful as
 CC molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854
 CC represent PCR primers for groE sequences which are used in the
 CC exemplification of the present invention. AAH56855 to AAH56870 represent
 CC groE nucleotide sequence given in the present invention

XX Sequence 20 BP; 6 A; 2 C; 2 G; 10 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2046 TATTTTCATTTTTGTCAG 2063
 ||||| |||||
 Db 1 TATTTTCAACTTTTGAG 18

RESULT 1949
 AAF80861/c
 ID AAF80861 standard; DNA; 20 BP.
 XX AAF80861;
 XX
 DT 02-MAY-2001 (first entry)
 XX Human mdm2 phosphorothioate oligonucleotide #235.
 DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 KW Homo sapiens.
 XX

US6184212-B1.
 PD 06-FEB-2001.
 XX 26-MAR-1999; 99US-00280805.
 PF 26-MAR-1998; 98US-00048810.
 PR (ISIS-) ISIS PHARM INC.
 XX

PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsett LM;
 XX WPI; 2001-190948/19.
 DR

PT Novel antisense compound 8-30 nucleobases in length targeted to a nucleic
 PT acid molecule encoding human mdm-2 useful for modulating the expression
 PT of human mdm-2 and reducing hyperproliferation of human cells.

XX Example 9; Col 31; 77pp; English.

XX The present invention relates to an antisense compound 8-30 nucleobases
 CC in length targeted to nucleobases 1-308 of the 5' untranslated region,
 CC 1776-1806 of the translation termination codon region or 1818-2370 of the
 CC 3' untranslated region of a nucleic acid molecule encoding human mdm-2.

CC The invention is useful for reducing hyperproliferation of human cells,
 CC modulating the expression of mdm2 in human cells or tissues or in vitro.
 CC The hyperproliferative disorder includes cancer or psoriasis

SQ Sequence 20 BP; 11 A; 2 C; 1 G; 6 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1613 TTTTAAATATAAATAT 1630
 ||||| |||||
 Db 19 TTTCTTAAATATGTATAT 2

RESULT 1950
 AAF80870
 ID AAF80870 standard; DNA; 20 BP.
 XX AAF80870;
 XX
 DT 02-MAY-2001 (first entry)
 XX Human mdm2 phosphorothioate oligonucleotide #244.
 DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 KW Homo sapiens.
 XX

US6184212-B1.
 PD 06-FEB-2001.
 XX 26-MAR-1999; 99US-00280805.
 PF 26-MAR-1998; 98US-00048810.
 PR (ISIS-) ISIS PHARM INC.
 XX

PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsett LM;
 XX WPI; 2001-190948/19.
 DR

PT Novel antisense compound 8-30 nucleobases in length targeted to a nucleic
 PT acid molecule encoding human mdm-2 useful for modulating the expression
 PT of human mdm-2 and reducing hyperproliferation of human cells.

XX Example 9; Col 31; 77pp; English.

XX The present invention relates to an antisense compound 8-30 nucleobases
 CC in length targeted to nucleobases 1-308 of the 5' untranslated region,
 CC 1776-1806 of the translation termination codon region or 1818-2370 of the
 CC 3' untranslated region of a nucleic acid molecule encoding human mdm-2.
 CC The invention is useful for reducing hyperproliferation of human cells,
 CC modulating the expression of mdm2 in human cells or tissues or in vitro.
 CC The hyperproliferative disorder includes cancer or psoriasis

SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1951 GCCTCAAGTGAGCCCAAGA 1968
 ||||| |||||
 Db 3 GCTTCAGTGAGCCCAAGA 20

RESULT 1951
 AAC92609/c
 ID AAC92609 standard; DNA; 20 BP.
 XX AAC92609;
 AC


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AAC92591/c
ID AAC92591 standard; DNA; 20 BP.
XX AC AAC92591;
XX DT 27-MAR-2001 (first entry)
XX XX
DE Human nucleolin phosphorothioate antisense oligonucleotide, SEQ ID NO:41.
XX XX
XX Human nucleolin; P92; C23; phosphoprotein; ribosome biogenesis;
XX ribosome transport; cytokinesis; nucleogenesis; cell proliferation;
XX cell growth; transcriptional repression; replication;
XX signal transduction; chromatin decondensation; Ag-NOR family;
XX nucleolin antibody; systemic connective tissue disease; SLE;
XX systemic lupus erythematosus;
XX scleroderma-like chronic graft versus host disease;
XX expression inhibition; tumour formation; cancer; inflammation;
XX immune disorder; phosphorothioate; antisense oligonucleotide; ss.
XX OS Homo sapiens.
XX XX
XX US6165786-A.
XX PD 26-DEC-2000.
XX PF 03-NOV-1999; 99US-00433699.
XX PR 03-NOV-1999; 99US-00433699.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Cowsett LM;
XX WPI; 2001-079848/09.
XX DR
XX Novel antisense compound targeted to human nucleolin which specifically
XX hybridizes with and inhibits the expression of human nucleolin, useful
XX for modulating the expression of nucleolin in cells.
XX PS Claim 14; Col 41-42; 41pp; English.
XX CC
XX Sequences AAC92560-C92639 represent antisense oligonucleotides targeted
XX to the human nucleolin gene, which inhibit its expression. The antisense
XX oligonucleotides were designed to target different regions of the human
XX nucleolin mRNA, and were analysed for their effect on nucleolin mRNA
XX levels by quantitative real-time PCR. Nucleolin (also known as P92 or
XX C23) is the most abundant nucleolar phosphoprotein in actively growing
XX cells. Nucleolin primarily participates in ribosome biogenesis and
XX transport of ribosomal components, being able to transiently bind to pre-
XX ribosomes in the nucleolus via a ribonucleoprotein consensus sequence.
XX However, it has also been shown to be involved in cytokinesis,
XX nucleogenesis, cell proliferation and growth, transcriptional repression,
XX replication, signal transduction, and chromatin decondensation. Nucleolin
XX is a member of the Ag-NOR (active ribosomal gene located in the nucleolar
XX organiser region) family of proteins which are markers of active
XX ribosomal genes, and whose expression is associated with the prediction
XX of tumour growth rate. The presence of antibodies against nucleolin are
XX associated with systemic connective tissue diseases such as systemic
XX lupus erythematosus (SLE) and scleroderma-like chronic graft versus host
XX disease. The oligonucleotides of the invention are useful for diagnosis,
XX prevention and treatment of conditions associated with nucleolin
XX expression, such as tumour formation, immune disorders and inflammation
XX
XX Sequence 20 BP; 1 A; 9 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1246 GATGAGGACGACGAC 1263
DB 19 GACGAGGATGACGACGAC 2

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RESULT 1954
AAC83918
ID AAC83918 standard; DNA; 20 BP.
XX AC AAC83918;
XX DT 02-MAR-2001 (first entry)
XX XX
DE VDR gene PCR primer #1.
XX XX
XX Osteoporosis; human; polymorphism; vitamin D receptor; VDR;
XX oestrogen receptor; apolipoprotein E; ApoE; PCR primer; detection probe;
XX ss.
XX OS Homo sapiens.
XX XX
XX EP1054066-A2.
XX PD 22-NOV-2000.
XX PF 18-MAY-2000; 2000EP-00110219.
XX PR 18-MAY-1999; 99JP-00136653.
XX PR 11-JUN-1999; 99JP-00165642.
XX PA (NISS-) NISSHO CORP.
XX PI Shiraki M, Ouchi Y, Hosoi T, Kusaba N, Baba T, Yoshida H;
XX WPI; 2001-018132/03.
XX DR
XX Diagnosing sensitivity to a medicine for osteoporosis involves analyzing
XX genetic polymorphisms of vitamin D receptor gene, estrogen receptor gene
XX and apolipoprotein E gene.
XX PS Claim 18; Page 42; 51pp; English.
XX XX
XX The present invention relates to a method for anticipating the
XX sensitivity to a medicine for osteoporosis. The method involves analysing
XX combinations of genetic polymorphisms of a vitamin D receptor gene (VDR),
XX an oestrogen receptor (ER) gene, and an apolipoprotein E (ApoE) gene from
XX a human genome DNA sample. PCR primers AAC83918-C83926 and AAC83937-
XX C83942 were used in the method of the present invention to amplify the
XX VDR, ER and ApoE genes, and detection probes AAC83927-C83936 were used
XX for detecting VDR, ER and ApoE genetic polymorphism. By relating a
XX combination of the genetic polymorphisms detected using the detection
XX probes described in AAC83927-C83936, a remedy for a bone-associated
XX disease can be selected
XX
XX Sequence 20 BP; 3 A; 3 C; 10 G; 4 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1205 TGCAGGCGATTCCTGAGG 1222
DB 2 TGCAGGCGATTCGTTAGG 19

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RESULT 1955
AAF63722
ID AAF63722 standard; DNA; 20 BP.
XX AC AAF63722;
XX DT 04-MAY-2001 (first entry)
XX XX
XX Human hHAIERbs-iso PCR primer SEQ ID NO:4.
XX DE Human; hHAIERbs-iso; HAIERbs; HAIERbs isomer; detection; PCR primer;
XX high affinity immunoglobulin epsilon receptor beta subunit; ss.

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XX OS Homo sapiens.
 XX PN CN1269410-A.
 XX PD 11-OCT-2000.
 XX PF 17-MAR-2000; 2000CN-00114959.
 XX PR 17-MAR-2000; 2000CN-00114959.
 XX PA (SREN-) SOUTHERN RES CENT NAT HUMAN GENE GROUP.
 XX PI Xiao H, Liu F, Song H;
 XX DR WPI; 2001-050545/07.
 XX PT New human immunoglobulin receptor subunit protein and its nucleic acid.
 XX PS Example 1; Page 11; 22pp; Chinese.
 XX CC The present invention describes a human high affinity immunoglobulin epsilon receptor beta subunit isomer, designated hHA1ERbs-iso. hHA1ERbs-iso is isolated from in human pheochromocytoma. The present invention also describes methods for the preparation and detection of hHA1ERbs-iso protein and nucleotide sequences. The present sequence represents a PCR primer for human hHA1ERbs-iso, which is used in an example from the present invention
 XX SQ Sequence 20 BP; 8 A; 3 C; 7 G; 2 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. NO. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 322 TACAGCAGCAGATGCAG 339
 DB 1 TACAGCAGGAAGTGCAG 18
 RESULT 1956
 AA197988
 ID AA197988 standard; DNA; 20 BP.
 AC AA197988;
 XX 20-NOV-2001 (first entry)
 XX Lawsonia intracellullaris protein related oligonucleotide SEQ ID NO: 32.
 XX HtrA; PonA; HypC; YefW; ABC1; Omp100; Lawsonia intracellullaris infection; vaccine; PCR primer; probe; ss.
 XX Lawsonia intracellullaris.
 XX JP2001169787-A.
 XX 26-JUN-2001.
 XX 20-OCT-2000; 2000JP-00320736.
 XX 22-OCT-1999; 99US-0160922P.
 XX (PFIZ) PFIZER PROD INC.
 XX WPI; 2001-592540/67.
 XX Lawsonia intracellullaris polynucleotide and encoded protein, used to prevent Lawsonia intracellullaris infection.
 XX Example 1; Page 52; 67pp; Japanese.
 XX The present invention provides isolated polynucleotides encoding HtrA,

CC PonA, HypC, Lyss, YefW, ABC1 or Omp100 protein of Lawsonia intracellullaris. The sequences can be used in vaccines for the prevention of Lawsonia intracellullaris infection. The present sequence is an oligonucleotide described in the exemplification of the invention
 XX Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. NO. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1083 TTTCAGCTCCACATCAG 1100
 DB 3 TTCAAGATCTACTTCAG 20
 RESULT 1957
 AA69341/C
 ID AA69341 standard; DNA; 20 BP.
 XX AA69341;
 AC AA69341;
 XX 18-APR-2001 (first entry)
 XX Integrin-linked kinase coding region targeted oligonucleotide #54.
 XX Antisense; integrin-linked kinase; hIK; infection; tumour; inflammation; ss.
 XX Homo sapiens.
 XX US6177273-B1.
 XX 23-JAN-2001.
 XX 26-OCT-1999; 99US-00428219.
 XX 26-OCT-1999; 99US-00428219.
 XX (ISIS-) ISIS PHARM INC.
 XX Bennett CF, Cowser LM;
 XX WPI; 2001-137069/14.
 XX Novel antisense compounds capable of modulating expression of human Integrin-linked kinase, useful for diagnosis, prophylaxis and treatment of diseases, e.g. tumors, associated with expression of the kinase.
 XX Claim 3; Col 43; 40pp; English.
 XX The present invention relates to an antisense compound 8 to 30 bases in length targeted to the 5' untranslated (UTR) region, the coding region or the 3' UTR region human Integrin-linked kinase (hIK). The antisense oligonucleotides are useful for inhibiting the expression of human hIK in human cells or tissues, in vitro. The oligonucleotides can be utilized for diagnostics, therapeutics for the treatment of diseases associated with the expression of hIK, prophylaxis e.g. to prevent or delay infection, inflammation or tumor formation and as research reagent
 XX Sequence 20 BP; 6 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. NO. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 407 GTGCTTCTGTGGCAAGTC 424
 DB 19 GTGCTTCTGTGGCAAGTC 2
 RESULT 1958
 AAH37989

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ID AAH37989 standard; DNA; 20 BP.
XX
AC AAH37989;
XX
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific upper PCR primer SEQ ID 785.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
OS Homo sapiens.
XX
XX W0200129262-A2.
XX
XX 26-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US028436.
XX
XX 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX Picoult-Newburg L, Pohl M;
XX
XX WPI; 2001-290930/30.
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
XX absence or identity of single polynucleotide polymorphism in a nucleic
XX acid sample.
XX
XX Claim 1; Page 54; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX primer extension (SNPE) primers, and the sequences of regions flanking
XX sites of single nucleotide polymorphisms SNPs. The present invention
XX includes kits for determining the presence or absence of a SNP, using the
XX oligonucleotides of the invention. The PCR primers are used to amplify a
XX SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX The oligonucleotides are useful for genotyping a nucleic acid sample by
XX performing a single-nucleotide primer extension reaction. The
XX oligonucleotides are useful for determining the presence, absence or
XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX assess by association analysis the genotype of an individual or group of
XX individuals, having a pathological phenotypic trait suspected of being
XX caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
XX dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX traits also include symptoms of or susceptibility to multifactorial
XX diseases, including a component is or may be genetic such as autoimmune
XX disease, including, rheumatoid arthritis, multiple sclerosis,
XX inflammation, cancer, nervous system diseases and infection by pathogenic
XX microorganism. The method is also useful in forensic investigations and
XX paternity analysis. The present sequence represents a PCR primer specific
XX for a human SNP containing DNA sequence
XX
SQ Sequence 20 BP; 1 A; 6 C; 5 G; 8 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1529 CTGGCTTCCTGCTGAGTC 1546
Db 3 CTGGCTTCCTGCTGTC 20
RESULT 1959

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AAH40673
ID AAH40673 standard; DNA; 20 BP.
XX
AC AAH40673;
XX
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific upper PCR primer SEQ ID 3469.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
OS Homo sapiens.
XX
XX W0200129262-A2.
XX
XX 26-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US028436.
XX
XX 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX Picoult-Newburg L, Pohl M;
XX
XX WPI; 2001-290930/30.
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
XX absence or identity of single polynucleotide polymorphism in a nucleic
XX acid sample.
XX
XX Claim 1; Page 67; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX primer extension (SNPE) primers, and the sequences of regions flanking
XX sites of single nucleotide polymorphisms SNPs. The present invention
XX includes kits for determining the presence or absence of a SNP, using the
XX oligonucleotides of the invention. The PCR primers are used to amplify a
XX SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX The oligonucleotides are useful for genotyping a nucleic acid sample by
XX performing a single-nucleotide primer extension reaction. The
XX oligonucleotides are useful for determining the presence, absence or
XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX assess by association analysis the genotype of an individual or group of
XX individuals, having a pathological phenotypic trait suspected of being
XX caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
XX dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX traits also include symptoms of or susceptibility to multifactorial
XX diseases, including a component is or may be genetic such as autoimmune
XX disease, including, rheumatoid arthritis, multiple sclerosis,
XX inflammation, cancer, nervous system diseases and infection by pathogenic
XX microorganism. The method is also useful in forensic investigations and
XX paternity analysis. The present sequence represents a PCR primer specific
XX for a human SNP containing DNA sequence
XX
SQ Sequence 20 BP; 3 A; 3 C; 4 G; 10 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1063 TTGTAATCTTTGGACCA 1080
Db 3 TTGTAATGTTTGGCCCA 20

```

RESULT 1960
AADO5680
ID AAD05680 standard; DNA; 20 BP.
XX
AC AAD05680;
XX
DT 31-JUL-2001 (first entry)
XX
DE Mouse zmsel cDNA clone sequencing primer, ZC19,192.
XX
KW Mouse; zmsel protein; Cdc42/Rac interactive binding protein; CRIB;
KW Wiskott-Aldrich Syndrome; cancer; tumour; invasion; metastasis; asthma;
KW digestion; actin polymerisation; cytoskeletal reorganisation; arthritis;
KW testicular function; muscle inflammation; inflammatory bowel disease;
KW diverticulitis; male infertility; male contraceptive agent; myocarditis;
KW spermatogenesis; sperm capacitation; reperfusion ischaemia; psoriasis;
KW melanoma; atherosclerosis; pelvic inflammatory disease; PID; eczema;
KW scleroderma; cytostatic; vasotropic; dermatological; gene therapy;
KW primer; ss.
XX
OS Mus musculus.
XX
XX
XX WO200134803-A2.
XX
XX 17-MAY-2001.
XX
XX 09-NOV-2000; 2000WO-US030945.
XX
XX 10-NOV-1999; 99US-00438564.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Holloway JL, Gao Z, Whitmore TE;
XX
XX WPI; 2001-335928/35.
XX
XX Novel human CRIB protein, zmsel and polynucleotide encoding the protein,
XX PT for detecting human chromosomal abnormalities and for treating cancer,
XX PT cardiovascular and inflammatory conditions.
XX
XX Example 4; Page 128; 132pp; English.
XX
XX The present invention relates to DNA and protein for zmsel, a novel human
XX Cdc42/Rac interactive binding (CRIB) protein. CRIB proteins are
XX implicated in human disease such as Wiskott-Aldrich Syndrome. Zmsel
XX modulators are useful for modulating tumour cell motility, invasion and
XX metastasis, gene transcription, contractility of various tissues, actin
XX polymerisation and cytoskeletal reorganisation, digestion, testicular
XX function and fertility. Zmsel sequence and its modulators are useful for
XX treating cancer, inflammation during and after surgery, arthritis, asthma,
XX inflammation, inflammation during and after surgery, arthritis, asthma,
XX inflammatory bowel diseases or diverticulitis, myocarditis, scleroderma,
XX atherosclerosis, pelvic inflammatory disease (PID), eczema and other
XX inflammatory diseases, male infertility or as male contraceptive agents
XX and for modulating spermatogenesis and sperm capacitation. zmsel and anti
XX -zmsel antibodies are useful in diagnosing inflammatory diseases, such as
XX reperfusion ischaemia, psoriasis, arthritis, melanoma and other
XX inflammatory diseases, male reproductive cancers such as prostate and
XX testicular cancers. Zmsel polynucleotide sequences are useful as probes
XX or primers for detecting human chromosomal abnormalities. zmsel sequence
XX is used in gene therapy. The present sequence is ZC19,192 primer used for
XX sequencing mouse zmsel cDNA clone
XX
XX Sequence 20 BP; 4 A; 3 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1486 GTCAAGGAGGAGGTCAGG 1503
Db 3 GTCAAGGAGGTCAGG 20

RESULT 1961
AAS42733/c
ID AAS42733 standard; DNA; 20 BP.
XX
AC AAS42733;
XX
DT 17-DEC-2001 (first entry)
XX
DE Sequencing primer for T.gondii gene MGIS4-4 #1.
XX
KW Immunogenic protein; oocyst; faeces; ss; enteric apicomplexa oocyst;
KW Cryptosporidium oocyst; Toxoplasma oocyst; Giardia cyst; vaccine;
KW oocyte shedding; sequencing primer.
XX
OS Toxoplasma gondii.
XX
XX US2001014447-A1.
XX
XX 16-AUG-2001.
XX
XX 18-DEC-1998; 98US-00216393.
XX
XX 19-DEC-1997; 97US-00994825.
XX
XX (MILH/) MILHAUSEN M J.
XX
XX Milhausen MJ;
XX
XX WPI; 2001-529100/58.
XX
XX Detecting parasite oocysts or cysts in feces, comprises eluting DNA from
XX sample into aqueous solution by heating, amplifying DNA with primers
XX specific for oocysts or cysts being detected, and detecting amplification
XX product.
XX
XX Example 15; Page 156; 188pp; English.
XX
XX The invention relates to detection of parasite oocysts or cysts in a
XX faeces sample comprising contacting the sample with a solid support,
XX drying and then washing the sample with an aqueous wash solution, adding
XX an aqueous elution solution and eluting DNA from the sample by heating
XX and amplifying by PCR oocyst/cyst-specific DNA and detecting the
XX amplification products. The method is useful for detecting parasite
XX oocysts e.g., enteric apicomplexa oocysts such as Cryptosporidium oocysts
XX or Toxoplasma oocysts, or for detecting parasite cysts e.g. Giardia
XX cysts. The method is also useful for developing vaccines to prevent
XX oocyte shedding in cats. The present sequence is a sequencing primer used
XX to sequence DNAs encoding immunogenic proteins from Toxoplasma gondii
XX
XX Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 807 AATGAGATGTTTCAGCC 824
Db 19 AATGAGATGTTTCAGCC 2
XX
RESULT 1962
AAD10163
ID AAD10163 standard; DNA; 20 BP.
XX
AC AAD10163;
XX
DT 12-SEP-2001 (first entry)
XX
DE PCR primer, 924 used to produce transgenic mouse embryos.
XX
XX Sonic hedgehog; Shh; morphogenic signal; neuron; mouse;
XX embryonic patterning; cell culture; cell differentiation; ischaemia;

KW cell proliferative disorder; intracerebral grafting; Huntington's chorea;
 KW neurological disorder; Alzheimer's disease; Parkinson's disease;
 KW amyotrophic lateral sclerosis; ALS; multiple sclerosis; PCR primer; ss.

OS Mus sp.

XX US6261786-B1.

XX 17-JUL-2001.

XX 02-JUL-1996; 96US-00674509.

XX 30-DEC-1993; 93US-00176427.

XX 14-DEC-1994; 94US-00356060.

XX 04-MAY-1995; 95US-00435093.

XX 05-JUN-1995; 95US-00460900.

XX 05-JUN-1995; 95US-00462386.

XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

XX (HARD) HARVARD COLLEGE.

XX Marigo V, Tabin CJ, Ingham PW, McMahon AP;

XX WPI; 2001-440859/47.

XX Screening compounds that potentiate or inhibit binding of hedgehog
 PT polypeptide to naturally occurring patched receptor, comprises contacting
 PT polypeptide with receptor and test compound, and detecting change in
 PT binding.

XX Example 2; Col 80; 127pp; English.

XX The present invention relates to assay for screening compounds that
 CC potentiate or inhibit binding of hedgehog polypeptide to naturally
 CC occurring patched receptor. The hedgehog proteins comprise morphogenic
 CC signals produced by embryonic patterning centres, and are involved in the
 CC formation and maintenance of ordered spatial arrangements of
 CC differentiated tissues in vertebrates, both adult and embryonic. The
 CC proteins can be used to generate and/or maintain an array of different
 CC vertebrate tissues both in vitro and in vivo. The invention also relates
 CC to a method for modulating growth, differentiation or survival of a
 CC mammalian cell (e.g. neuron, testicular cell) responsive to hedgehog
 CC induction. Hedgehog agonists and antagonists can be used in cell culture
 CC techniques to enhance survival and maintenance of neurons and various
 CC vertebrate organogenic pathways. The hedgehog gene is useful in
 CC determining whether a patient is at the risk of disorder characterised by
 CC unwanted cell proliferation or aberrant control of differentiation. The
 CC hedgehog proteins or mimetics can be used to induce foetal neurons
 CC especially neuronal stem cells in intracerebral grafting. The protein or
 CC its mimetic can be used in the treatment of neurological conditions e.g.
 CC injury to nervous system, ischaemia resulting from stroke, Alzheimer's
 CC disease, Parkinson's disease, Huntington's chorea, amyotrophic lateral
 CC sclerosis (ALS) and multiple sclerosis. The present sequence is a PCR
 CC primer used to produce transgenic mouse embryos

XX Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1436 AAGTCACCGAAGAGGAGA 1453

DB 1 AAGTCAGCCAGAGGAGA 18

RESULT 1963

AAH26928

ID AAH26928 standard; DNA; 20 BP.

XX AAH26928;

XX 21-DEC-2001 (first entry)

XX

DE Brevibacillus borstelensis 16S rDNA C-terminal PCR primer.

XX 16S rDNA; dipeptidase; D-stereospecific; thermostable enzyme;

KW D-amino acid; sweetener; dipeptide; PCR primer; ss.

XX Brevibacillus borstelensis.

XX WO200170937-A1.

XX 27-SEP-2001.

XX 06-JUL-2000; 2000WO-KR000730.

XX 24-MAR-2000; 2000KR-00015174.

XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX Sung M, Lee S, Kwon S, Baek D, Hong S, Cho S, Jung M;

XX WPI; 2001-611489/70.

XX Novel thermophilic Brevibacillus borstelensis BCS-1 that produces D-
 PT stereospecific dipeptidase useful for synthesis of D-amino acid-
 PT containing peptides, peptide-sweeteners or L-D-dipeptides.

XX Example 1; Page 42; 51pp; English.

XX 16S rDNA from newly isolated thermophilic microorganism BCS-1 was PCR
 CC amplified using the present sequence as C-terminal primer and the
 CC sequence given in AAH26927 as N-terminal primer. Sequencing of the
 CC product helped to identify BCS-1 as novel Brevibacillus borstelensis,
 CC which was deposited as KCTC 0673BP. The bacterium had been isolated on
 CC the basis of its ability to produce enzymes capable of hydrolysing D-
 CC peptide derivatives. It produces a D-stereospecific dipeptidase (see
 CC AAB82974) that has properties (thermostability, pH stability and
 CC substrate specificity) making it industrially useful for the synthesis L-
 CC D-configuration dipeptides. Various peptides containing D-amino acids,
 CC such as antibiotics, neuroactive peptides and peptide sweeteners, can be
 CC produced economically in high yield, without protection/deprotection and
 CC without environmental pollution, using the novel dipeptidase

XX Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 807 AATGGAGATGTTCCAGCC 824

DB 3 AAAGGAGGTGATCCAGCC 20

RESULT 1964

AAH23181/c

ID AAH23181 standard; DNA; 20 BP.

XX AAH23181;

XX 19-MAR-2001 (first entry)

XX Oligonucleotide for detection of Mycobacterium vaccae.

XX ITS; internal transcribed spacer region; Mycobacterium fortuitum;
 KW Mycobacterium chelonae; Mycobacterium abscessus; Mycobacterium vaccae;
 KW Mycobacterium flavescens; Mycobacterium asiaticum; tuberculosis;
 KW Mycobacterium porcinum; Mycobacterium acapulcensis; identification;
 KW Mycobacterium diernhoferi; PCR primer; probe; detection; ss.

OS Mycobacterium vaccae.

XX WO200073436-A1.

XX

XX 20-OCT-1997; 97US-00954698.
PF
XX 30-DEC-1993; 93US-00176427.
PR
XX 14-DEC-1994; 94US-00356060.
PR
XX 04-MAY-1995; 95US-00435093.
PR
XX 05-JUN-1995; 95US-00462386.
PR
XX (HARD) HARVARD COLLEGE.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
XX Ingham PW, McMahon AP, Tabin CJ;
XX WPI; 2001-456723/49.
DR
XX Novel nucleic acid encoding a hedgehog polypeptide, used to produce the
PT polypeptide, which is used to promote proliferation, survival, and/or
PT differentiation of neuronal and mesodermal tissue.
XX
XX Example 2; Col 71; 118pp; English.
PS
XX The invention relates to nucleic acids encoding hedgehog proteins
CC selected from sonic hedgehog (Shh), indian hedgehog (Ihh), desert
CC hedgehog (Dhh) polypeptides. The hedgehog genes are involved in the
CC formation of ordered spatial arrangements of differentiated tissue in
CC vertebrates. The nucleic acid sequences are useful for producing hedgehog
CC proteins, used for promoting differentiation of, or survival of
CC differentiated, neuronal cells, and for promoting proliferation, survival
CC or differentiation of mesenchymal, endodermal or ectodermal tissue,
CC particularly chondrocytes, or testicular germ line cells. Sequences
CC AAH76123-124 represent PCR primers amplifying a 345 bp fragment spanning
CC the insertion junction of the chicken Shh cDNA in the WEXP2 expression
CC vector
XX
XX Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1436 AAGTCACCCGAGGAGGAGA 1453
DB 1 AAGTCACCCGAGGAGGAGA 18
RESULT 1966
AAF80021
ID AAF80021 standard; DNA; 20 BP.
XX
AC AAF80021;
XX
DT 11-JUN-2001 (first entry)
XX
DE Primer used to amplify cDNA encoding an odorant binding polypeptide.
XX
XX Odorant binding polypeptide; ORP; hydrophobic ligand; odorant; allergy;
XX asthma; cancer; perfume; hyperlipidemia; obesity; food additive;
XX anticancer; foetus detoxification; pregnancy marker; PCR primer; ss.
OS Homo sapiens.
XX
PN WO200112806-A2.
XX
PD 22-FEB-2001.
XX
XX 11-AUG-2000; 2000WO-FR002319.
PF
XX 12-AUG-1999; 99FR-00010439.
PR
XX (UYAU-) UNIV AUVERGNE.
PA (PITI/) PITIOT G.
XX
XX Pitiot G, Lacazette E, Gachon F;
PI

XX 07-DEC-2000.
PF
XX 16-MAY-2000; 2000WO-KR000477.
PR
XX 29-MAY-1999; 99KR-00019631.
PR
XX 29-MAY-1999; 99KR-00019632.
PR
XX 29-MAY-1999; 99KR-00019633.
PR
XX 29-MAY-1999; 99KR-00019634.
PR
XX 29-MAY-1999; 99KR-00019635.
PR
XX 07-APR-2000; 2000KR-00018189.
XX
XX (SUHI-) SJ HIGHTECH CO LTD.
PA (KIMC/) KIM C M.
PA (PARK/) PARK H K.
XX
XX Kim CM, Park HK, Jang HJ;
XX
XX WPI; 2001-061527/07.
DR
XX Novel oligonucleotide sequences of internal transcribing spacer region of
PT non-tuberculosis mycobacteria (NTM) used as probes or primers for
PT detecting and identifying mycobacteria and distinguish TB complex from
PT NTM.
XX
XX Claim 16; Page 43; 89pp; English.
PS
XX The present sequence is an oligonucleotide developed using a
CC Mycobacterium ITS (internal transcribed spacer region) nucleotide
CC sequence. ITS DNA sequences from M. fortuitum, M. chelonae, M. abscessus,
CC M. vaccae, M. flavescens, M. asiaticum, M. porcinum, M. acapulcensis, M.
CC diernhoferi genes were identified. The oligonucleotides derived from
CC these sequences were used to develop PCR primers and hybridisation probes
CC for detection and identification of Mycobacterium. ITS has a more
CC polymorphic region than 16S rRNA and also has a conserved region. It is
CC therefore highly effective as a target DNA for distinction of genotype.
CC The oligonucleotide probes, attached to solid substrate, hybridise only
CC with nucleotide sequences in ITS of specific mycobacteria, and thus they
CC can detect and identify the specific mycobacteria sensitively. The
CC oligonucleotides can also detect and identify the specific mycobacteria
CC by PCR amplification. Using the oligonucleotide primers or probes made
CC from ITS of mycobacteria, it is possible to detect mycobacteria.
CC distinguish tuberculosis (TB) complex from non-tuberculosis mycobacteria
CC (NTM), and to identify mycobacteria species accurately and effectively
XX
XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 140 AAGGCCACCCCAATGAGC 157
DB 19 AAGGCCATCCACGATC 2
RESULT 1965
AAH76124
ID AAH76124 standard; DNA; 20 BP.
XX
AC AAH76124;
XX
DT 29-OCT-2001 (first entry)
XX
DE Chicken-Shh specific primer 924.
XX
XX Hedgehog protein; sonic hedgehog; Shh; indian hedgehog; Ihh; Dhh;
XX desert hedgehog; cell differentiation; PCR primer; ss.
XX
XX Synthetic.
XX
XX US6271363-B1.
PN
XX 07-AUG-2001.
PD

CC human ornithine decarboxylase (odc) gene. The amplified fragment
CC comprised the polymorphism site, leading to A allele or G allele. The G
CC allele differs from the A allele in that it has a G at position +321. The
CC presence of the minor (A allele) in an individual is predictive of a high
CC incidence of carcinogenesis in the individual. The primers were used in
CC the method of the invention. The specification describes a method for
CC assessing the relative susceptibility of a mammal to an epithelial
CC cancer. The method comprises determining whether the mammal contains an A
CC allele of the odc gene, where if the mammal contains the A allele, then
CC the mammal has a greater susceptibility to the epithelial cancer than a
CC mammal of the same type which does not contain the A allele. The method
CC is useful for assessing the relative susceptibility of a mammal to an
CC epithelial cancer
XX
SQ Sequence 20 BP; 6 A; 2 C; 10 G; 2 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1556 TCTTCCCAACCCCTCAG 1573
Db 18 TCTTCCCAACCCCTCG 1
RESULT 1970
AAS29476/c
ID AAS29476 standard; DNA; 20 BP.
AC AAS29476;
XX
XX 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31617.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= All phosphorothioate linkages,
FT additionally bases 1-6 and bases 15-20 are 2'-O-
FT methoxyethyl bases, and bases 7-14 are deoxynucleotides"
XX
XX US2001016575-A1.
XX
XX 23-AUG-2001.
XX
XX 02-JAN-2001; 2001US-00752983.
XX
XX 26-MAR-1998; 98US-00048810.
XX 26-MAR-1999; 99US-00280805.
XX
XX (MIRA/) MIRAGLIA L J.
XX (NERO/) NERO P.
XX (GRAH/) GRAHAM M J.
XX (MONT/) MONIA B P.
XX (COWS/) COWSERT L M.
XX
XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsert LM;
XX WPI; 2001-535565/59.
XX
XX An antisense compound, useful for treating e.g. cancer, comprises
XX nucleobases targeted a region (e.g. translation termination codon region)
XX of a nucleic acid encoding human mdm2.
XX
XX Example 9; Page 18; 81pp; English.
PS

DR WPI; 2001-079847/09.
XX
XX Polynucleotides encoding hedgehog proteins, useful for treating diseases
XX of nervous system such as Alzheimer's disease, Parkinson's disease,
XX Huntington's chorea, amyotrophic lateral sclerosis, multiple sclerosis.
XX
XX Example 2; Col 157-158; 119pp; English.
XX
XX PCR primers AAC87088-89 were used to amplify cDNA encoding a hedgehog
XX related-protein. The specification describes a sonic hedgehog protein
XX (Shh), a desert hedgehog protein (Dhh), and an indian hedgehog protein
XX (Ihh). The hedgehog polynucleotides are useful in diagnostic, in
XX antisense therapy and in therapeutic assays for detecting and treating
XX disorders involving, e.g., aberrant expression of vertebrate hedgehog
XX homologue. Hedgehog polypeptides are useful therapeutically to enhance
XX survival of neurons and other neuron cells and in treating neurological
XX conditions deriving from acute, subacute, or chronic injury to the
XX nervous system, including traumatic injury, chemical injury, vascular injury
XX and deficits (such as the ischemia resulting from stroke), together with
XX infectious/inflammatory and induced-induced injury, aging of the nervous
XX system including Alzheimer's disease, chronic neurodegenerative diseases
XX of the nervous system, including Parkinson's disease, Huntington's
XX chorea, amyotrophic lateral sclerosis, spinocerebellar degenerations,
XX and chronic immunological diseases of the nervous system or affecting the
XX nervous system, including multiple sclerosis
XX
SQ Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1436 AAGTCACCGAAGGAGGA 1453
Db 1 AAGTCACCGAAGGAGGA 18
RESULT 1969
AAH78569/c
ID AAH78569 standard; DNA; 20 BP.
XX
XX AAH78569;
XX
XX 10-DEC-2001 (first entry)
XX
XX PCR primer used to amplify a 546 bp fragment of the human odc gene.
XX
XX Human; A allele; ornithine decarboxylase gene; odc gene; G allele;
XX carcinogenesis; epithelial cancer; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX US6277581-B1.
XX
XX 21-AUG-2001.
XX
XX 01-MAR-2000; 2000US-00516357.
XX
XX 01-MAR-1999; 99US-0122309P.
XX
XX (LANK-) LANKENAU MEDICAL RES CENT.
XX
XX O'brien TG, Guo YJ;
XX WPI; 2001-588918/66.
XX
XX Assessing relative susceptibility of mammal to epithelial cancer,
XX involves determining if the mammal comprises an A-allele of the mammal's
XX odc gene.
XX
XX Claim 7; Col 14; 15pp; English.
XX
XX PCR primers AAH78568-69 were used to amplify a 546 bp fragment of the
XX

XX The present invention relates to antisense compounds, 8-30 nucleobases in
 CC length targeted to the 5' untranslated region, coding region or translation termination
 CC codon region, 3' untranslated region, coding region or translation start
 CC site of a nucleic acid encoding human mdm2, where the antisense compound
 CC modulates the expression of human mdm2. The antisense oligonucleotides of
 CC the invention are useful for encoding human mdm2 and for inhibiting the
 CC expression of human mdm2. They may be used for treating an animal having
 CC a disease or condition associated with amplification of mdm2 gene or
 CC overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer
 CC (blood, brain, breast, lung, or a soft tissue cancer) and psoriasis,
 CC fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma
 CC and chronic myelogenous leukemia. The antisense compound may be
 CC administered with a chemotherapeutic agent to overcome drug resistance.
 CC The antisense compound reduces hyperproliferation of human cells. The
 CC method, which involves the use of the antisense compound, is also useful
 CC for detecting the role of mdm2 expression in various cell functions and
 CC physiological processes and useful in both clinical research and
 CC diagnostic tools. AAS29242-AAS29507 represent the human mdm2 antisense
 CC oligonucleotides of the present invention
 XX
 SQ Sequence 20 BP; 11 A; 2 C; 1 G; 6 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1613 TTTTATTAAATATATATAT 1630
 DB 19 TTTCTTAATATGTATAT 2
 RESULT 1971
 AAS29485
 ID AAS29485 standard; DNA; 20 BP.
 AC AAS29485;
 DT 21-NOV-2001 (first entry)
 XX Human mdm2 antisense oligonucleotide 31468.
 XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;
 KW anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= All phosphorothioate linkages,
 FT additionally bases 1-6 and bases 15-20 are 2'-O-
 FT methoxyethyl bases, and bases 7-14 are deoxynucleotides"
 XX
 PN US2001016575-A1.
 XX
 XX 23-AUG-2001.
 XX
 PF 02-JAN-2001; 2001US-00752983.
 XX
 PR 26-MAR-1998; 98US-00048810.
 PR 26-MAR-1999; 99US-00280805.
 XX
 XX (MIRA/) MIRAGLIA L J.
 PA (NERO/) NERO P.
 PA (GRAH/) GRAHAM M J.
 PA (MONI/) MONIA B P.
 PA (COWS/) COWSERT L M.
 XX
 XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsert LM;
 PI
 XX

DR WPI; 2001-535565/59.
 XX An antisense compound, useful for treating e.g. cancer, comprises
 PT nucleobases targeted a region (e.g. translation termination codon region)
 PT of a nucleic acid encoding human mdm2.
 XX
 PS Claim 4; Page 19; 81pp; English.
 XX
 CC The present invention relates to antisense compounds, 8-30 nucleobases in
 CC length targeted to the 5' untranslated region, translation termination
 CC codon region, 3' untranslated region, coding region or translation start
 CC site of a nucleic acid encoding human mdm2, where the antisense compound
 CC modulates the expression of human mdm2. The antisense oligonucleotides of
 CC the invention are useful for encoding human mdm2 and for inhibiting the
 CC expression of human mdm2. They may be used for treating an animal having
 CC a disease or condition associated with amplification of mdm2 gene or
 CC overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer
 CC (blood, brain, breast, lung, or a soft tissue cancer) and psoriasis,
 CC fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma
 CC and chronic myelogenous leukemia. The antisense compound may be
 CC administered with a chemotherapeutic agent to overcome drug resistance.
 CC The antisense compound reduces hyperproliferation of human cells. The
 CC method, which involves the use of the antisense compound, is also useful
 CC for detecting the role of mdm2 expression in various cell functions and
 CC physiological processes and useful in both clinical research and
 CC diagnostic tools. AAS29242-AAS29507 represent the human mdm2 antisense
 CC oligonucleotides of the present invention
 XX
 SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1951 GCCTCAAGTGAGCCAGA 1968
 DB 3 GCTTGCACTGAGCCAGA 20
 RESULT 1972
 ABZ72159
 ID ABZ72159 standard; DNA; 20 BP.
 XX
 AC ABZ72159;
 XX
 DT 03-APR-2003 (first entry)
 XX
 DE Gene 216 SSCP detection primer SEQ ID NO 131.
 XX
 KW Human; Gene 216; chromosome 20p13-p12; antiasthmatic; anorectic;
 KW antiinflammatory; gastrointestinal; gene therapy; vaccine; asthma;
 KW obesity; inflammatory bowel disease; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200178894-A2.
 XX
 XX 25-OCT-2001.
 XX
 PF 13-APR-2001; 2001WO-US012245.
 XX
 PR 13-APR-2000; 2000US-00548797.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Keith T;
 XX
 DR WPI; 2001-639428/73.
 XX
 XX Isolated genes (Gene 216) from human chromosome 20p13-p12 and the
 PT proteins they encode, useful for the prevention, diagnosis and treatment
 PT of asthma, obesity and inflammatory bowel disease.
 XX


```

XX SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
XX AC
XX ABK93609;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1819 GCTTTGGAAAGTGCCCT 1836
XX ||| ||||| |||||
XX 18 GCTGAGGAAGTGCTCT 1
XX
XX RESULT 1975
XX ABA82574
XX ID ABA82574 standard; DNA; 20 BP.
XX AC
XX ABA82574;
XX
XX 25-JAN-2002 (first entry)
XX
XX Zmax1 gene region physical map preparation STS marker #533.
XX
XX Human; high bone mass; HBM gene; Zmax1 gene; chromosome 11; 11q13.3;
XX sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
XX antisense therapy; vaccine; bone disorder; Paget's disease; adapter;
XX sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss.
XX
XX Homo sapiens.
XX OS
XX Synthetic.
XX
XX WO200177327-A1.
XX
XX 18-OCT-2001.
XX
XX 21-JUN-2000; 2000WO-US016951.
XX
XX 05-APR-2000; 2000US-00543771.
XX
XX 03-APR-2000; 2000US-00544398.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Carulli JP, Little RD, Recker RR, Johnson ML;
XX
XX WPI; 2001-657171/75.
XX
XX New high bone mass (HBM) and Zmax1 genes and proteins useful for
XX modulating bone mass for the treatment of e.g. osteoporosis.
XX
XX Disclosure; Page 37; 443pp; English.
XX
XX The present invention describes the human Zmax1 gene and the high bone
XX mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM
XX genes have osteopathic activities. The genes can be used in gene therapy,
XX antisense therapy and in the production of vaccines. They can be used in
XX the diagnosis and treatment of bone disorders including osteoporosis,
XX Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.
XX ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences used in
XX the exemplification of the present invention
XX
XX Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 35 ACTGACGGTAGGACGGG 52
XX ||| ||||| |||||
XX 3 AGTGACACTAGGACGGG 20
XX
XX RESULT 1976
XX ABK93609
XX ID ABK93609 standard; DNA; 20 BP.
XX
XX SQ Sequence 20 BP; 5 A; 4 C; 2 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 935 TTAACCTGCTATGCTGA 952
XX ||| ||||| |||||
XX 3 TTAAACTGCTATTCTGA 20
XX
XX RESULT 1977
XX AAI70922
XX ID AAI70922 standard; DNA; 20 BP.
XX
XX AAI70922;
XX
XX 12-MAR-2002 (first entry)
XX
XX Sentinel Virus II PCR primer 33.2.
XX

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KW SVII; H101.c33; hepatitis virus; infection; therapy; diagnosis; vaccine;
XX PCR primer; ss.
XX Sentinel virus II.
XX WO200185770-A2.
XX 15-NOV-2001.
XX 04-MAY-2001; 2001WO-EP005029.
XX 05-MAY-2000; 2000US-0202271P.
XX (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX Liu J, Lewis S, Bohenzky R, Lin Y, Ramaswamy L, Montiel J;
XX Batz H, Chen B;
XX WPI; 2002-062234/08.
XX A new virus associated with cryptogenic non-A/non-G hepatitis, designated
XX Sentinel Virus II is useful to detect and treat Sentinel Virus II
XX infection.
XX Example 2; Page 29; 20pp; English.
XX The present sequence is that of PCR primer 33.2 used in the nested PCR
XX amplification of Sentinel virus II (SVII) DNA. In the nested PCR, the
XX first round used primer pair 33.1/33.2 and the second round used primer
XX pair 33.3/33.4 (see AAI70921-24). The PCR was performed to assay for SVII
XX in serum samples during the physical characterisation of SVII virus
XX particles. SVII is a new hepatitis virus associated with cryptogenic, non
XX A/non-G hepatitis. The invention provides SVII viruses, polynucleotides,
XX proteins, and antibodies which bind SVII virus and viral proteins. These
XX can be used to detect SVII virus or infection by SVII virus. DNA- and
XX protein-based vaccines for prevention and/or treatment of SVII infection
XX are also provided
XX Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 732 TGTTAACTACCGCTCCG 749
XX |||||
XX 1 TGTCAAATACCGCTCAG 18
XX
XX RESULT 1978
XX ABK49728/c
XX ID ABK49728 standard; DNA; 20 BP.
XX AC ABK49728;
XX XX
XX 15-JUL-2002 (first entry)
XX Herpes simplex virus thymidine kinase PCR primer MLCTKR1.
XX
XX Thymidine kinase; TK; parenchymal; bioincubator; transplantation; ss;
XX totipotent human embryonic stem cell; fertilised human ova; PCR; primer;
XX MLCTKR1; myosin light chain.
XX
XX Herpes simplex virus.
XX
XX WO200222789-A1.
XX
XX 21-MAR-2002.
XX
XX 13-SEP-2001; 2001WO-JF007947.
XX
XX 14-SEP-2000; 2000JP-00280295.
XX
XX (YUKI/) YUKI A.
XX Yuki A;
XX WPI; 2002-362343/39.
XX Producing normal parenchymal cells, tissues and organs as close as
XX possible to homoplasia by bioincubator, useful in transplantation in
XX human.
XX Example 1; Page 15; 42pp; Japanese.
XX The present invention relates to a new method of producing normal
XX parenchymal cells, tissues or organs originating from a human or non-
XX human mammal. The method of the invention involves culturing cells from
XX an organ, and specific cells from an incubator, and constructing the
XX target organ from the cells from the organ in the bioincubator without
XX containing cells originating from cells from the incubator. The invention
XX is useful as the normal parenchymal cells, tissues and organs it produces
XX are useful in transplantation in human. By using the bioincubator,
XX neither fertilised human ova nor the presence of totipotent human
XX embryonic stem cells are needed to enable large scale production. The
XX present nucleic acid sequence represents the herpes simplex virus
XX thymidine kinase PCR primer MLCTKR1 (myosin light chain thymidine
XX kinase). This sequence was used in the methods of the invention for
XX amplification of herpes simplex virus thymidine kinase
XX Sequence 20 BP; 1 A; 6 C; 5 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1430 AGAAGAAGTCAACGGAAG 1447
XX |||||
XX 19 AGCAGAAGCCACGGAAG 2
XX
XX RESULT 1979
XX ABS52255/c
XX ID ABS52255 standard; DNA; 20 BP.
XX AC ABS52255;
XX XX
XX 05-NOV-2002 (first entry)
XX Plant vector PCR primer #19.
XX
XX Plant; PCR; primer; ss; plastome; plastid genome; antibiotic;
XX herbicide resistance gene.
XX
XX Synthetic.
XX
XX WO200257466-A2.
XX
XX 25-JUL-2002.
XX
XX 18-JAN-2002; 2002WO-EP000481.
XX
XX 19-JAN-2001; 2001DE-01002389.
XX
XX (ICON-) ICON GENETICS AG.
XX
XX Bibl C, Huang F, Klaus S, Muehlbauer S, Herz S, Koop H;
XX WPI; 2002-590747/63.
XX
XX Transforming multicellular plants, by altering the function of a plastid
XX gene, selecting plants expressing altered phenotype, transforming plants
XX with a vector capable of restoring function and separating transformed
XX plants.
XX
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PS Example 3; Page 33; 56pp; English.
CC The invention relates to producing multicellular plants, organs or
CC tissues transformed on their plastome, comprising altering/disrupting the
CC function of a gene in a plastid genome for producing a selectable
CC phenotype and selecting plants with plastids expressing the phenotype,
CC transforming the plastid genomes of selected plants with a transformation
CC vector with a restoring sequence for restoring function and separating
CC transformed plants. This method is useful for producing multicellular
CC plants, organs or tissues transformed on their plastome and for selection
CC of antibiotics and herbicide resistance genes. Sequences ABS52237-
CC ABS52269 represent PCR primers used to amplify plant vector genes of the
CC invention
XX
SQ Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1845 ATTCTAGAGGGTGGCT 1862
Db 20 ATTCTAGAGGATTGCT 3

RESULT 1980
ABA83532
ID ABA83532 standard; DNA; 20 BP.
XX
AC ABA83532;
XX
DT 08-FEB-2002 (first entry)
DE Human MP-1 antisense oligonucleotide SEQ ID NO 91.
XX
XX Human; mouse; rat; antisense gene therapy; MP-1; MAP kinase Partner 1;
KW antiinflammatory; cytostatic; antimicrobial; infection; tumour;
KW phosphorothioate; ss.
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone linkage, all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-MOE wings"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-MOE wings"
XX
US5306606-B1.
XX
PD 23-OCT-2001.
XX
PF 22-NOV-2000; 2000US-00721822.
PR 22-NOV-2000; 2000US-00721822.
XX
PA (ISIS-) ISIS PHARM INC.
PA (UYVI-) UNIV VIRGINIA.
XX
PI Weber MJ, Wyatt J, Cowser LM;
XX WPI; 2002-040199/05.
XX
XX New antisense oligonucleotides for modulating the expression of MP-1 (MAP

```

```

PT kinase partner 1), for preventing, delaying or treating infection,
PT inflammation or tumor formation, especially in humans.
XX
PS Example 15; Col 43-44; 47pp; English.
XX
CC The invention relates to an antisense compound (ABA83459-ABA83576) which
CC is up to 30 nucleobases in length and that inhibits the expression of MP-
CC 1 (MAP kinase Partner 1) in cells or tissues comprising contacting the
CC cells or tissues in vitro with the antisense compound so that expression
CC of MP-1 is inhibited. The antisense compounds have potential
CC antiinflammatory, cytostatic and antimicrobial activity. The antisense
CC compounds are useful for diagnostics, therapeutics, prophylaxis or as
CC research reagents or kits. The antisense oligonucleotides are useful in
CC gene therapy for treating an animal, particularly a human, suspected of
CC having or being prone to a disease or condition associated with the
CC expression of MP-1. In particular, the antisense oligonucleotides are
CC useful for preventing, delaying or treating infection, inflammation or
CC tumor formation. The present sequence is that of a human MP-1 antisense
CC oligonucleotide, comprising a chimeric oligonucleotide gapper 20
CC nucleotides in length, composed of a central gap region of ten 2'-
CC deoxynucleotides flanked by five nucleotide 2'-MOE wings
XX
SQ Sequence 20 BP; 8 A; 1 C; 0 G; 11 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2034 TTTTTCGAGATCTATTTT 2051
Db 2 TTTTAAAAATCTATTTT 19

RESULT 1981
ABN74818/c
ID ABN74818 standard; DNA; 20 BP.
XX
AC ABN74818;
XX
DT 26-JUL-2002 (first entry)
DE Human caspase 2 antisense inhibitor oligonucleotide #9.
XX
XX Caspase 2; antisense; cytostatic; osteopathic; cerebroprotective;
KW neuroprotective; antileptic; antiinflammatory; antimicrobial;
KW haematopoietic disorder; bone metabolism disorder; cholesterol disorder;
KW hyperproliferative disorder; cancer; blood disorder; stroke;
KW brain injury; neurodegenerative disease; infection; inflammation; tumour;
KW ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= m5C, OTHER
FT /note= "Nucleotides 1-5 and 16-20 are five-nucleotide
FT wings consisting 2'-methoxyethyl (2'-MOE) nucleotides, 6-
FT 15 are 2'-deoxynucleotides, backbone linkages are
FT phosphodiester, all cytosines are 5-methylcytidines"
XX
PN WO200224720-A1.
XX
PD 28-MAR-2002.
XX
PF 14-SEP-2001; 2001WO-US028631.
XX
PR 20-SEP-2000; 2000US-00667018.
XX
PA (ISIS-) ISIS PHARM INC.
XX Zhang H, Watt AT;
PI
XX

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DR WPI; 2002-351998/38.
XX
XX Novel antisense compounds targeted to nucleic acid molecule encoding
PT caspase 2, useful for treating diseases or conditions associated with
PT caspase 2, e.g. cancer, blood disorders, stroke, brain injury and
PT neurodegenerative diseases.
XX
XX Claim 3; Page 98; 146pp; English.
XX
XX The invention relates to a compound 8-50 nucleobases in length targeted
CC to a nucleic acid molecule encoding caspase 2, which specifically
CC hybridises with and inhibits the expression of caspase 2, or specifically
CC hybridises with at least an 8-nucleobase portion of an active site on a
CC nucleic acid molecule encoding caspase 2. The activity of antisense
CC oligonucleotides of the invention may be described as, cytostatic,
CC osteoprotective, cerebroprotective, neuroprotective, antilepemic,
CC antiinflammatory and antimicrobial. The antisense compounds are useful
CC for treating an animal having a disease or condition associated with
CC caspase 2, such as haematopoietic disorder, bone metabolism disorder,
CC cholesterol disorder, or a hyperproliferative disorder. These compounds
CC may further be used as research reagents and diagnostics, to distinguish
CC between functions of various members of a biological pathway, in the
CC treatment of a disease or disorder which can be treated by modulating the
CC expression of caspase 2, including cancer, blood disorders, stroke, brain
CC injury and neurodegenerative diseases. They may also be used for
CC prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
CC formation. Records ABN74810-ABN74952 represent caspase 2 mRNA inhibitor
CC oligonucleotides
XX
XX Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1675 TGGGTGAGCTCTTCAGG 1692
||| ||||| |||||
Db 19 TGAGGGAGCTCATCCAGG 2

RESULT 1982
AAS96810
ID AAS96810 standard; DNA; 20 BP.
XX
XX AAS96810;
AC
XX
XX 26-FEB-2002 (first entry)
DT
XX
XX Human STAT3 antisense phosphorothioate oligodeoxynucleotide #43.
DE
XX
XX STAT3; human; signal transducer and activator of transcription; ss; STAT;
KW antisense gene therapy; Fas-mediated apoptosis; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; cancer; breast; prostate; head;
KW neck; brain; leukaemia; myeloma; melanoma; lymphoma; apoptosis;
KW antiinflammatory; immunosuppressive; antineuritic; antiarthritic;
KW cytostatic.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX US2001029250-A1.
PN
XX
XX 11-OCT-2001.
PD
XX
XX 11-JAN-2001; 2001US-00758881.
PF
XX
XX 08-APR-1999; 99US-00288461.
PR
XX 06-APR-2000; 2000WO-US009054.
PR
XX (KARR/) KARRAS J G.
XX
XX Karras JG;
PI
XX

```

```

DR WPI; 2002-009991/01.
XX
XX Novel antisense compound useful for treating and diagnosing inflammatory
PT diseases and cancers, is targeted to a nucleic acid molecule encoding
PT signal transducer and activator of transcription proteins.
XX
XX Example 2; Page 13; 21pp; English.
XX
XX The invention relates to antisense compounds targeted to a nucleic acid
CC molecule encoding a signal transducer and activator of transcription
CC (STAT) protein, specifically STAT3, where the antisense compounds inhibit
CC the expression of STAT3. The antisense sequences are useful for
CC inhibiting the expression of STAT3 in cells or tissues, inducing Fas-
CC mediated apoptosis in cells, and sensitising cells to apoptosis. They are
CC also useful for treating an animal having a disease or condition
CC associated with STAT3. These disorders include inflammatory or autoimmune
CC disease, particularly rheumatoid arthritis, cancers, such as those of the
CC breast, prostate, brain and head and neck and leukaemias, myelomas,
CC melanomas and lymphomas. Also treatable are human diseases or conditions
CC characterised by a reduction in apoptosis or an insensitivity to
CC apoptotic signals. The sequences of the invention can be used in clinical
CC research, for detecting and determining the role of STAT3 in various cell
CC functions and physiological processes and for diagnosing conditions
CC associated with the expression of STAT3. The sequences represent cDNA
CC encoding human STAT3 and human STAT3 oligonucleotides
XX
XX Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 497 CCGAGGACATCGGCTTCT 514
||| ||||| |||||
Db 3 CCCAGGACATTTGGCATCT 20

RESULT 1983
AAS97922/C
ID AAS97922 standard; DNA; 20 BP.
XX
XX AAS97922;
AC
XX
XX 12-MAR-2002 (first entry)
DT
XX
XX Murine SAC1 gene-specific oligonucleotide PCR primer #475.
DE
XX
XX Human; mouse; SAC1; carbohydrate; sweeter; ethanol; alcoholism; ss;
KW obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
KW blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
KW protein replacement therapy.
XX
XX Mus sp.
OS
XX
XX WO200183749-A2.
PN
XX
XX 08-NOV-2001.
PD
XX
XX 25-APR-2001; 2001WO-US013387.
PF
XX
XX 28-APR-2000; 2000US-0200794P.
PR
XX 28-JUL-2000; 2000US-0221419P.
PR
XX 10-NOV-2000; 2000US-0247443P.
PR
XX
XX (WARN ) WARNER LAMBERT CO.
PA
XX (MONE-) MONELL CHEM SENSES CENT.
XX
XX Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PJ, Li S, Li X;
PI Ohman JD, Reed DR, Ross D, Tordoff MG;
XX
XX WPI; 2002-075162/10.
XX
XX Novel isolated polypeptide comprising variant form of mouse or human SAC1
PT

```


PT polypeptide, and is associated with altered preference for carbohydrates
 XX or other sweeteners, useful for preventing obesity, diabetes, alcoholism.

PS Claim 14; Page 92; 239pp; English.

XX The invention relates to an isolated polypeptide, comprising a variant
 CC form of mouse or human SAC1 polypeptide. The variant form is associated
 CC with altered preference for carbohydrates, other sweeteners or ethanol.
 CC The polypeptide and its associated DNA sequence can be produced by
 CC recombinant techniques and is useful for preventing obesity, diabetes or
 CC alcoholism associated with SAC1 expression. The sequences are useful in
 CC screening for drugs and sweeteners. Recombinant cell lines and transgenic
 CC embryos may be used in screening for and identifying agents that induce
 CC or repress function of SAC1. Predisposition to diabetes, obesity or
 CC alcoholism can be ascertained by testing any fluid or tissue of a human
 CC (such as blood, pancreas or tongue) for sequence variations of the SAC1
 CC gene. A sequence variation of the SAC1 locus may indicate a
 CC predisposition to diabetes, obesity and/or alcoholism and may provide a
 CC diagnostic mark. The polynucleotide can be detected in a biological
 CC sample by contacting the DNA with a probe to form a hybridisation complex
 CC which is then detected. The sequences represent cDNA encoding human and
 CC mouse SAC1 polypeptides and PCR primers specific for the SCAL genes

SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 1.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1630 TCCCGAGGACAGAAACC 1647

DB 19 TCACGAGGACAGAGAGC 2

RESULT 1984

AAS97965/C

ID AAS97965 standard; DNA; 20 BP.

AC AAS97965;

DT 12-MAR-2002 (first entry)

XX Murine SAC1 gene-specific oligonucleotide PCR primer #518.

XX Human; mouse; SAC1; carbohydrate; sweetener; ethanol; alcoholism; ss;
 KW obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
 KW blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
 KW protein replacement therapy.

XX Mus sp.

PN WO200183749-A2.

PD 08-NOV-2001.

XX 25-APR-2001; 2001WO-US013387.

XX 28-APR-2000; 2000US-0200794P.

PR 28-JUL-2000; 2000US-0221419P.

PR 10-NOV-2000; 2000US-0247443P.

XX (WARN) WARNER LAMBERT CO.

PA (MONE-) MONELL CHEM SENSES CENT.

XX Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PU, Li S, Li X;
 PI Ohmen UD, Reed DR, Ross D, Tordoff MG;

XX WPI; 2002-075162/10.

XX Novel isolated polypeptide comprising variant form of mouse or human SAC1
 PT polypeptide, and is associated with altered preference for carbohydrates
 PT or other sweeteners, useful for preventing obesity, diabetes, alcoholism.

XX

PS Claim 14; Page 94; 239pp; English.

XX The invention relates to an isolated polypeptide, comprising a variant
 CC form of mouse or human SAC1 polypeptide. The variant form is associated
 CC with altered preference for carbohydrates, other sweeteners or ethanol.
 CC The polypeptide and its associated DNA sequence can be produced by
 CC recombinant techniques and is useful for preventing obesity, diabetes or
 CC alcoholism associated with SAC1 expression. The sequences are useful in
 CC screening for drugs and sweeteners. Recombinant cell lines and transgenic
 CC embryos may be used in screening for and identifying agents that induce
 CC or repress function of SAC1. Predisposition to diabetes, obesity or
 CC alcoholism can be ascertained by testing any fluid or tissue of a human
 CC (such as blood, pancreas or tongue) for sequence variations of the SAC1
 CC gene. A sequence variation of the SAC1 locus may indicate a
 CC predisposition to diabetes, obesity and/or alcoholism and may provide a
 CC diagnostic mark. The polynucleotide can be detected in a biological
 CC sample by contacting the DNA with a probe to form a hybridisation complex
 CC which is then detected. The sequences represent cDNA encoding human and
 CC mouse SAC1 polypeptides and PCR primers specific for the SCAL genes

SQ Sequence 20 BP; 5 A; 0 C; 11 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 1.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1555 TTCTTCCCAACCCCTCA 1572

DB 20 TTCTTCCCAACCCCTCA 3

RESULT 1985

AAL40073

ID AAL40073 standard; DNA; 20 BP.

AC AAL40073;

DT 13-SEP-2002 (first entry)

XX Breast tissue library BS135 gene-specific clone related primer SEQ ID 36.

XX Cytostatic; BS135 nucleic acid; breast disease; breast tissue library;
 KW cancer; PCR; primer; ss.

XX Homo sapiens.

XX US2002045165-A1.

XX 18-APR-2002.

XX 16-DEC-1998; 98US-00215652.

XX 26-DEC-1997; 97US-00998496.

XX (BILL/) BILLINGEL P A.

XX (COHE/) COHEN M.

XX (COLP/) COLPITTS T L.

XX (KLAS/) KLASS M R.

XX (FRIE/) FRIEDMAN P N.

XX (GORD/) GORDON J.

XX (GRAN/) GRANADOS E N.

XX (HODG/) HODGES S C.

XX (KRAT/) KRATOCHVIL J D.

XX (RUSSELL) RUSSELL J C.

XX (STRO/) STROUPE S D.

XX Billington PA, Cohen M, Colpitts TL, Klass MR, Friedman PN;
 PI Gordon J, Granados EN, Hodges SC, Kratochvil JD, Russell JC;
 PI Stroupe SD;

XX WPI; 2002-507235/54.

XX A set of contiguous and partially overlapping cDNA sequences designated

PT BS135 are transcribed in breast tissue and useful to detect and treat
 PT breast disease including cancer.
 XX
 XX Example 2; Page 48; 61pp; English.
 XX
 CC The invention relates to novel purified polynucleotides derived from a
 CC BS135 nucleic acid. The purified polynucleotides derived from a BS135
 CC nucleic acid comprise the 16 sequences fully defined in the
 CC specification, their fragment or complement. Also provided by the
 CC invention are antibodies which specifically bind to BS135-encoded
 CC proteins, and agonists or inhibitors which prevent action of the tissue
 CC specific BS135 polypeptide. It is these molecules that can be used to
 CC detect breast disease, particularly cancer. This polynucleotide sequence
 CC represents a breast tissue library BS135 related PCR primer of the
 CC invention
 XX
 SQ Sequence 20 BP; 1 A; 6 C; 5 G; 8 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1985 TGCTGCTCTCTCTCTAAT 2002
 DB 3 TGCTGCTCTCTCTCTCAT 20
 RESULT 1986
 AAD41799/C
 ID AAD41799 standard; DNA; 20 BP.
 XX
 AC AAD41799;
 XX
 DT 30-OCT-2002 (first entry)
 XX
 DE Human RECQL2 antisense oligonucleotide, ISIS #137579.
 XX
 KW Antisense; RECQL2; Bloom's disorder; prophylaxis; infection; tumour;
 KW inflammation; therapy; human; phosphorothioate; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone"
 FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotides"
 FT modified_base 2
 FT /*tag= d
 FT /mod_base= m5c
 FT modified_base 12..13
 FT /*tag= e
 FT /mod_base= m5c
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotides"
 FT modified_base 17
 FT /*tag= f
 FT /mod_base= m5c
 XX
 XX US6399378-B1.
 XX
 PD 04-JUN-2002.
 XX
 XX 01-MAR-2001; 2001US-00798096.
 XX
 XX 01-MAR-2001; 2001US-00798096.
 PR

XX (ISIS-) ISIS PHARM INC.
 XX
 XX Ward DT, Watt AT;
 XX
 XX WPI; 2002-535979/57.
 DR
 XX Antisense compounds targeted to nucleic acids encoding RECQL2 associated
 PT with Bloom's disorder, for modulating RECQL2 expression and treating
 PT diseases e.g. tumors associated with expression of the RECQL2 in humans.
 XX
 XX Claim 3; Col 45; 86pp; English.
 PS
 XX The invention relates to antisense compounds targetted to nucleic acid
 CC encoding RECQL2 (gene associated with Bloom's disorder) to inhibit the
 CC expression of RECQL2. Antisense compounds of the invention are useful for
 CC treating diseases associated with expression of RECQL2, in humans. They
 CC are useful for diagnostics, therapeutics and as research reagent, e.g.
 CC prophylactically to prevent or delay infection, inflammation or tumour
 CC formation. They are also useful in antisense therapy. The present
 CC sequence is an antisense oligonucleotide targetted to human RECQL2 DNA
 XX
 SQ Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2074 ATAAATGGTACATTCT 2091
 DB 20 ATAGCATGGTACATTACT 3
 RESULT 1987
 AAD41790/C
 ID AAD41790 standard; DNA; 20 BP.
 XX
 AC AAD41790;
 XX
 DT 30-OCT-2002 (first entry)
 XX
 DE Human RECQL2 antisense oligonucleotide, ISIS #137570.
 XX
 KW Antisense; RECQL2; Bloom's disorder; prophylaxis; infection; tumour;
 KW inflammation; therapy; human; phosphorothioate; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone"
 FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotides"
 FT modified_base 9
 FT /*tag= d
 FT /mod_base= m5c
 FT modified_base 11
 FT /*tag= e
 FT /mod_base= m5c
 FT modified_base 15
 FT /*tag= f
 FT /mod_base= m5c
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotides"
 FT modified_base 20
 FT /*tag= g

```

PT XX /mod_base= m5c
PN XX
XX US6399378-B1.
XX
XX 04-JUN-2002.
XX
XX 01-MAR-2001; 2001US-00798096.
XX
XX 01-MAR-2001; 2001US-00798096.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ward DT, Watt AT;
XX
XX WPI; 2002-535979/57.
XX
XX Antisense compounds targeted to nucleic acids encoding RECQL2 associated
PT with Bloom's disorder, for modulating RECQL2 expression and treating
PT diseases e.g. tumors associated with expression of the RECQL2 in humans.
XX
XX Example 15; Col 45; 86pp; English.
XX
XX The invention relates to antisense compounds targetted to nucleic acid
CC encoding RECQL2 (gene associated with Bloom's disorder) to inhibit the
CC expression of RECQL2. Antisense compounds of the invention are useful for
CC treating diseases associated with expression of RECQL2, in humans. They
CC are useful for diagnostics, therapeutics and as research reagent, e.g.
CC prophylactically to prevent or delay infection, inflammation or tumour
CC formation. They are also useful in antisense therapy. The present
CC sequence is an antisense oligonucleotide targetted to human RECQL2 DNA
XX
XX Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 922 TTGTCAAGAGCTTTAAC 939
DB 19 TTTAGCATGAGCTTTAAC 2
RESULT 1988
ABA93202
ID ABA93202 standard; DNA; 20 BP.
XX
XX ABA93202;
XX
XX 17-APR-2002 (first entry)
XX
XX Human vitamin D receptor gene PCR primer SEQ ID NO:11.
XX
XX Human; vitamin D receptor; apolipoprotein E; oestrogen receptor; VDR;
XX ApoE; bone-related disease; polymorphism; detection; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX JP2001333798-A.
XX
XX 04-DEC-2001.
XX
XX 26-MAY-2000; 2000JP-00155871.
XX
XX 26-MAY-2000; 2000JP-00155871.
XX
XX (NISS-) NISSHO KK.
XX
XX WPI; 2002-135948/18.
XX
XX A reagent for detecting simultaneously a gene polymorphism of the vitamin
PT D receptor gene, apolipoprotein E gene and estrogen receptor gene.
XX
XX Claim 3; Page 2; 13pp; Japanese.
XX

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```

XX The present invention describes a reagent for detecting simultaneously
CC the gene polymorphism of the vitamin D receptor (VDR) gene,
CC apolipoprotein E (ApoE) gene and oestrogen receptor (ER) gene. Also
CC described is a method for detecting simultaneously the gene polymorphism
CC of VDR gene, ApoE gene and ER gene in which the reagent is used to detect
CC the gene polymorphism of VDR, ApoE and ER in a sample. The reagent can be
CC used for selecting a treating agent for bone-related diseases. The
CC present sequence represents a specifically claimed PCR primer for the
CC human VDR gene, for use in a reagent of the present invention
XX
XX Sequence 20 BP; 3 A; 3 C; 10 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1205 TGCAGGCGATTCTCTGAGG 1222
DB 2 TGCAGGCGATTCTGTTAGG 19
RESULT 1989
ABV73220
ID ABV73220 standard; DNA; 20 BP.
XX
XX AC ABV73220;
XX
XX 08-JAN-2003 (first entry)
XX
XX Human blood coagulation factor X gene detecting 5' primer.
XX
XX Cell proliferation; liver; hepatotropic; cell therapy; drug metabolism;
XX liver failure; haemophilia; galactosemia; blood coagulation factor X;
XX PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200274968-A1.
XX
XX 26-SEP-2002.
XX
XX 15-MAR-2002; 2002WO-US006639.
XX
XX 16-MAR-2001; 2001US-00809187.
XX
XX (KOBAYASHI N.
XX (LEBOULCH P.
XX (TANAKA N.
XX (FUJIWARA T.
XX (TOTSUGAWA T.
XX
XX Kobayashi N, Leboulch P, Tanaka N, Fujiwara T, Totsugawa T;
XX WPI; 2002-740860/80.
XX
XX Proliferating a liver cell useful as a model for drug metabolism in human
PT liver and for treating liver insufficiency, comprises transferring a cell
PT proliferation factor gene into a liver cell to obtain an in vitro
PT immortalized liver cell.
XX
XX Example 2; Page 23; 45pp; English.
XX
XX The invention relates to proliferating a liver cell and involves
CC transferring a cell proliferation factor gene into a mammalian liver cell
CC to obtain an in vitro immortalized liver cell, proliferating the in vitro
CC immortalized liver cell, and removing the cell proliferation factor gene
CC from the in vitro immortalized liver cell. The method is useful in
CC proliferating a liver cell to produce an in vitro immortalized liver cell
CC which can be used as an assay model for drug metabolism in human liver.
CC The in vitro liver cell may also be used for treating liver insufficiency
CC (liver failure and liver-based metabolic diseases such as haemophilia or
CC galactosemia) and as an artificial liver. Sequences ABV73206-225

```

CC represent PCR primers used in an assay for detecting the expression of
 CC various genes which were important to metabolism in a liver, i.e. albumin
 CC gene, ASGP gene, bilirubin UGT gene, CYP3A4 gene, GK gene, GS gene, GST-
 CC pie gene, human blood coagulation factor X gene, beta-actin gene and
 CC hTERT gene
 CC
 SQ Sequence 20 BP; 5 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 608 GCGTGAAGAGGCTTCT 625
 |||||
 Db 3 GCATGAAGAGACCTGCT 20

RESULT 1990
 ABA02922/c
 ID ABA02922 standard; DNA; 20 BP.

AC ABA02922;
 DT 15-FEB-2002 (first entry)
 DE Human HO-1 RT-PCR primer SEQ ID NO 41.

KW Human; acute transplant rejection; gene expression;
 KW pro-apoptotic gene cluster; cytoprotective; IL-7/17; IL-8; IL-10; IL-15;
 KW T cell; urinary system; renal graft; antimicrobial; antiviral;
 KW antifungal; competitive template RT-PCR; PCR primer; ss.
 XX Synthetic.

XX WO200181916-A2.
 XX 01-NOV-2001.

XX 23-APR-2001; 2001WO-US013014.
 XX 24-APR-2000; 2000US-0199327P.
 XX 06-OCT-2000; 2000US-0238718P.
 XX 12-OCT-2000; 2000US-0239635P.
 XX 16-OCT-2000; 2000US-0240735P.
 XX 06-FEB-2001; 2001US-00778013.

XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX Ma N, Strom T, Soares MC, Ferran C, Suthanthiran M;
 XX Vasconcellos L, Avhingsanon Y;
 XX WPI; 2002-034457/04.

XX Evaluating acute transplant rejection in a host especially in a recipient
 XX of a urinary system graft, by determining a heightened magnitude of
 XX expression of genes in rejection-associated gene clusters.
 XX Claim 35; Fig 7; 101pp; English.

XX The invention relates to evaluating acute transplant rejection in a host,
 XX comprising obtaining a sample, determining the magnitude of gene
 XX expression of at least two genes from one or more rejection associated-
 XX gene clusters, where the genes were selected from the pro-apoptotic
 XX cluster, the cytoprotective cluster, the IL-7/17, IL-8, IL-10, IL-15 and
 XX T cell clusters, comparing the results to a baseline magnitude of gene
 XX expression of the two genes and detecting upregulation of the two genes.
 XX The method is useful for evaluating acute transplant rejection in a host
 XX especially in a recipient of a urinary system (renal) graft, where gene
 XX expression in the urine sample of at least two genes of a pro-apoptotic
 XX gene cluster is determined. The method is further useful for treating a
 XX transplant-related condition in a host. The method comprises
 XX choosing a therapy comprising adding to the host's baseline therapeutic
 XX regimen an effective dose of an anti-rejection agent appropriate, for

CC treating rejection state. The anti-rejection agent is selected from
 CC azathioprine, cyclosporine, FK506, mycophenolate mofetil, anti-CD25
 CC antibody, antithymocyte globulin, rapamycin, ACE inhibitors, perillyl
 CC alcohol, anti-CD14 antibody, anti-CD40L antibody, anti-thrombin III,
 CC tissue plasminogen activator, antioxidants, anti-CD154, anti-CD3
 CC antibody. The therapy may further comprise modifying the host's baseline
 CC therapeutic regimen by adding pharmacological agent selected from
 CC antimicrobial agents, antiviral agents and antifungal agents or by
 CC reducing a dose of a baseline anti-rejection agent. The method accurately
 CC quantitate marker gene expression in biopsy tissue, urine, urine
 CC sediment, peripheral blood mononuclear and other body fluids and
 CC correlates the magnitude of expression of these genes with rejection of
 CC allografts. Moreover, the evaluation of the expression of marker genes in
 CC a post-transplant sample, along with the evaluation of the expression of
 CC an infectious agent gene also accurately detects allografts rejection.
 CC The is rapid and reliable for diagnosing acute rejection, even in cases
 CC where allograft biopsies show only mild cellular infiltrates. The present
 CC sequence is that of a PCR primer used for quantitation of gene expression
 CC by competitive template RT-PCR in a method of the invention
 SQ Sequence 20 BP; 1 A; 5 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1642 GAACCAAGGCCCGAGC 1659
 |||||
 Db 18 GACACCAAGGACGAGC 1

RESULT 1991
 ABK68200/c
 ID ABK68200 standard; DNA; 20 BP.

XX ABK68200;
 XX 02-JUL-2002 (first entry)
 XX Mouse HYPLIPI locus specific primer C4b-f.

XX Mouse; primer; antilipemic; cardiant; hypotensive; anorectic; HYPLIPI;
 XX FCHL1; lipid disorder; familial combined hyperlipidaemia;
 XX coronary artery disease; atherogenic lipoprotein phenotype; cancer;
 XX hyperapobetalipoproteinaemia; hypertriglyceridaemia; obesity; ss;
 KW familial dyslipidaemic hypertension; syndrome X; insulin resistance;
 KW hypercholesterolaemia; chromosome 3.

OS Mus sp.
 XX WO200220847-A2.
 XX 14-MAR-2002.

XX 07-SEP-2001; 2001WO-US028181.
 XX 08-SEP-2000; 2000US-0231322P.
 XX (REGC) UNIV CALIFORNIA.

XX Bodnar JS, Castellani LW, Chatterjee A, De Jong P, Lusis AJ;
 XX Ohmen J, Ross D, Tafuri S, Wu C;
 XX WPI; 2002-339808/37.

XX Novel HYPLIPI and FCHL1 genes and their sequence variations associated
 XX with lipid disorder and cancer, useful for prognosis, diagnosis and
 XX treatment of lipid disorders.
 XX Claim 11; Page 74; 102pp; English.

XX This invention relates to the cDNA and protein sequences of novel
 CC proteins HYPLIPI or FCHL1 and to sequence variations within these genes

CC that have been shown to be associated with lipid disorders.
CC Oligonucleotide probes that hybridise to the cDNA sequence are useful for
CC analysing the expression of FCHL1 by detecting the expression of the mRNA
CC transcript in the sample. A host cell transformed with the cDNA of the
CC invention is useful for producing the protein by recombinant means.
CC Pharmaceutical compositions based on the sequences of the invention are
CC useful for treating or preventing a lipid disorder associated with
CC expression of FCHL1 such as familial combined hyperlipidaemia, coronary
CC artery disease, atherogenic lipoprotein phenotype,
CC hyperapobetalipoproteinaemia, hypertriglyceridaemia, familial
CC dyslipidaemic hypertension, syndrome X, obesity, insulin resistance and
CC hypercholesterolaemia. The cDNA sequence is useful in the diagnosis or
CC prognosis of predisposition to lipid disorders and cancers, and also to
CC identify a molecule which enhances or decreases the HYPLIPI or FCHL1
CC activity. The present sequence represents an oligonucleotide primer
CC specific for the mouse HYPLIPI locus of the invention. The mouse HYPLIPI
CC locus is situated on chromosome 3
XX
SQ Sequence 20 BP; 8 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred.No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1522 TCAGCTCTGGCTTCCTG 1539
Db 19 TCACCTCTGTTCCTG 2

RESULT 1992
AAD39526/c
ID AAD39526 standard; DNA; 20 BP.
XX
AC AAD39526;
XX
DT 04-OCT-2002. (first entry)
XX
DE Human calreticulin antisense oligonucleotide, ISIS 109319.
KW Human; calreticulin; antisense compound; hyperproliferative disorder;
KW cancer; autoimmune disease; viral infection; cardiovascular disease;
KW antisense therapy; cytostatic; immunosuppressive; virucide; antisense;
KW phosphorothioate backbone; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT modified_base 5
FT /note= "2'methoxyethyl nucleotides"
FT /*tag= d
FT /mod_base= m5c
FT modified_base 6..20
FT /*tag= c
FT /mod_base= OTHER
FT modified_base 8
FT /note= "2'methoxyethyl nucleotides"
FT /*tag= e
FT /mod_base= m5c
FT modified_base 11
FT /*tag= f
FT /mod_base= m5c
FT modified_base 12
FT /*tag= g
FT /mod_base= m5c
FT modified_base 14

FT /*tag= h
FT /mod_base= m5c
FT modified_base 15
FT /*tag= i
FT /mod_base= m5c
FT modified_base 17
FT /*tag= j
FT /mod_base= m5c
FT modified_base 18
FT /*tag= k
FT /mod_base= m5c
XX
WO200236743-A2.
XX
PD 10-MAY-2002.
XX
PF 30-OCT-2001; 2001WO-US049045.
XX
PR 30-OCT-2000; 2000US-00702327.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowsett LM;
XX
DR WPI; 2002-479759/51.
XX
PT Novel antisense compound targeted to nucleic acid encoding calreticulin,
PT useful for treating a human having disease or condition associated with
PT calreticulin e.g. cancer, viral infection, autoimmune disease.
XX
PS Claim 3; Page 82; 109pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of calreticulin. The compositions comprise
CC antisense compounds, particularly antisense oligonucleotides, targeted
CC to nucleic acids encoding calreticulin. The antisense compound is useful
CC for inhibiting the expression of calreticulin in human cells or tissues.
CC It is also useful for treating a human having a disease or condition
CC associated with calreticulin, e.g., hyperproliferative disorder e.g.
CC cancer, autoimmune disease, viral infection or cardiovascular disease, by
CC inhibiting expression of calreticulin. It is useful for diagnostics,
CC therapeutics, prophylaxis and as research reagents and kits. It is also
CC used in antisense therapy. The present sequence is an antisense compound
CC targeted to human calreticulin. This sequence is used to study the
CC antisense inhibition of calreticulin expression-phosphorothioate 2'-MOE
CC gapmer oligonucleotides
XX
SQ Sequence 20 BP; 0 A; 8 C; 1 G; 11 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred.No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1424 AGGAGAAGAAGAGTCA 1441
Db 19 AGGAGGAGGAGAGACACA 2

RESULT 1993
ABL43113
ID ABL43113 standard; DNA; 20 BP.
XX
AC ABL43113;
XX
DT 11-APR-2002 (first entry)
XX
DE Human chromosome 1p36-35 PCR primer SEQ ID NO:157.
XX
KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX

```

PN  JP2001321190-A.
XX  20-NOV-2001.
XX  12-MAR-2001; 2001JP-00068285.
XX  10-MAR-2000; 2000JP-00066716.
XX  (RIKA ) RIKAGAKU KENKYUSHO.
XX  (GENO-) GENOTEX YG.
XX  WPI; 2002-144136/19.
XX  Arraying genome clones.
XX  Claim 4; Page 8; 528pp; Japanese.
XX  The present invention describes a method of arraying genome clones. The
XX  method comprises: (a) clones of the genomic libraries contained in
XX  multiwell plates numbered for discrimination are mixed in each of the
XX  multiwell plates; (b) a primer designed based on the chromosome marker
XX  sequence is added to the mixture to carry out an amplification reaction;
XX  (c) a signal corresponding to the marker is detected from the resultant
XX  amplified product to specify the discrimination Nos. of the multiwell
XX  plates containing the clones having said marker sequence; (d) the order
XX  of the markers is changed so that the same discrimination Nos. succeed to
XX  the maximum in the specified discrimination Nos. to array the multiwell
XX  plates; (e) the clones in the multiwell plates of the specified
XX  discrimination Nos. are mixed respectively in each wells of longitudinal
XX  and lateral directions; (f) the mixed clones are cultured and the
XX  resultant cultures are amplified by using the above primer; (g) signals
XX  are detected from the amplified products; (h) the clones in the multiwell
XX  plates are specified from the detected result; and (i) the clones are
XX  reconstituted as the positions on the chromosome and arrayed. The
XX  microarray is useful for gene analysis. ABL42957 to ABL45322 represent
XX  PCR primers for human chromosome lp36-35 DNA, and ABL45323 to ABL45634
XX  represent PCR primers for human chromosome 21q22.1, which are
XX  specifically claimed for use in the present invention
XX  Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
SQ  Query Match 0.6%; Score 13.2; DB 1; Length 20;
    Best Local Similarity 83.3%; Pred. No. 1.3e+03;
    Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  351 TGGTGAGGAGCTGTCCAGT 368
    |||||
Db  2 TGGTGAGGAGCTCCAGT 19

RESULT 1994
ABL44019
ID  ABL44019 standard; DNA; 20 BP.
XX  ABL44019;
AC  ABL44019;
XX  11-APR-2002 (first entry)
XX  Human chromosome lp36-35 PCR primer SEQ ID NO:1063.
XX  Human; chromosome lp36-35; chromosome 21q22.1; genetic analysis; genome;
XX  PCR primer; ss.
XX  Homo sapiens.
XX  JP2001321190-A.
XX  20-NOV-2001.
XX  12-MAR-2001; 2001JP-00068285.
XX  10-MAR-2000; 2000JP-00066716.
XX  (RIKA ) RIKAGAKU KENKYUSHO.
XX  (GENO-) GENOTEX YG.
XX  WPI; 2002-144136/19.
XX  Arraying genome clones.
XX  Claim 4; Page 16; 528pp; Japanese.

PA  (RIKA ) RIKAGAKU KENKYUSHO.
XX  (GENO-) GENOTEX YG.
XX  WPI; 2002-144136/19.
XX  Arraying genome clones.
XX  Claim 4; Page 26; 528pp; Japanese.
XX  The present invention describes a method of arraying genome clones. The
XX  method comprises: (a) clones of the genomic libraries contained in
XX  multiwell plates numbered for discrimination are mixed in each of the
XX  multiwell plates; (b) a primer designed based on the chromosome marker
XX  sequence is added to the mixture to carry out an amplification reaction;
XX  (c) a signal corresponding to the marker is detected from the resultant
XX  amplified product to specify the discrimination Nos. of the multiwell
XX  plates containing the clones having said marker sequence; (d) the order
XX  of the markers is changed so that the same discrimination Nos. succeed to
XX  the maximum in the specified discrimination Nos. to array the multiwell
XX  plates; (e) the clones in the multiwell plates of the specified
XX  discrimination Nos. are mixed respectively in each wells of longitudinal
XX  and lateral directions; (f) the mixed clones are cultured and the
XX  resultant cultures are amplified by using the above primer; (g) signals
XX  are detected from the amplified products; (h) the clones in the multiwell
XX  plates are specified from the detected result; and (i) the clones are
XX  reconstituted as the positions on the chromosome and arrayed. The
XX  microarray is useful for gene analysis. ABL42957 to ABL45322 represent
XX  PCR primers for human chromosome lp36-35 DNA, and ABL45323 to ABL45634
XX  represent PCR primers for human chromosome 21q22.1, which are
XX  specifically claimed for use in the present invention
XX  Sequence 20 BP; 4 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
SQ  Query Match 0.6%; Score 13.2; DB 1; Length 20;
    Best Local Similarity 83.3%; Pred. No. 1.3e+03;
    Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1742 GTGCCAGGTCGTGGTGAA 1759
    |||||
Db  3 GTGCCAGGTCGTGGTGAA 20

RESULT 1995
ABL43525
ID  ABL43525 standard; DNA; 20 BP.
XX  ABL43525;
AC  ABL43525;
XX  11-APR-2002 (first entry)
XX  Human chromosome lp36-35 PCR primer SEQ ID NO:569.
XX  Human; chromosome lp36-35; chromosome 21q22.1; genetic analysis; genome;
XX  PCR primer; ss.
XX  Homo sapiens.
XX  JP2001321190-A.
XX  20-NOV-2001.
XX  12-MAR-2001; 2001JP-00068285.
XX  10-MAR-2000; 2000JP-00066716.
XX  (RIKA ) RIKAGAKU KENKYUSHO.
XX  (GENO-) GENOTEX YG.
XX  WPI; 2002-144136/19.
XX  Arraying genome clones.
XX  Claim 4; Page 16; 528pp; Japanese.

```

XX The present invention describes a method of arraying genome clones. The
 CC method comprises: (a) clones of the genomic libraries contained in
 CC multiwell plates numbered for discrimination are mixed in each of the
 CC multiwell plates; (b) a primer designed based on the chromosome marker
 CC sequence is added to the mixture to carry out an amplification reaction;
 CC (c) a signal corresponding to the marker is detected from the resultant
 CC amplified product to specify the discrimination Nos. of the multiwell
 CC plates containing the clones having said marker sequence; (d) the order
 CC of the markers is changed so that the same discrimination Nos. succeed to
 CC the maximum in the specified discrimination Nos. to array the multiwell
 CC plates; (e) the clones in the multiwell plates of the specified
 CC discrimination Nos. are mixed respectively in each wells of longitudinal
 CC and lateral directions; (f) the mixed clones are cultured and the
 CC resultant cultures are amplified by using the above primer; (g) signals
 CC are detected from the amplified products; (h) the clones in the multiwell
 CC plates are specified from the detected result; and (i) the clones are
 CC reconstituted as the positions on the chromosome and arrayed. The
 CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
 CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
 CC represent PCR primers for human chromosome 21q22.1, which are
 CC specifically claimed for use in the present invention
 XX
 SQ Sequence 20 BP; 8 A; 2 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1467 GAAGCAGAGCAAGCAAGG 1484
 ||||| ||||| ||||| |||||
 Db 3 GAAGTCAGAGCAATGG 20
 RESULT 1996
 AAD29652
 ID AAD29652 standard; DNA; 20 BP.
 XX
 AC AAD29652;
 XX
 DT 17-MAY-2002 (first entry)
 XX
 DE Human DGAT gene polymorphism identifying p16 PCR primer.
 XX
 KW Human; diacylglycerol acyltransferase; DGAT; hypotensive; gene therapy;
 KW severe leanness; atherosclerosis; hypertension; coronary artery disease;
 KW enzyme; anorectic; antilipemic; abnormal fat storage; PCR primer;
 KW obesity; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200204682-A2.
 XX
 PD 17-JAN-2002.
 XX
 PF 10-JUL-2001; 2001WO-US021915.
 XX
 PR 11-JUL-2000; 2000US-00613444.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Ludwig EH, Farese RV, Innerarity TL, Cases S;
 XX WPI; 2002-188471/24.
 XX
 PT Detecting polymorphism associated with abnormal fat storage in an
 PT individual by analyzing polynucleotide sample from individual for
 PT presence of polymorphism in diacylglycerol acyltransferase gene.
 XX
 PS Example 1; Page 38; 63pp; English.
 XX
 CC The invention relates to a method for detecting a polymorphism associated
 CC with abnormal fat storage (a condition associated with diacylglycerol

CC acyltransferase (DGAT)) in an individual. The method involves analysing a
 CC polynucleotide sample from the individual for the presence of a
 CC polymorphism in DGAT gene, where the polymorphism is associated with a
 CC condition associated with DGAT activity. The method is useful for
 CC detecting a propensity of an individual to develop a condition associated
 CC with DGAT activity such as obesity, severe leanness, atherosclerosis,
 CC hypertension, excessive levels of serum triglycerides, high HDL (high
 CC density lipoprotein) levels, or coronary artery disease; and for
 CC genetically diagnosing a condition associated with DGAT activity in an
 CC individual. The present sequence is a PCR primer used for identifying
 CC human DGAT gene polymorphism
 XX
 SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 566 AGAGGCTTCTGTGCATTG 583
 ||||| ||||| ||||| |||||
 Db 2 AGAGGCTTCTGTGCATTG 19
 RESULT 1997
 ABX85923/c
 ID ABX85923 standard; DNA; 20 BP.
 XX
 AC ABX85923;
 XX
 DT 16-AUG-2002 (first entry)
 XX
 DE Methicillin resistant Staphylococcus aureus detection primer #23.
 XX
 KW Methicillin resistant Staphylococcus aureus; MRSA; primer; ss; mecA;
 KW probe.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP1160333-A2.
 XX
 PD 05-DEC-2001.
 XX
 PF 29-MAY-2001; 2001EP-00112100.
 XX
 PR 29-MAY-2000; 2000JP-00163149.
 PR 09-JUN-2000; 2000JP-00179394.
 XX
 PA (TOYU) TOSOH CORP.
 XX
 PI Taya T, Ishiguro T, Saito J;
 XX WPI; 2002-396248/43.
 XX
 PT New oligonucleotide specific for the mecA methicillin-resistance gene,
 PT useful for cleavage, detection and amplification of the gene or related
 PT mRNA.
 XX
 PS Claim 5; Page 20; 28pp; English.
 XX
 CC This invention relates to oligonucleotides used for cleaving, detecting
 CC and amplifying the mecA gene (associated with methicillin resistance in
 CC Staphylococcus aureus) or its derived RNA. The invention also comprises a
 CC detection method employing an RNA amplification process, using RNA
 CC derived from the mecA gene as template. Also disclosed is a detection
 CC method for a methicillin-resistant S. aureus (MRSA), comprising an RNA
 CC amplification process in the presence of a complementary oligonucleotide
 CC probe labelled with an intercalated fluorescent dye, where complementary
 CC binding of the probe to the RNA transcription product results in a change
 CC in the fluorescent property relative to that of a situation where a
 CC complex formation is absent, and then measuring the fluorescence
 CC intensity of the reaction solution. The oligonucleotides may be used as
 CC primers or probes, for detecting methicillin-resistant S. aureus in
 CC clinical samples. They may also be used therapeutically to inhibit RNA

CC methods for modulating the expression of MEKK4 (also referred as mitogen-
CC activated protein kinase kinase 4; MAP3K4; MAP three kinase 1; MAP/ERK
CC kinase kinase 4; MAPKKK4; MKK1). The antisense oligos are useful for
CC inhibiting the expression of MEKK4 in cells or tissues. They are also
CC useful for treating an animal having a disease or condition associated
CC with MEKK4 such as immunological, inflammatory, hyperproliferative
CC disorder or cancer. Sequences of the invention are also useful for
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC They are also useful in antisense therapy. The present sequence is an
CC antisense oligonucleotide targeted to human MEKK4 DNA. This sequence is
CC used in the exemplification of the invention
XX
SQ Sequence 20 BP; 5 A; 3 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2039 GAGATACCTATTTTCATT 2056
|| ||||| ||||| |||||
Db 1 GACATACCTTTTGATT 18

RESULT 2000
ABN87561
ID ABN87561 standard; DNA; 20 BP.
AC ABN87561;
XX
XX

DT 06-AUG-2002 (first entry)

DE Chicken sonic hedgehog (Shh) related oligonucleotide SEQ ID NO:28.

XX Sonic hedgehog; Shh; desert hedgehog; Dhh; Indian hedgehog; Ihh;
XX antiparkinsonian; antiarrhythmic; neuroprotective; anticonvulsant;
KW cytosolic; nontropic; spermatogenesis; peripheral nervous system;
KW central nervous system; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; arrhythmia; nerve degeneration; multiple sclerosis;
KW immunological disorder; neoplastic; hyperplastic; ss.

XX Gallus gallus.

OS Synthetic.

XX US6384192-B1.

XX 07-MAY-2002.

XX 20-OCT-1997; 97US-00957874.

XX 30-DEC-1993; 93US-00176427.

PR 14-DEC-1994; 94US-00356060.

PR 04-MAY-1995; 95US-00435099.

PR 05-JUN-1995; 95US-00462386.

XX (HARD) HARVARD COLLEGE.

PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

XX Ingham PW, McMahon AP, Tabin CJ;

XX WPI; 2002-442817/47.

XX New vertebrate hedgehog-related proteins, useful e.g. for promoting
PT differentiation, survival and proliferation of cells, e.g. for treating
PT neurodegeneration.

XX Example 2; Col 71; 116pp; English.

XX The present invention describes an isolated and/or recombinant

CC polypeptide (I) comprising a hedgehog (hh) amino acid (aa) sequence
CC encoded by a nucleic acid (II) that hybridizes under stringent conditions
CC to 1 of 6 sequences (see ABN87544, and ABN87546 to ABN87550). (I) binds
CC to a natural patched receptor. Specifically claimed example of (I) are
CC given in ABN79132 and ABN79134 to ABN79138. (I) has antiparkinsonian,

CC nontropic, neuroprotective, anticonvulsant, antiarrhythmic and cytostatic
CC activities. (I) induces the expression of the BMP-2 and -4 genes, and of
CC the Hoxd gene. (I) can be used: (i) to promote differentiation of
CC neuronal cells and survival of the differentiated cells, specifically
CC dopaminergic or motor neurons, proliferation of chondrocytes, and
CC proliferation, differentiation and/or survival of mesodermal or
CC ectodermal cells, either in cell cultures (particularly for preparation
CC of transplants) or therapeutically; (ii) for detecting loss of response
CC in tissues or cells, to hh proteins; (iii) in drug screening (to identify
CC antagonists, useful e.g. for inhibition of spermatogenesis); and (iv)
CC for isolation of cognate receptors. (I) may be used therapeutically to
CC treat e.g. injuries/defects in the central or peripheral nervous systems,
CC including Alzheimer's, Parkinson's and Huntington's diseases, or
CC arrhythmias caused by nerve degeneration; immunological disorders of the
CC nervous system, e.g. multiple sclerosis; neoplastic and hyperplastic
CC alterations in the central nervous system, also to promote attachment of
CC prostheses. The present sequence represents an oligonucleotide which is
CC used in an example from the present invention
XX
SQ Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1436 AAGTCACCGAAGAGGAGA 1453
||||| ||||| ||||| |||||
Db 1 AAGTCACCGCAGAGGAGA 18

RESULT 2001

ABQ80503

ID ABQ80503 standard; DNA; 20 BP.

XX ABQ80503;

DT 31-OCT-2002 (first entry)

DE NB-1 reverse PCR primer.

XX PCR; primer; allergic disease; allergy; NB-1; E48 antigen; c-fos;

KW involucrin; BENE; HBP17; fibronectin; IdL; ss.

XX Synthetic.

XX JP2002191398-A.

XX 09-JUL-2002.

XX 26-DEC-2000; 2000JP-00396167.

PR 26-DEC-2000; 2000JP-00396167.

XX (GENO-) GENOX SOYAKU KENKYUSHO KK.

XX WPI; 2002-594354/64.

XX Inspection of allergic diseases, and a reagent for the inspection of
PT allergic diseases.

XX Example 2; Page 13; 31pp; Japanese.

XX The present invention relates to a method for the inspection of allergic
CC diseases. The method involves measuring the expression level of a gene
CC selected from the group consisting of NB-1, E48 antigen, c-fos,
CC involucrin, BENE, HBP17, fibronectin and IdL in a biopsy sample, and
CC comparing it with the expression level of the gene in a biopsy sample of
CC a healthy person. The present primer was used in an example from the
CC invention

SQ Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;

```
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 529 ATGCTCTTGCCCATCTG 546
Db 3 ATCTTCTGCGCATCATG 20

RESULT 2002
ABT12854
ID ABT12854 standard; DNA; 20 BP.
XX
AC ABT12854;
XX
DT 16-JAN-2003 (first entry)
XX
DE Human RECQL gene antisense oligonucleotide #35.
XX
KW Human; antisense therapy; ss; RECQL; hyperproliferative disorder; cancer;
KW premature ageing; infection; inflammation; tumour formation; 2'-MOE;
KW antisense oligonucleotide; phosphorothioate backbone; 2'-methoxyethyl.
XX
OS Homo sapiens.
XX
PN WO200268590-A2.
XX
PD 06-SEP-2002.
XX
PF 21-FEB-2002; 2002WO-US005225.
XX
PR 23-FEB-2001; 2001US-00793807.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ward DT, Watt AT;
XX
DR WPI; 2002-750415/81.
XX
New antisense oligonucleotides targeted to a nucleic acid encoding RECQL,
PT useful for modulating the expression of RECQL protein, or for treating a
PT disease or condition associated with the expression of RECQL, e.g.
PT cancer.
XX
PS Example 15; Page 91; 138pp; English.
XX
The invention comprises antisense oligonucleotides which inhibit
CC expression of the human RECQL gene. The antisense oligonucleotides of the
CC invention are useful for modulating the expression of RECQL protein and
CC in treating hyperproliferative disorders (e.g. cancer and conditions
CC involving premature ageing. The antisense oligonucleotides of the
CC invention are also useful for diagnostics, therapeutics and prophylaxis
CC (e.g. to prevent or delay infection, inflammation or tumour formation).
CC The present DNA sequence represents an RECQL antisense oligonucleotide of
CC the invention. NOTE: The present DNA sequence contains a phosphorothioate
CC backbone, nucleotides 1-5 and 16-20 are 2'-methoxyethyl (2'-MOE)
CC nucleotides
XX
SQ Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1275 CATCTCGATCTGCTCTC 1292
Db 2 CATCTCGACCTGCGAGTC 19

RESULT 2003
ABQ62423
ID ABQ62423 standard; DNA; 20 BP.
XX
AC ABQ62423;
```

```
XX
DT 16-AUG-2002 (first entry)
XX
DE Mouse syntaxin 4 interacting protein antisense oligonucleotide 10.
XX
KW Mouse; antisense gene therapy; Syntaxin 4 interacting protein; ss;
KW antisense oligonucleotide; diabetes; obesity; skeletal muscle disorder;
KW inflammation; tumour formation; phosphorothioate backbone;
KW 2'-O-methoxyethyl wing.
XX
OS Mus musculus.
XX
PN WO200224864-A2.
XX
PD 28-MAR-2002.
XX
PF 19-SEP-2001; 2001WO-US029251.
XX
PR 22-SEP-2000; 2000US-00668313.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Wyatt JR;
XX
PN WPI; 2002-404952/43.
XX
DR Novel antisense compound that hybridizes and inhibits nucleic acid
PT molecule encoding Syntaxin 4 interacting protein, useful for treating
PT diabetes, obesity and skeletal muscle disorder.
XX
PS Claim 3; Page 87; 154pp; English.
XX
The invention comprises antisense oligonucleotides designed to inhibit
CC expression of Syntaxin 4 interacting protein. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of Syntaxin 4 interacting protein in cells or tissues. The
CC antisense oligonucleotides are also useful for treating an animal having
CC a disease or condition associated with Syntaxin 4 interacting protein
CC (e.g. diabetes, obesity or a skeletal muscle disorder). The antisense
CC oligonucleotides can also be used to prevent or delay infection,
CC inflammation and tumour formation. The present DNA sequence represents a
CC mouse Syntaxin 4 interacting protein antisense oligonucleotide. NOTE: The
CC present sequence contains a phosphorothioate backbone and 2'-O-
CC methoxyethyl wings
XX
SQ Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 456 CGCTGTGAATTGGGCTGG 473
Db 1 CCCTGTCAAGTGGGCTGG 18

RESULT 2004
ABQ62324/c
ID ABQ62324 standard; DNA; 20 BP.
XX
AC ABQ62324;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human syntaxin 4 interacting protein antisense oligonucleotide 63.
XX
KW Human; antisense gene therapy; Syntaxin 4 interacting protein; ss;
KW antisense oligonucleotide; diabetes; obesity; skeletal muscle disorder;
KW inflammation; tumour formation; phosphorothioate backbone;
KW 2'-O-methoxyethyl wing.
XX
OS Homo sapiens.
XX
```

```
PN WO200224864-A2.
XX
XX
PD 28-MAR-2002.
XX PF 19-SEP-2001; 2001WO-US029251.
XX PR 22-SEP-2000; 2000US-00668313.
XX (ISIS-) ISIS PHARM INC.
XX PA Monia BP, Freier SM, Wyatt JR;
XX PI
XX DR WPI; 2002-404952/43.
XX
XX Novel antisense compound that hybridizes and inhibits nucleic acid
PT molecule encoding Syntaxin 4 interacting protein, useful for treating
PT diabetes, obesity and skeletal muscle disorder.
XX
XX Claim 3; Page 84; 154pp; English.
XX
XX The invention comprises antisense oligonucleotides designed to inhibit
CC expression of Syntaxin 4 interacting protein. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of Syntaxin 4 interacting protein in cells or tissues. The
CC antisense oligonucleotides are also useful for treating an animal having
CC a disease or condition associated with Syntaxin 4 interacting protein
CC (e.g. diabetes, obesity or a skeletal muscle disorder). The antisense
CC oligonucleotides can also be used to prevent or delay infection,
CC inflammation and tumour formation. The present DNA sequence represents a
CC human Syntaxin 4 interacting protein antisense oligonucleotide. NOTE: The
CC present sequence contains a phosphorothioate backbone and 2'-O-
CC methoxyethyl wings
XX
XX Sequence 20 BP; 11 A; 3 C; 1 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1598 GTATTATATATAAAATTT 1615
DB 19 GTATTTTGTGAAACTTT 2
RESULT 2005
ABQ62287/C
ID ABQ62287 standard; DNA; 20 BP.
XX
XX ABQ62287;
XX
XX 16-AUG-2002 (first entry)
XX
XX Human syntaxin 4 interacting protein antisense oligonucleotide 26.
DE
XX
XX Human; antisense gene therapy; Syntaxin 4 interacting protein; ss;
KW antisense oligonucleotide; diabetes; obesity; skeletal muscle disorder;
KW inflammation; tumour formation; phosphorothioate backbone;
KW 2'-O-methoxyethyl wing.
XX
XX Homo sapiens.
OS
XX WO200224864-A2.
XX
XX 28-MAR-2002.
PD
XX
XX 19-SEP-2001; 2001WO-US029251.
PF
XX
XX 22-SEP-2000; 2000US-00668313.
PR
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM, Wyatt JR;
XX
XX
```

```
DR WPI; 2002-404952/43.
XX
XX Novel antisense compound that hybridizes and inhibits nucleic acid
PT molecule encoding Syntaxin 4 interacting protein, useful for treating
PT diabetes, obesity and skeletal muscle disorder.
XX
XX Claim 3; Page 83; 154pp; English.
XX
XX The invention comprises antisense oligonucleotides designed to inhibit
CC expression of Syntaxin 4 interacting protein. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of Syntaxin 4 interacting protein in cells or tissues. The
CC antisense oligonucleotides are also useful for treating an animal having
CC a disease or condition associated with Syntaxin 4 interacting protein
CC (e.g. diabetes, obesity or a skeletal muscle disorder). The antisense
CC oligonucleotides can also be used to prevent or delay infection,
CC inflammation and tumour formation. The present DNA sequence represents a
CC human Syntaxin 4 interacting protein antisense oligonucleotide. NOTE: The
CC present sequence contains a phosphorothioate backbone and 2'-O-
CC methoxyethyl wings
XX
XX Sequence 20 BP; 2 A; 8 C; 1 G; 9 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1421 CAGAGGAGAGAGAGAG 1438
DB 19 CAGAGGAGAGAGAGAGG 2
RESULT 2006
AAD39626
ID AAD39626 standard; DNA; 20 BP.
XX
XX AAD39626;
XX
XX 04-OCT-2002 (first entry)
XX
XX Human SR-cyp antisense oligonucleotide, ISIS #123890.
XX
XX Human; antisense; SR-cyp; Ck-associated RS cyclophilin; inflammation;
KW hyperproliferative disorder; cancer; prophylaxis; infection; therapy;
KW tumour; CARS-cyp; phosphorothioate backbone; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /*note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /*note= "2'methoxyethyl nucleotides"
FT modified_base 3
FT /*tag= d
FT /mod_base= m5c
FT modified_base 12
FT /*tag= e
FT /mod_base= m5c
FT modified_base 14
FT /*tag= f
FT /mod_base= m5c
FT modified_base 16..20
FT /*tag= c
FT /*note= "2'methoxyethyl nucleotides"
FT modified_base 18
FT /*tag= g
FT
```

```

FT      /mod_base= m5c
FT      20
FT      /*tag= h
FT      /mod_base= m5c
XX      WO200236809-A2.
XX      10-MAY-2002.
XX      30-OCT-2001; 2001WO-US047335.
XX      03-NOV-2000; 2000US-00706197.
XX      (ISIS-) ISIS PHARM INC.
XX      (COLD-) COLD SPRING HARBOR LAB.
XX      Bennett CF, Spector DL, Wyatt JR;
XX      WPI; 2002-479763/51.
XX      Novel antisense compounds targeted to nucleic acids encoding SR-cyp, Clk-
XX      associated RS cyclophilin for modulating the gene expression and treating
XX      hyperproliferative disorders such as cancer.
XX      Claim 3; Page 90; 117pp; English.
XX      The invention relates to antisense compounds targetted to a nucleic acid
XX      molecule encoding human SR-cyp (Clk-associated RS cyclophilin) to inhibit
XX      its expression. SR-cyp is also referred to as CARS-cyp. Antisense
XX      compounds of the invention are used for treating diseases or conditions
XX      associated with SR-cyp. The diseases treated include hyperproliferative
XX      disorders e.g. cancer or hyperproliferative disorders resulting from an
XX      alternative splicing event. They are useful for diagnostics, therapeutics
XX      and as research reagents, e.g. prophylactically to prevent or delay
XX      infection, inflammation or tumour formation. They are also used in
XX      antisense therapy. The present sequence is an antisense oligonucleotide
XX      targetted to human SR-cyp
XX      Sequence 20 BP; 2 A; 5 C; 4 G; 9 T; 0 U; 0 Other;
XX      Query Match      0.6%; Score 13.2; DB 1; Length 20;
XX      Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX      Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX      QY      1672 TGCTGGGTGAGCTCTTCC 1689
XX      |||||
XX      Db      1 TTCTGTGTGAGCTCTTAC 18
XX      RESULT 2007
XX      ABZ31179
XX      ID      ABZ31179 standard; DNA; 20 BP.
XX      AC      ABZ31179;
XX      XX      30-JAN-2003 (first entry)
XX      DE      Candida albicans GRACE strain PCR primer SEQ ID NO 5398.
XX      KW      Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
XX      KW      signal transduction; DNA replication; cell division; growth;
XX      KW      proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
XX      OS      Candida albicans.
XX      WO200253728-A2.
XX      11-JUL-2002.
XX      26-DEC-2001; 2001WO-US049486.
XX      29-DEC-2000; 2000US-0259128P.
XX      20-FEB-2001; 2001US-00792024.
PR      22-AUG-2001; 2001US-0314050P.
XX      (ELIT-) ELITRA PHARM INC.
XX      Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
XX      WPI; 2002-566694/60.
XX      Constructing strains for identifying gene products as effective targets
XX      for therapeutic intervention, by inactivating in the strain one allele of
XX      a gene and placing other allele of the gene under conditional expression.
XX      Claim 36; SEQ ID NO 5398; 167pp + Sequence Listing; English.
XX      The invention relates to constructing (M1) a strain of diploid fungal
XX      cells in which both alleles of a gene are modified, comprising modifying
XX      one allele by insertion or replacement by a cassette having an
XX      expressible selectable marker and modifying other allele by
XX      recombination, of a promoter replacement fragment with a heterologous
XX      promoter, so that expression of the second allele is regulated by the
XX      promoter. (M1) is useful for constructing a strain of diploid fungal
XX      cells in which both alleles of a gene are modified. The diploid fungal
XX      cells having both alleles modified are useful for identifying a gene that
XX      is essential to the survival or growth of a fungus, a gene that
XX      contributes to the virulence and/or pathogenicity of a fungus, a gene
XX      that contributes to the resistance of a diploid fungus to an antifungal
XX      agent, an antifungal agent that inhibits the growth of a diploid fungus
XX      and for identifying a therapeutic agent for treatment of a mammalian
XX      disease. (M1) is useful for identifying a compound which modulates the
XX      activity of a gene product, preferably enzymatic activity, carbon
XX      compound catabolism, biosynthetic, transporter, transcriptional,
XX      translational, signal transduction, DNA replication and cell division
XX      activity. The method is useful for identifying a compound having the
XX      ability to inhibit growth or proliferation of C. albicans cells and for
XX      treating infection by C. albicans. The present sequence is that of a PCR
XX      primer used in the method of the invention. Note: The sequence data for
XX      this patent is not represented in the printed specification but is based
XX      on sequence information supplied to Derwent by the European Patent Office
XX      Sequence 20 BP; 8 A; 9 C; 2 G; 1 T; 0 U; 0 Other;
XX      Query Match      0.6%; Score 13.2; DB 1; Length 20;
XX      Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX      Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX      QY      1286 GCTCCTCTGTGACAAACGAA 1303
XX      |||||
XX      Db      1 GCCCTCCACAAACGAA 18
XX      RESULT 2008
XX      AAD22548/c
XX      ID      AAD22548 standard; RNA; 20 BP.
XX      AC      AAD22548;
XX      XX      12-FEB-2002 (first entry)
XX      DE      Human R1alpha/protein kinase A (PKA) gene sense RNA fragment.
XX      KW      RNase inhibitor; anti-HIV; cytostatic; hepatotropic; antiinflammatory;
XX      KW      virucide; oncogene; cancer; transcription; translation; leukaemia virus;
XX      KW      human immunodeficiency virus; duck; hepatitis B virus; polymerase; human;
XX      KW      viral reverse transcriptase; protein kinase A; PKA; antisense; ss.
XX      OS      Homo sapiens.
XX      US6291438-B1.
XX      18-SEP-2001.
XX      06-OCT-1998; 98US-00167375.

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PR 24-FEB-1993; 93US-00022055.
 PR 23-FEB-1994; 94US-00200650.
 PR 22-FEB-1996; 96US-00604871.
 XX
 PA (WANG/J) WANG J H.
 XX Wang JH;
 XX WPI; 2002-009339/01.
 XX
 PT Derivatized antisense oligoribonucleotide useful to inhibit e.g. viral
 PT reverse transcriptase comprises at the 2'-O position of the
 PT oligoribonucleotide, a hydrophobic carrier reagent containing a poly
 PT substituted phenyl compound.
 XX
 PS Example 9; Col 39; 56pp; English.
 XX
 CC The invention relates to derivatised antisense oligoribonucleotides with
 CC enhanced membrane permeability and stability. The derivatised antisense
 CC oligoribonucleotide complementary to a sequence of nucleotides found in a
 CC virus or a cell is useful for inhibiting e.g., viral reverse
 CC transcriptase. Derivatized antisense oligoribonucleotide is conjugated at
 CC the 2'-O position with a hydrophobic carrier reagent containing a poly
 CC substituted phenyl compound. The derivatised oligoribonucleotides are
 CC used to decrease the expression of oncogenes and thereby decrease the
 CC expression of cancer cells which rely upon oncogene expression for their
 CC phenotypic and pathological properties. The oligoribonucleotides are also
 CC targeted for increasing the effectiveness of antisense oligonucleotide
 CC targeted to a gene associated with a disease or a condition in an
 CC animal. To alter gene transcription and/or translation for any gene or
 CC gene segment responsible for expression, to inhibit viral reverse
 CC transcriptase, to inhibit the expression of leukaemia virus, hepatitis
 CC virus, oncogenes and human immunodeficiency virus. The present sequence
 CC is human R1alpha/protein kinase A (PKA) gene sense RNA fragment used in
 CC the treatment of human breast cancer cells in vitro
 XX
 SQ Sequence 20 BP; 4 A; 5 C; 10 G; 0 T; 1 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1936 CGTACCTTCCCACTGGCC 1953
 DB 19 CGTGCCTCTCACTGGCC 2
 RESULT 2009
 AAS16023
 ID AAS16023 standard; DNA; 20 BP.
 XX
 AC AAS16023;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Mouse microsatellite genotyping PCR primer D2Mit12 forward.
 XX
 KW Mouse; ss; D2Mit12; genotyping; PCR primer; Ext2; bone mineral density;
 KW BMD; osteoporosis; hereditary multiple exostoses; HME; osteopathic;
 KW Gene therapy; hormone replacement therapy.
 XX
 OS Mus sp.
 XX
 PN WO200178575-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 17-APR-2001; 2001WO-US012447.
 XX
 PR 17-APR-2000; 2000US-0197917P.
 PR 04-OCT-2000; 2000US-0237848P.
 XX
 PA (UYOR-) UNIV OREGON HEALTH SCI.

PA (USGO) US DEPT VETERANS AFFAIRS.
 XX
 PI Klein RF, Orwoll ES, Belknap JK;
 XX
 DR WPI; 2002-025943/03.
 XX
 PT Detecting a biological condition such as a predisposition to osteoporosis
 PT or low bone marrow density for enabling therapeutic intervention to
 PT prevent, reduce or delay osteoporosis, comprises detecting a polymorphism
 PT in the Ext2 gene.
 XX
 PS Example 1; Page 19; 54pp; English.
 XX
 CC The invention relates to detecting a biological condition associated with
 CC an abnormal Ext2 nucleic acid or an abnormal Ext2 expression comprising
 CC detecting the abnormal Ext2 nucleic acid or expression. For example
 CC predicting a predisposition to osteoporosis or an increased likelihood of
 CC having low bone mineral density (BMD) in a subject by detecting a
 CC polymorphism in an Ext2 gene sequence or performing a hybridisation
 CC assay. Ext2 polymorphisms in humans are also associated with hereditary
 CC multiple exostoses (HME). The method is useful for diagnosing an
 CC increased predisposition to osteoporosis or an increased likelihood of
 CC having low bone mineral density. Such screening is especially useful to
 CC identify individuals having a genetic predisposition to osteoporosis to
 CC enable therapeutic intervention (e.g. by hormone replacement therapy to
 CC prevent or reduce osteoporosis, or delay its onset. The present sequence
 CC is a PCR primer used to genotype mice which are a result of a genetic
 CC cross which selected for low bone density or high bone density
 XX
 SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 673 TACTTCCCAGGACTGGG 690
 DB 2 TACTTCCCAGGCTTGG 19
 RESULT 2010
 ABA93167
 ID ABA93167 standard; DNA; 20 BP.
 XX
 AC ABA93167;
 XX
 DT 17-APR-2002 (first entry)
 XX
 DE Human vitamin D receptor gene PCR primer SEQ ID NO:1.
 XX
 KW Human; vitamin D receptor; apolipoprotein E; oestrogen receptor; VDR;
 KW ApoE; osteoporosis; polymorphism; allele; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2001333799-A.
 XX
 PD 04-DEC-2001.
 XX
 PF 26-MAY-2000; 2000JP-00155993.
 XX
 PR 26-MAY-2000; 2000JP-00155993.
 XX
 PA (NISS-) NISSHO KK.
 XX
 DR WPI; 2002-135949/18.
 XX
 PT Estimate of sensitivity to drugs for osteoporosis and a reagent kit.
 XX
 PS Example 1; Page 7; 13pp; Japanese.
 XX
 CC The present invention describes a method for the estimation of
 CC sensitivity to drugs for osteoporosis in which each gene polymorphism of

CC vitamin D receptor (VDR) gene, oestrogen receptor (ER) gene and
CC apolipoprotein E3 (ApoE3) allele (2/2, 2/3, 2/4, 3/3, 3/4 or 4/4) are
CC analysed from the genomic DNA contained in a sample collected from a
CC human and based on these combinations of gene polymorphisms, it is
CC estimated that the sample is derived from an individual showing a
CC specific priority on the sensitivity against a plural of treating agents
CC for osteoporosis. Also described is a reagent kit for analysing gene
CC polymorphisms of VDR, ApoE and ER genes containing primers specific to
CC each of the genes and detecting probes for detecting each gene
CC polymorphisms. The reagent can be used for selecting an effective drug
CC for osteoporosis. The present sequence represents a PCR primer for human
CC VDR which is used in the exemplification of the present invention
XX
XX
SQ Sequence 20 BP; 3 A; 3 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1205 TGCAGGCGATTCCTGAGG 1222
| | | | | | | | | | | | | | | | | | | | | |
Db 2 TGCAGGCGATTCCTGAGG 19

RESULT 2011
ABL56378/c
ID ABL56378 standard; DNA; 20 BP.
XX
AC ABL56378;
XX
DT 22-JUL-2002 (first entry)
XX
DE PCR primer used to amplify a cDNA fragment of the MDR3 gene.
XX
KW MDR3 gene; multiple drug resistance 3 gene; hepatic syndrome;
KW phosphatidylcholine transporter; cholesterol-type biliary microlithiasis;
KW CBM; intrahepatic cholestasis; IHC; abortion; pregnancy; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200212556-A1.
XX
PD 14-FEB-2002.
XX
PF 06-AUG-2001; 2001WO-FR002553.
XX
PR 08-AUG-2000; 2000FR-00010428.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
XX
PI Poupon R, Hermelin B, Rosmorduc O;
XX
DR WPI; 2002-269095/31.
XX
PT Screening for new hepatic syndrome, by detecting a mutation in multiple
PT drug resistance-3 gene, also treatment of the syndrome with
PT ursodeoxycholic acid.
XX
PS Claim 5; Page 12; 30pp; French.
XX
CC PCR primers ABL56374-81 were used to amplify cDNA fragments from the
CC human MDR (multiple drug resistance) 3 gene. The primers were used in the
CC method of the invention. The specification describes a method for
CC screening for a hepatic syndrome. The method comprises detecting, in a
CC sample of nucleic acid from peripheral blood mononuclear cells, at least
CC one heterozygous mutation in the MDR3 gene and/or a homozygous mutation
CC that does not abolish expression of protein by this gene. The MDR3 gene
CC encodes a protein which is a transporter of phosphatidylcholine. The
CC screening is performed on adults having cholesterol-type biliary
CC microlithiasis (CBM) and intrahepatic cholestases (IHC). The method is
CC used to detect, and to assess the risk of developing, the new syndrome in
CC families at risk of CBM and/or unexplained hepatic anomalies. Detection
CC and prevention of the new syndrome should avoid repeated abortions
XX

CC associated with cholestases of pregnancy
XX
SQ Sequence 20 BP; 5 A; 1 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1695 CCACCTTGCACCAATTC 1712
| | | | | | | | | | | | | | | | | | | | | |
Db 19 CAACCTTGTCAACCAATTC 2

RESULT 2012
ABK23083/c
ID ABK23083 standard; DNA; 20 BP.
XX
AC ABK23083;
XX
DT 09-APR-2002 (first entry)
XX
DE Human Zmax1 cDNA forward PCR primer #123.
XX
KW Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke;
KW lipid-associated condition; arteriosclerosis; cardiovascular disease; ss;
KW osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up;
KW neurovascular condition; wound healing; gene therapy; PCR primer; probe;
KW bone development disorder; antiarteriosclerotic; cardiovascular;
KW osteopathic; cerebroprotective.
XX
OS Homo sapiens.
XX
PN WO200192891-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016946.
XX
PR 26-MAY-2000; 2000US-00578900.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
XX
PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX
DR WPI; 2002-097784/13.
XX
PT Identifying molecules involved in lipid regulation, useful for
PT diagnosing, treating or preventing e.g., arteriosclerosis, comprises
PT identifying a molecule that binds to high bone mass gene or its
PT corresponding wild type gene.
XX
PS Disclosure; Page 39; 409pp; English.
XX
CC The invention relates to a method for identifying a molecule involved in
CC lipid regulation comprising identifying a molecule that binds to or
CC inhibits binding of a molecule to high bone mass (HBM) or its wild type
CC gene, Zmax1. Compounds identified by the method are useful for treating,
CC diagnosing, preventing or screening for normal and abnormal lipid-
CC associated conditions, including arteriosclerosis, cardiovascular
CC disease, stroke, and osteoporosis. The compounds may also be used in the
CC treatment or prevention of diabetic atherosclerosis, neurovascular
CC conditions caused by plaque build-up, poor circulation due to plaque
CC build-up and associated poor wound healing. The methods may be used in
CC gene therapy, pharmaceutical development, and diagnostic assays for bone
CC development disorders. Molecules identified by comparison of Zmax1 and
CC HBM systems can be used as surrogate markers in pharmaceutical
CC development, in diagnosis of human or animal bone disease, and in the
CC treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA
CC molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers
CC and adapters of the invention
XX
SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. NO. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1819 GCTTTGGAAAGGTGCCCT 1836
Db 18 GCTGAGGAAAGGTGCTCT 1

RESULT 2013
ABK22844
ID ABK22844 standard; DNA; 20 BP.

AC ABK22844;

DT 09-APR-2002 (first entry)

Human Zmax1 cDNA reverse PCR primer #3.

KW	
KW	Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke;
KW	Liped-associated condition; arteriosclerosis; cardiovascular disease; ss
KW	osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up
KW	neurovascular condition; wound healing; gene therapy; PCR primer; probe;
KW	wound development disorder; antiarteriosclerotic; cardiovascular;
KW	osteoapathic; cerebroprotective.

Homo sapiens.

AA
PN
WO200192891-A2.

XX PD 06-DEC-2001.

XX
PF
25-MAY-2001:XX
PR 26-MAY-2000: 2000TS-00578900

XX PA (GENO-) GENOME THERAPEUTICS CORP

PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
yy

PI Carulli JP, Little RD, Recker RR, Johnson ML;

DR WPI; 2002-097784/13.

PT Identifying molecules involved in lipid regulation, useful for
PT diagnosing, treating or preventing e.g., arteriosclerosis, comprises
PT identifying a molecule that binds to high bone mass gene or its
PT corresponding wild type gene.

PS · Disclosure; Page 38; 409pp; English.

The invention relates to a method for identifying a molecule involved in lipid regulation comprising identifying a molecule that binds to or inhibits binding of a molecule to high bone mass (HBM) or its wild type gene, Zmx1. Compounds identified by the method are useful for treating, diagnosing, preventing or screening for normal and abnormal lipid-associated conditions, including arteriosclerosis, cardiovascular disease, stroke, and osteoporosis. The compounds may also be used in the treatment or prevention of diabetic atherosclerosis, neurovascular conditions caused by plaque build-up, poor circulation due to plaque build-up and associated poor wound healing. The methods may be used in gene therapy, pharmaceutical development, and diagnostic assays for bone development disorders. Molecules identified by comparison of Zmx1 and HBM systems can be used as surrogate markers in pharmaceutical development, in diagnosis of human or animal bone diseases, and in the treatment of bone diseases. Sequences ABK2776-ABK23411 represent cDNA molecules encoding human Zmx1 and HBM, and PCR primers, probes, linkers and adapters of the invention.

SQ Sequence 20 BP; 2 A; 3 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;

	Matches	15;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	2002	TTCTGCAGGTGAGGTTG	2019							
Db	1	TTCTGCAGGTGCTGTTG	18							

RESULT 2014	
ABK23371	
ID	ABK23371 standard; DNA; 20 BP.
XX	
XX	
AC	ABK23371;
XX	
XX	09-APR-2002 (first entry)
DT	
DT	
XX	
DE	Human Zmax1 cDNA forward PCR primer #267

Human; mouse; Zmx1; HBM; high bone mass gene; lipid regulation; stroke; lipid-associated condition; arteriosclerosis; cardiovascular disease; ss osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up neurovascular condition; wound healing; gene therapy; PCR primer; probe; bone development disorder; antiarteriosclerotic; cardiovascular; osteopathic; cerebroprotective.

OS Homo sapiens.

XX
PN
WO200192891-A2.

XX
PD
06-DEC-2001XX
PF
25-MAY-2001:XX
PP 26-MAY-2000. 2000US - 00578000XX
DA
(CENO) CENOME EUPD3 DRYMTCC

PA (UYCR-) UNIV CREIGHTON SCHOOL MED

PI Carulli JP, Little RD, Recker RR, Jo

DR WPI; 2002-097784/13.

Identifying molecules involved in lipid regulation, useful for PT diagnosing, treating or preventing e.g., arteriosclerosis, comprises PT identifying a molecule that binds to high bone mass gene or its PT corresponding wild type gene.

PS Disclosure; Page 42; 409pp; English.

The invention relates to a method for identifying a molecule involved in lipid regulation comprising identifying a molecule that binds to or inhibits binding of a molecule to high bone mass (HBM) or its wild type gene, Zmx1. Compounds identified by the method are useful for treating, diagnosing, preventing or screening for normal and abnormal lipid-associated conditions, including arteriosclerosis, cardiovascular disease, stroke, and osteoporosis. The compounds may also be used in the treatment or prevention of diabetic atherosclerosis, neurovascular conditions caused by plaque build-up, poor circulation due to plaque build-up and associated poor wound healing. The methods may be used in gene therapy, pharmaceutical development, and diagnostic assays for bone development disorders. Molecules identified by comparison of Zmx1 and HBM systems can be used as surrogate markers in pharmaceutical development, in diagnosis of human or animal bone disease, and in the treatment of bone diseases. Sequences ABK2776-ABK23411 represent CDNA molecules encoding human Zmx1 and HBM, and PCR primers, probes, linkers and adapters of the invention

Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other; SQ

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;

QY 35 ACTGACGGTAGGGACGGG 52

XX 15-JUL-2002 (first entry)
 XX Mouse HYPLIP1 locus PCR primer #177.
 DE Human; mouse; HYPLIP1; FCHL1; familial combined hyperlipidaemia; cancer;
 XX lipid disorder; PCR; primer; ss.
 XX Mus sp.
 XX WO200220848-A2.
 XX 14-MAR-2002.
 XX 07-SEP-2001; 2001WO-US028182.
 XX 08-SEP-2000; 2000US-0231322P.
 XX (REGC) UNIV CALIFORNIA.
 XX Bodnar JS, Castellani LW, Chatterjee A, De Jong P, Lusis AJ;
 PI Ohmen J, Ross D, Tafuri S, Wu C;
 XX WPI; 2002-329882/36.
 XX New mouse HYPLIP1 and human FCHL1 (familial combined hyperlipidemia)
 PT genes and their sequence variations, useful for diagnosing, treating or
 PT preventing lipid disorders and cancers.
 XX Claim 11; Page 74; 102pp; English.
 XX The invention relates to an isolated polynucleotide comprising a sequence
 CC variation of a mouse HYPLIP1 cDNA or a human FCHL1 (familial combined
 CC hyperlipidaemia) gene. The FCHL1 polynucleotide, the FCHL1 polypeptide or
 CC antibody immunoreactive to the FCHL1 polypeptide are useful for treating
 CC or preventing cancer associated with expression of FCHL1, as well as for
 CC treating lipid disorder. The mouse HYPLIP1 cDNA or human FCHL1 gene are
 CC also useful for diagnosing or prognosing a predisposition to lipid
 CC disorder and cancer. ABK70902-ABK71303 represent mouse HYPLIP1, human
 CC FCHL1 coding sequences and PCR primers of the invention
 XX Sequence 20 BP; 8 A; 4 C; 7 G; 1 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1522 TCCAGCTCTGGCTTCCTG 1539
 DB 19 TCCACCTCTGTGTTCTG 2
 RESULT 2018
 ABS73428/c
 ID ABS73428 standard; DNA; 20 BP.
 XX AC ABS73428;
 XX DT 03-DEC-2002 (first entry)
 XX Chimeric phosphorothioate oligonucleotide #9.
 XX Human; glioma-associated oncogene-2; antisense compound; infection;
 KW inflammation; tumour formation; antiinflammatory; anticancer;
 KW inhibitor of human glioma-associated oncogene-2 expression;
 KW antisense gene therapy; phosphorothioate; ss.
 XX Homo sapiens.
 OS Synthetic.
 OS Chimeric.
 XX US6440739-B1.
 XX

PD 27-AUG-2002.
 XX 17-JUL-2001; 2001US-00907843.
 XX 17-JUL-2001; 2001US-00907843.
 XX (ISIS-) ISIS PHARM INC.
 XX Bennett CF, Freier SM;
 XX WPI; 2002-697096/75.
 XX Novel antisense compound that hybridizes and inhibits nucleic acid
 PT encoding human glioma-associated oncogene-2, useful for treatment of
 PT diseases associated with human glioma-associated oncogene-2.
 XX Claim 3; Col 45; 43pp; English.
 XX The present invention relates to a new antisense compound targeted to
 CC human glioma-associated oncogene-2. The invention is useful for
 CC inhibiting the expression of human glioma-associated oncogene-2 in cells
 CC or tissues. The invention is also useful for treatment of diseases
 CC associated with human glioma-associated oncogene-2. The invention is
 CC further useful for diagnostics, therapeutics, prophylaxis, as research
 CC reagents and kits, for distinguishing functions of various members of a
 CC biological pathway, and in antisense gene therapy. The invention is also
 CC useful prophylactically, e.g., to prevent or delay infection,
 CC inflammation or tumour formation. The present nucleic acid sequence
 CC represents an oligonucleotide that was used in the methods of the
 CC invention to inhibit human glioma-associated oncogene-2
 XX Sequence 20 BP; 1 A; 7 C; 3 G; 9 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1469 AGCAGAGCCAAAGGGG 1486
 DB 20 AGCAGAGCCAAAGTG 3
 RESULT 2019
 ABX97219
 ID ABX97219 standard; DNA; 20 BP.
 XX AC ABX97219;
 XX DT 20-MAY-2003 (first entry)
 XX Human NOV-associated forward primer from primer-probe set Ag3421.
 DE NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;
 KW hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;
 KW human; PCR; primer; ss.
 XX Homo sapiens.
 XX WO200272757-A2.
 XX 19-SEP-2002.
 XX 08-MAR-2002; 2002WO-US006908.
 XX 08-MAR-2001; 2001US-0274101P.
 PR 08-MAR-2001; 2001US-0274194P.
 PR 08-MAR-2001; 2001US-0274281P.
 PR 08-MAR-2001; 2001US-0274322P.
 PR 09-MAR-2001; 2001US-0274849P.
 PR 12-MAR-2001; 2001US-0275235P.
 PR 13-MAR-2001; 2001US-0275578P.
 PR 13-MAR-2001; 2001US-0275579P.
 PR 13-MAR-2001; 2001US-0275601P.

PR 14-MAR-2001; 2001US-0276000P.
PR 16-MAR-2001; 2001US-0276776P.
PR 19-MAR-2001; 2001US-0276994P.
PR 20-MAR-2001; 2001US-0277239P.
PR 20-MAR-2001; 2001US-0277321P.
PR 20-MAR-2001; 2001US-0277327P.
PR 21-MAR-2001; 2001US-0277791P.
PR 22-MAR-2001; 2001US-0278152P.
PR 23-MAR-2001; 2001US-0278152P.
PR 26-MAR-2001; 2001US-0278894P.
PR 27-MAR-2001; 2001US-0278999P.
PR 27-MAR-2001; 2001US-0279036P.
PR 28-MAR-2001; 2001US-0279344P.
PR 30-MAR-2001; 2001US-0277338P.
PR 30-MAR-2001; 2001US-0279995P.
PR 30-MAR-2001; 2001US-0280233P.
PR 02-APR-2001; 2001US-0280802P.
PR 02-APR-2001; 2001US-0280822P.
PR 02-APR-2001; 2001US-0280900P.
PR 04-APR-2001; 2001US-0281194P.
PR 13-APR-2001; 2001US-0283675P.
PR 30-APR-2001; 2001US-0287424P.
PR 02-MAY-2001; 2001US-0288066P.
PR 03-MAY-2001; 2001US-0288342P.
PR 03-MAY-2001; 2001US-0288528P.
PR 15-MAY-2001; 2001US-0291190P.
PR 16-MAY-2001; 2001US-0291099P.
PR 16-MAY-2001; 2001US-0291240P.
PR 30-MAY-2001; 2001US-0294485P.
PR 31-MAY-2001; 2001US-0294889P.
PR 31-MAY-2001; 2001US-0294899P.
PR 18-JUN-2001; 2001US-0299027P.
PR 19-JUN-2001; 2001US-0299303P.
PR 19-JUN-2001; 2001US-0299310P.
PR 10-JUL-2001; 2001US-0304354P.
PR 31-JUL-2001; 2001US-0309198P.
PR 16-AUG-2001; 2001US-0312903P.
PR 10-SEP-2001; 2001US-0318462P.
PR 12-SEP-2001; 2001US-0318770P.
PR 27-SEP-2001; 2001US-0325430P.
PR 27-SEP-2001; 2001US-0325681P.
PR 18-OCT-2001; 2001US-0330380P.
PR 31-OCT-2001; 2001US-0335301P.
PR 14-NOV-2001; 2001US-0332172P.
PR 14-NOV-2001; 2001US-0332271P.
PR 14-NOV-2001; 2001US-0332722P.
PR 14-NOV-2001; 2001US-0333184P.
PR 14-NOV-2001; 2001US-0333272P.
PR 21-NOV-2001; 2001US-0332094P.
PR 03-DEC-2001; 2001US-0337426P.
PR 03-DEC-2001; 2001US-0338092P.
PR 04-DEC-2001; 2001US-0337185P.
PR 03-JAN-2002; 2002US-0345705P.
PR 07-MAR-2002; 2002US-00092900.
XX XX

(CURA-) CURAGEN CORP.

XX Padigar M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L;
XX Zernhusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;
PI Patturajan M, Gangoli E, Vernet CAM, Guo X, Tchernev V;
PI Fernandes ER, Cawman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;
PI Spaderna SK, Carteron E, Burgess C, Leite M, Zhong H, Alsobrook JP;
PI Lepley DM, Rieger DK;
XX WPI; 2002-723332/78.
XX

XX NOVX polypeptides and polynucleotides, useful for preventing or treating
PT a disorder associated with aberrant NOVX expression or activity e.g.,
PT cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
PT asthma.
XX

XX Example C; Page 516; 1103pp; English.

XX

CC This invention describes novel human NOVX polypeptides which have
CC cytotatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive
CC activity. Pharmaceutical compositions comprising the NOVX proteins or
CC nucleic acid molecules or NOVX antibodies are useful for preventing or
CC treating a disorder associated with aberrant NOVX expression or activity
CC e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
CC asthma. The products of the invention can be used for gene therapy or in
CC a vaccine. ABX13460-ABX13462 and ABX97186-ABX97593 represent PCR primers
CC and probes used in the amplification and isolation of the NOVX
CC polynucleotides represented in ABX97008-ABX97185 which encode the
CC polypeptides represented in ABU65041-ABU65218
XX XX

SQ Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 1.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 412 TCTGTGGCAAGTGTGTG 429

|||||

Db 2 TCTGCTGCAGTGTATG 19

RESULT 2020

ABK52885/C

ID ABK52885 standard; DNA; 20 BP.

XX

AC ABK52885;

XX

DT 27-AUG-2002 (first entry)

XX

DE Human osteonectin gene RT-PCR primer #1.

XX

RT-PCR; reverse transcription; primer; osteonectin; human; bone mass;
KW bone repair; osteopathic; pre-osteoblast cell line; bone; osteoblast;
KW bone formation; osteoporosis; ss.
XX

OS Homo sapiens.

XX

PN WO200234891-A2.

XX

PD 02-MAY-2002.

XX

PF 26-OCT-2001; 2001WO-EP012441.

XX

PR 27-OCT-2000; 2000EP-00123570.

XX

PA (NEST) SOC PROD NESTLE SA.

XX

PI Offord Cavin E, Darimont-Nicolau C, Mace C;

XX

DR WPI; 2002-463357/49.

XX

PT New immortalized preosteoblast cell line derived from periosteal layer of
PT bones capable of differentiating to osteoblasts, useful in assays for
PT detecting substances enabling improved bone formation.
XX

PS Example 6; Page 11; 26pp; English.

XX

This invention relates to a novel immortalised preosteoblast cell line
CC derived from the peritoneum of the bone, expressing at least one gene,
CC uncoupling the normal cell cycle and containing a construct with which
CC telomerase gene may be expressed, and which is capable of differentiating
CC to osteoblasts. The pre-osteoblast cell line of the invention is useful
CC in an assay for detecting substances controlling the differentiation of
CC preosteoblasts to osteoblasts, or substances enabling improved bone
CC formation, maintenance of bone mass, bone repair and for preventing the
CC onset of osteoporosis. The cell lines are capable of being cultured for
CC at least 60, preferably at least 100 passages in culture. They are
CC immortal and may be cultured in vitro as long as desired. They may by
CC prepared from any source from which preosteoblasts derived from the
CC peristal layer of bones may be obtained. They are capable of
CC differentiating to osteoblasts the cell responsible for bone mass

CC formation. The present sequence represents a reverse transcription (RT)
 CC PCR primer used to amplify human osteonectin mRNA from the cell lines of
 CC the invention

XX SQ Sequence 20 BP; 7 A; 1 C; 9 G; 3 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1553 GTTCTCTCCCAACCCCT 1570
 |||||
 Db 18 GTTCTCTCCCAACCCCT 1

RESULT 2021

AB53175/c
 ID AB53175 standard; DNA; 20 BP.

XX AC AB53175;

XX 29-NOV-2002 (first entry)

XX DE Nested PCR primer, #2, used to amplify the human +317 odc gene region.

XX KW Human; PCR; primer; ornithine decarboxylase; odc; ss; susceptibility;
 KW epithelial cancer; A-allele; G-allele; polyamine level; carcinogenesis;
 KW single nucleotide polymorphism; SNP; molecular beacon probe; skin;
 KW digestive system; oesophageal; gastric; colon; prostate; breast;
 KW haematopoietic; lung; cervical; cancer; melanoma; carcinoma.

XX OS Homo sapiens.

XX PN US2002081611-A1.

XX PD 27-JUN-2002.

XX PF 24-JUL-2001; 2001US-00911935.

XX PR 01-MAR-2000; 2000US-00516357.

XX PA (LANK-) LANKENAU MEDICAL RES CENT.

XX PI O'Brien TG, Guo YJ;

XX DR WPI; 2002-635464/68.

XX PT Assessing susceptibility of humans to epithelial cancer comprises the
 PT determination of A- or G-alleles of the ornithine decarboxylase (odc)
 PT gene which is an indicator of susceptibility to epithelial cancer.

XX PS Example 1; Page 9; 28pp; English.

XX CC The invention discloses a method for assessing the relative
 CC susceptibility of a human to an epithelial cancer. The method involves
 CC determining whether the human comprises an A-allele of the ornithine
 CC decarboxylase (odc) gene, where its presence indicates a greater
 CC susceptibility to epithelial cancer than one without the allele. Odc is
 CC involved in establishing cellular polyamine levels and the susceptibility
 CC of a tissue to carcinogenesis is related to these polyamine levels. This
 CC can be achieved by determining the sequence of a region of the gene
 CC containing the single nucleotide polymorphism (SNP) or by contacting a
 CC polynucleotide derived from the human's genome with a first molecular
 CC beacon probe which is complementary to a SNP target region of the odc
 CC gene (e.g. at positions -3175, -3004, -1936, +263, +317, +5294, +5915,
 CC +6697, +7486 relative to the transcription start site of the
 CC gene). The invention discloses a kit for assessing susceptibility of a
 CC human to an epithelial cancer which comprises the primer and
 CC oligonucleotide probes for determining the presence or absence of the A-
 CC allele. The method is useful in assessing the relative susceptibility of
 CC a human to an epithelial cancer, such as skin, digestive system,
 CC oesophageal, gastric, colon, prostate, breast, haematopoietic, lung and
 CC cervical cancers, carcinoma or melanoma and in assessing whether a test

CC compound is an inhibitor or an inducer of carcinogenesis. The sequence
 CC presented is the nested PCR primer, #2, which was used to amplify the
 CC human odc gene region containing the +317 SNP

XX SQ Sequence 20 BP; 6 A; 2 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1556 TCTTCCCAACCCCTCAG 1573
 |||||
 Db 18 TCTTCCCAACCCCTCG 1

RESULT 2022

ABI93616/c
 ID ABI93616 standard; DNA; 20 BP.

XX AC ABI93616;

XX 15-FEB-2002 (first entry)

XX DE Capture oligonucleotide Zip ID#703 oligo #9.

XX KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
 KW oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.

XX OS Synthetic.

XX PN WO200179548-A2.

XX PD 25-OCT-2001.

XX PF 04-APR-2001; 2001WO-US010958.

XX PR 14-APR-2000; 2000US-0197271P.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;

XX DR WPI; 2002-034366/04.

XX PT Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch.

XX PS Example 5; Fig 29; 300pp; English.

XX CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridise with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.

XX CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a

CC presence or absence of the target nucleotide sequences. ABI82074 to
 CC ABI97546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention
 XX
 SQ Sequence 20 BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 326 GCACGACAGTCACAGAT 343
 ||||| ||||| |||||
 Db 18 GCAAGCCGATGCACCGAT 1

RESULT 2025
 ABI93491
 ID ABI93491 standard; DNA; 20 BP.
 XX AC ABI93491;
 XX
 DT 15-FEB-2002 (first entry)
 XX
 DE Capture oligonucleotide Zip ID#578 oligo #9.
 XX
 KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
 KW oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.
 XX
 OS Synthetic.
 XX
 PN WO200179548-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 04-APR-2001; 2001WO-US010958.
 XX
 PR 14-APR-2000; 2000US-0197271P.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
 XX
 DR WPI; 2002-034366/04.
 XX
 PT Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch.
 XX
 PS Example 5; Fig 29; 300pp; English.
 XX
 CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridize with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a

CC presence or absence of the target nucleotide sequences. ABI82074 to
 CC ABI97546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention
 XX
 SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1659 CTCAGGGCAGCTGTGCTG 1676
 ||||| ||||| |||||
 Db 2 CTRACGGCAGCTGCGCTG 19

RESULT 2026
 ABI94112
 ID ABI94112 standard; DNA; 20 BP.
 XX AC ABI94112;
 XX
 DT 16-FEB-2002 (first entry)
 XX
 DE Capture oligonucleotide Zip ID#1199 oligo #9.
 XX
 KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
 KW oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.
 XX
 OS Synthetic.
 XX
 PN WO200179548-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 04-APR-2001; 2001WO-US010958.
 XX
 PR 14-APR-2000; 2000US-0197271P.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
 XX
 DR WPI; 2002-034366/04.
 XX
 PT Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch.
 XX
 PS Example 5; Fig 29; 300pp; English.
 XX
 CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridize with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a

CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention
XX
SQ Sequence 20 BP; 5 A; 7 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 690 GGACCTACGGATATCGG 707
|||||
Db 3 GGACCTACGGACCAACGG 20
RESULT 2027
ABI96674
ID ABI96674 standard; DNA; 20 BP.
XX
AC ABI96674;
XX
DT 16-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#3761 oligo #9.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US010958.
XX
PR 14-APR-2000; 2000US-0197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch.
XX
PS Example 5; Fig 29; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchovirus volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a

CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1742 GTGCCAGGTCTGGGTGAA 1759
|||||
Db 1 GTGCCAGGTCTGAGTGGA 18
RESULT 2028
AAD29425/C
ID AAD29425 standard; DNA; 20 BP.
XX
AC AAD29425;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human BMPR2 exon1 amplifying PCR primer #1.
XX
KW Human; bone morphogenic protein receptor II; BMPR-2; FPPH;
KW familial primary pulmonary hypertension; PCR primer; exon1; ss.
XX
OS Homo sapiens.
XX
PN WO200206534-A2.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-US022492.
XX
PR 17-JUL-2000; 2000US-0218740P.
PR 21-JUL-2000; 2000US-0220133P.
XX
PA (UYVA-) UNIV VANDERBILT.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
PA (UYLE-) UNIV LEICESTER.
XX
PI Loyd JE, Lane KB, Phillips JA, Nichols WC, Pauciulo MW, Foroud T;
PI Trembath RC, Machado RD, Thomson JR;
XX
DR WPI; 2002-171821/22.
XX
PT Identifying subject having increased susceptibility for developing
PT pulmonary hypertension by detecting mutant bone morphogenic protein
PT receptor (BMPR)-II polypeptide or mutated BMPR2 nucleic acid in subject.
XX
PS Example 1; Page 24; 65pp; English.
XX
CC The invention relates to a method of identifying a subject having an
CC increased susceptibility for developing pulmonary hypertension involves
CC detecting a mutant bone morphogenic protein receptor II (BMPR-II)
CC polypeptide or mutated BMPR2 nucleic acid in the subject. The method is
CC identifying a subject having an increased susceptibility for developing
CC pulmonary hypertension, familial primary pulmonary hypertension (FPPH) or
CC non-familial or sporadic PPH. The present sequence is a PCR primer used
CC to amplify human BMPR2 exon1 DNA
XX
SQ Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 244 GCTGAGGAGATGACCAAG 261
|||||
Db 20 GCTGATGAGGAGCCTAG 3

RESULT 2029
ABK47079/c
ID ABK47079 standard; DNA; 20 BP.
XX
AC ABK47079;
XX
DT 05-JUN-2002 (first entry)
XX
DE Mouse R1-OS-B1-A1 forward PCR primer.
XX
KW PCR; primer; ss; nucleic acid library; immune response; asthma;
KW airway hyperresponsiveness; bronchoalveolar manifestation;
KW signature sequence; SS; chronic obstructive pulmonary disease; COPD;
KW allergic disease; rhinitis; atopic dermatitis; urticaria;
KW autoimmune disease; multiple sclerosis; inflammatory bowel disease;
KW allograft rejection; infectious disease.
XX
OS Mus sp.
XX
PN WO200214366-A2.
XX
PD 21-FEB-2002.
XX
PF 16-AUG-2001; 2001WO-NL000610.
XX
PR 16-AUG-2000; 2000EP-00202867.
XX
PA (UYUT-) RIJKSUNIV UTRECHT.
XX
PI Groot PC, Van Bergenhenegouwen BJ, Van Oosterhout AJM;
XX
DR WPI; 2002-241888/29.
XX
PT Nucleic acid library comprising genes which are capable of initiation,
PT progression and suppression of an immune response, especially an immune
PT response observed with airway hyper-responsiveness of asthma.
XX
PS Example 8; Page 75; 120pp; English.
XX
CC The invention relates to a nucleic acid library comprising genes or their
CC fragments which are capable of modulating an immune response observed
CC with airway hyperresponsiveness and/or bronchoalveolar manifestations of
CC asthma. Also included are a method for modulating an immune response of
CC an individual comprising modulating a gene comprising a nucleic acid at
CC least functionally equivalent to a nucleic acid identifiable by a
CC signature sequence (SS) given in the specification such as R1-SO-R1-A11,
CC StOI-A10, SV02-1-C11, StOI-A12, and R1-SO-R1-B7, a substance (for use as
CC a medicament) capable of modulating a gene comprising a nucleic acid at
CC least functionally equivalent to a nucleic acid identifiable by SS and
CC the use of a proteinaceous substance derived from a nucleic acid at least
CC functionally equivalent to a nucleic acid identifiable by SS for the
CC production of an antagonist (for use as a medicament) against the
CC substance. The antagonist and substance are useful for the treatment of
CC an immune response observed with airway hyperresponsiveness and/or
CC bronchoalveolar manifestations of asthma. The method is useful for
CC product capable of modulating the immune response. The substance is
CC useful for treating an immune response, particularly asthma, chronic
CC obstructive pulmonary disease (COPD), allergic diseases (rhinitis, atopic
CC dermatitis, urticaria), autoimmune diseases (e.g. multiple sclerosis),
CC inflammatory bowel disease, allograft rejection and infectious disease.
CC The present sequence is a PCR primer used to amplify and/or characterise
CC a mouse signature sequence of the invention
XX
SQ Sequence 20 BP; 2 A; 9 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1423 GAGGAGAGAAAGAGTC 1440

Db 20 GAGGAGAGCAAGATGC 3
RESULT 2030
ABK69386
ID ABK69386 standard; DNA; 20 BP.
XX
AC ABK69386;
XX
DT 15-JUL-2002 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide #138 for caspase 9 inhibition.
XX
KW Antisense compound; caspase 9; C9; hyperproliferative disorder; stroke;
KW haematopoietic disorder; cholesterol disorder; bone metabolism disorder;
KW brain injury; neurodegenerative disease; infection; inflammation; tumour;
KW phosphorothioate backbone linkage; 2'-methoxyethyl; 2'-MOE; ss.
XX
OS Mus musculus.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate nucleotides, all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN WO200222641-A1.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028233.
XX
PR 11-SEP-2000; 2000US-00659845.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Zhang H, Watt AT;
XX
DR WPI; 2002-351874/38.
XX
PT New antisense oligonucleotide which modulates expression of caspase 9,
PT useful to treat tumor, inflammation or to prevent infection in humans.
XX
PS Claim 26; Page 95; 145pp; English.
XX
CC The present invention relates to a new antisense compound targeted to a
CC nucleic acid molecule encoding caspase 9 (C9). The compound specifically
CC hybridises with and inhibits the expression of caspase 9. The invention
CC also describes an antisense compound that specifically hybridises with an
CC 8 nucleotide portion of an active site of the nucleic acid. The invention
CC is useful for inhibiting the expression of C9 in cells or tissues and is
CC also useful for treating an animal having a disease or condition
CC associated with C9, including a hyperproliferative, haematopoietic or
CC cholesterol disorder, bone metabolism disorder, stroke, brain injury or
CC neurodegenerative disease. The compound is commonly useful as a research
CC and diagnostics reagent. It is also useful to distinguish between
CC functions of various members of a biological pathway. The invention is
CC also useful prophylactically e.g. to prevent or delay infection,
CC inflammation or tumour formation. The antisense compound of the invention
CC is often preferred over native form because of enhanced cellular uptake,
CC enhanced affinity for nucleic acid target and increased stability in

8 nucleotide portion of an active site of the nucleic acid. The invention is useful for inhibiting the expression of C9 in cells or tissues and is also useful for treating an animal having a disease or condition associated with C9, including a hyperproliferative, haematopoietic or cholesterol disorder, bone metabolism disorder, stroke, brain injury or neurodegenerative disease. The compound is commonly useful as a research and diagnostics reagent. It is also useful to distinguish between functions of various members of a biological pathway. The invention is also be useful prophylactically e.g. to prevent or delay infection, inflammation or tumour formation. The antisense compound of the invention is often preferred over native form because of enhanced cellular uptake, enhanced affinity for nucleic acid target and increased stability in presence of nucleases. The present nucleic acid sequence represents one of a collection (ABK69249-ABK69396) of chimeric phosphorothioate oligonucleotides having 2'-methoxyethyl (2'-MOE) wings. This sequence was used in the methods of the invention for inhibition of caspase 9

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1975 GCCTGCCCTCTGCTGTC 1992
|||||
Db 3 GCCTGGCGCTGGATGTC 20

RESULT 2032
ABZ88291/C
ID ABZ88291 standard; DNA; 20 BP.
XX AC ABZ88291;
XX DT 17-OCT-2003 (first entry)
XX DE Human oligonucleotide sequence.
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW anti-inflammatory steroid; ubiquinone; anti-inflammatory; antiallergic;
KW antiaslathmic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX OS Homo sapiens.
XX PN WO200285308-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013135.
XX PR 24-APR-2001; 2001US-0286137P.
XX PA (EPIG-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX DR WPI; 2003-229219/22.
XX PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX PS Disclosure; SEQ ID NO 3533; 872pp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

presence of nucleases. The present nucleic acid sequence represents one of a collection (ABK69249-ABK69396) of chimeric phosphorothioate oligonucleotides having 2'-methoxyethyl (2'-MOE) wings. This sequence was used in the methods of the invention for inhibition of caspase 9

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1686 TTCAGGAGCCACTTGC 1703
|||||
Db 1 TACCAGGAGCCACTTTC 18

RESULT 2031
ABK69251
ID ABK69251 standard; DNA; 20 BP.
XX AC ABK69251;
XX DT 15-JUL-2002 (first entry)
XX DE Chimeric phosphorothioate oligonucleotide #3 for inhibition of caspase 9.
XX KW Antisense compound; caspase 9; C9; hyperproliferative disorder; stroke;
KW haematopoietic disorder; cholesterol disorder; bone metabolism disorder;
KW brain injury; neurodegenerative disease; infection; inflammation; tumour;
KW phosphorothioate backbone linkage; 2'-methoxyethyl; 2'-MOE; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX OS Chimeric.
XX FH Key
XX FT modified_base Location/Qualifiers
FT 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate nucleotides, all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX PN WO200222641-A1.
XX PD 21-MAR-2002.
XX PF 10-SEP-2001; 2001WO-US028223.
XX PR 11-SEP-2000; 2000US-00659845.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Zhang H, Watt AT;
XX DR WPI; 2002-351874/38.
XX PT New antisense oligonucleotide which modulates expression of caspase 9,
XX useful to treat tumor, inflammation or to prevent infection in humans.
XX PS Claim 26; Page 91; 145pp; English.
XX CC The present invention relates to a new antisense compound targeted to a
CC nucleic acid molecule encoding caspase 9 (C9). The compound specifically
CC hybridises with and inhibits the expression of caspase 9. The invention
CC also describes an antisense compound that specifically hybridises with an

CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 4 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1659 CTGAGGCACGTGTCTG 1676
 ||| |||||
 Db 19 CTCCTGGCAGCTGTGCAG 2

RESULT 2033
 AB292552/c
 ID AB292552 standard; DNA; 20 BP.
 XX AC AB292552;
 XX DT 17-OCT-2003 (first entry)
 XX DE Human oligonucleotide sequence.
 XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX OS Homo sapiens.
 XX PN WO200285308-A2.
 XX PD 31-OCT-2002.
 XX PF 23-APR-2002; 2002WO-US013135.
 XX PR 24-APR-2001; 2001US-0286137P.
 XX PA (EPIG-) EPIGENESIS PHARM INC.
 XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX DR WPI; 2003-229219/22.
 XX PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX PS Disclosure; SEQ ID NO 7794; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 14 A; 0 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1574 ATTTTATATTTCTATT 1591
 ||| |||||
 Db 19 AATTTCTATTTTATATT 2

RESULT 2034
 AB287231/c
 ID AB287231 standard; DNA; 20 BP.
 XX AC AB287231;
 XX DT 17-OCT-2003 (first entry)
 XX DE Human oligonucleotide sequence.
 XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX OS Homo sapiens.
 XX PN WO200285308-A2.
 XX PD 31-OCT-2002.
 XX PF 23-APR-2002; 2002WO-US013135.
 XX PR 24-APR-2001; 2001US-0286137P.
 XX PA (EPIG-) EPIGENESIS PHARM INC.
 XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX DR WPI; 2003-229219/22.
 XX PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

PS Claim 15; SEQ ID NO 2473; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 20 BP; 0 A; 7 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1399 GAGCATGAAAGAGAAA 1416
||||| ||||| |||||
Db 20 GAGGAAGAAAAGAGAAA 3

RESULT 2035
ABZ92946
ID ABZ92946 standard; DNA; 20 BP.
XX
AC ABZ92946;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 8188; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 20 BP; 2 A; 5 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1671 GTGCTGGTGAGCTCTTC 1688
||||| ||||| ||||| |||||
Db 3 GTGCTGAGTGAGCGCCTC 20

RESULT 2036
ABZ98484
ID ABZ98484 standard; DNA; 20 BP.
XX
AC ABZ98484;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human ICAM oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 13726; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 496 TCCGAGGACCTCGCTTC 513

Db ||||| ||||| ||||| |||||
 3 TCTGAGACCTCGCTTC 20

RESULT 2037

ABZ87535/c

ID ABZ87535 standard; DNA; 20 BP.

XX AC ABZ87535;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 PI WPI; 2003-229219/22.

XX DR

XX PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX PS Disclosure; SEQ ID NO 2777; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 20 BP; 8 A; 6 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1814 TAGTAGCTTTGGAAAGCT 1831

Db ||||| ||||| ||||| |||||
 18 TAGTCGCTTTGGAGATT 1

RESULT 2038

ABZ88008/c

ID ABZ88008 standard; DNA; 20 BP.

XX AC ABZ88008;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 PI WPI; 2003-229219/22.

XX DR

XX PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX PS Disclosure; SEQ ID NO 3250; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1280 CGATCTGCTCTCTGACA 1297
DB 3 CAATCTGCTCTCACTCA 20

RESULT 2040
ABZ86973
ID ABZ86973 standard; DNA; 20 BP.
AC ABZ86973;
DT 17-OCT-2003 (first entry)
DE Human oligonucleotide sequence.
KW Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
OS Homo sapiens.
PN WO200285308-A2.
PD 31-OCT-2002.
PF 23-APR-2002; 2002WO-US013135.
PR 24-APR-2001; 2001US-0286137P.
PA (EPIG-) EPIGENESIS PHARM INC.
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
DR WPI; 2003-229219/22.
PT Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.
PS Claim 15; SEQ ID NO 2215; 872pp; English.
XX The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1632 CCCAGGGACAGAACCCAA 1649
DB 20 CCCTGGGACAGACCCCA 3

RESULT 2039
ABZ88025
ID ABZ88025 standard; DNA; 20 BP.
AC ABZ88025;
DT 17-OCT-2003 (first entry)
DE Human oligonucleotide sequence.
KW Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
OS Homo sapiens.
PN WO200285308-A2.
PD 31-OCT-2002.
PF 23-APR-2002; 2002WO-US013135.
PR 24-APR-2001; 2001US-0286137P.
PA (EPIG-) EPIGENESIS PHARM INC.
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
DR WPI; 2003-229219/22.
PT Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.
PS Disclosure; SEQ ID NO 3267; 872pp; English.
XX The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 5 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 704 TCGGGGCTGGCAAGGCA 721
 |||||
 Db 1 TCGGGGCTGCAGAGCA 18

RESULT 2041
 ABZ97398
 ID ABZ97398 standard; DNA; 20 BP.
 XX
 AC ABZ97398;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human IL4-R oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 PI
 DR WPI; 2003-229219/22.
 XX

Pharmaceutical composition for treating ailments associated with impaired PT respiration, has oligo(s) antisense to specific gene(s) or its PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or PT ubiquinone.

PS Disclosure; SEQ ID NO 12640; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a CC first active agent comprising an oligonucleotide antisense to the CC initiation codon, coding region, 5' or 3' end genomic flanking regions, CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 5 A; 3 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 347 ACGTTGGTGAGGACTGTC 364
 |||||
 Db 2 ACATTGGTGTGACTGTC 19

RESULT 2042
 ABZ97646/C
 ID ABZ97646 standard; DNA; 20 BP.
 XX
 AC ABZ97646;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human CCR3 oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 XX Miller S, Tang L, Shahabuddin S;
 XX

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired PT respiration, has oligo(s) antisense to specific gene(s) or its PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or PT ubiquinone.

PS Disclosure; SEQ ID NO 12888; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a CC first active agent comprising an oligonucleotide antisense to the CC initiation codon, coding region, 5' or 3' end genomic flanking regions, CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

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CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, increasing levels of ubiquinone or
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 20 BP; 1 A; 5 C; 4 G; 10 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1456 ACCAAGGAGAGAGCCCA 1473
| | | | | | | | | | | | | |
DB 20 ACCAAGGAGATGAAGCAA 3
RESULT 2043
ABZ87032
ID ABZ87032 standard; DNA; 20 BP.
XX
AC ABZ87032;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
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PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
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XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Claim 15; SEQ ID NO 2274; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
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CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
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CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, increasing levels of ubiquinone or
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 20 BP; 4 A; 7 C; 8 G; 1 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 604 GACGCGTGGAGAGGCC 621
| | | | | | | | | | | | | |
DB 1 GACAGCGTGGAGAGCCC 18
RESULT 2044
ABZ93491
ID ABZ93491 standard; DNA; 20 BP.
XX
AC ABZ93491;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
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PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
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XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Disclosure; SEQ ID NO 8733; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
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 CC antiinflammatory steroid and ubiquinone. A composition of the invention
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 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 7 A; 2 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 602 GTGACGGCTGGAGAGG 619
 Db 1 GCGAAGCGCATGGAAGG 18
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 |||||

RESULT 2045
 ABZ85445
 ID ABZ85445 standard; DNA; 20 BP.
 XX
 AC ABZ85445;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
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 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX

Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

PS Claim 15; SEQ ID NO 687; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 9 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1430 AGAAGAAGTCCCGAAG 1447
 Db 2 AGAAGGAATTCACCAAG 19
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 |||||

RESULT 2046
 ABZ88403/C
 ID ABZ88403 standard; DNA; 20 BP.
 XX
 AC ABZ88403;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
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 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX

Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

PS Disclosure; SEQ ID NO 3645; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, increasing levels of ubiquinone or receptor, producing bronchodilation, increasing levels of bronchoconstriction, lung surfactant in a subject's tissue, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 2 A; 5 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 472 GCGGGCCCTGCACCATGCA 489
||| ||||| ||| ||| |||
DB 2 GCGGGCCCTGCATTGCA 19

RESULT 2048
ABZ85440/c
ID ABZ85440 standard; DNA; 20 BP.
XX
AC ABZ85440;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 682; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, increasing levels of ubiquinone or receptor, producing bronchodilation, increasing levels of bronchoconstriction, lung surfactant in a subject's tissue, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 2 A; 1 C; 4 G; 13 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1776 AACCAATAGACAAACTCC 1793
||| ||||| ||| ||| |||
DB 20 AACCAATAGACAAATAAC 3

RESULT 2047
ABZ87954
ID ABZ87954 standard; DNA; 20 BP.
XX
AC ABZ87954;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
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PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3196; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antineoplastic therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 8 A; 3 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2072 TAATAAAATGTCATTT 2089

Db 18 TAATAAAATGTCATTT 1

RESULT 2049

ABZ87226/c

ID ABZ87226 standard; DNA; 20 BP.

XX AC ABZ87226;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;

XX KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

XX KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

XX KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

XX KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

XX KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

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XX PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired

XX PT respiration, has oligo(s) antisense to specific gene(s) or its

XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

XX PT ubiquinone.

XX PS Claim 15; SEQ ID NO 2468; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a

XX CC first active agent comprising an oligonucleotide antisense to the

XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

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Sequence 20 BP; 0 A; 8 C; 0 G; 12 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1408 AAAGAGAAAGACCAGAG 1425

Db 19 AAAGAGAAAGAGAGAG 2

RESULT 2050

ABZ91893/c

ID ABZ91893 standard; DNA; 20 BP.

XX AC ABZ91893;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;

XX KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

XX KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

XX KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

XX KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

XX KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPITG-) EPIGENESIS PHARM INC.

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XX PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired

XX PT respiration, has oligo(s) antisense to specific gene(s) or its

XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

XX PT ubiquinone.

XX PS Disclosure; SEQ ID NO 7135; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a

XX CC first active agent comprising an oligonucleotide antisense to the

XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

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Sequence 20 BP; 6 A; 6 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 654 CTTTCATAAGTATGGAGA 671
||||| ||||| ||||| |||||
DB 19 CTTTGACAGGATGGAGA 2

RESULT 2052
ABZ92124
ID ABZ92124 standard; DNA; 20 BP.
XX
AC ABZ92124;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
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PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 7366; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

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Sequence 20 BP; 10 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1543 AGTCCTCACGTTCTTC 1560
||||| ||||| ||||| |||||
DB 20 AGTCATTAATTTCTTC 3

RESULT 2051
ABZ88018/C
ID ABZ88018 standard; DNA; 20 BP.
XX
AC ABZ88018;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3260; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 20 BP; 5 A; 1 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1573 GATTATATTTCTATT 1590

Db 3 GATTTCATGTTATTT 20

RESULT 2053

ABZ92971/C

ID ABZ92971 standard; DNA; 20 BP.

XX AC ABZ92971;

XX AC ABZ92971;

DT 17-OCT-2003 (first entry)

XX Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction;
antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
antisense gene therapy; respiratory; lung; adenosine sensitivity;
adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

PF 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX Disclosure; SEQ ID NO 8213; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 20 BP; 5 A; 10 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1854 GGGCTGGCTGGCTTCA 1871

Db 20 GGGCTGGATGGGGCTTCA 3

RESULT 2054

ABZ93629

ID ABZ93629 standard; DNA; 20 BP.

XX AC ABZ93629;

XX AC ABZ93629;

DT 17-OCT-2003 (first entry)

XX Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction;
antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
antisense gene therapy; respiratory; lung; adenosine sensitivity;
adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

PF 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX Disclosure; SEQ ID NO 8871; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or receptor, producing bronchodilation, increasing levels of adenosine or lung surfactant in a subject's tissue, or a respiratory disease or condition, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 20 BP; 3 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1742 GTGCCAGGCTCTGGGTGAA 1759
||||| ||||| ||||| |||||
Db 20 GTGCCAGGCTTGGGGGAA 3

RESULT 2056
ABZ87600
ID ABZ87600 standard; DNA; 20 BP.
XX AC ABZ87600;
XX DT 17-OCT-2003 (first entry)
XX DE Human oligonucleotide sequence.
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
XX OS Homo sapiens.
XX PN WO200285308-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013135.
XX PR 24-APR-2001; 2001US-0286137P.
XX PA (EPIG-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX PT Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.
XX PS Disclosure; SEQ ID NO 2842; 872pp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or receptor, producing bronchodilation, increasing levels of adenosine or lung surfactant in a subject's tissue, or a respiratory disease or condition, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 20 BP; 3 A; 5 C; 11 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1339 GAGGAGAGGGGGCCGC 1356
||||| ||||| ||||| |||||
Db 2 GAGGTCGAGAGGGGGCCGC 19

RESULT 2055
ABZ98454/C
ID ABZ98454 standard; DNA; 20 BP.
XX AC ABZ98454;
XX DT 17-OCT-2003 (first entry)
XX DE Human ICAM oligonucleotide sequence.
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
XX OS Homo sapiens.
XX PN WO200285308-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013135.
XX PR 24-APR-2001; 2001US-0286137P.
XX PA (EPTG-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX PT Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.
XX PS Disclosure; SEQ ID NO 13696; 872pp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 4 A; 2 C; 2 G; 12 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1578 TATATTTCTATTCTCT 1595
 ||||| || |||||
 Db 2 TATATATTGATTCTCT 19
 RESULT 2057
 ABZ88661
 ID ABZ88661 standard; DNA; 20 BP.
 XX
 AC ABZ88661;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 3903; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1693 AGCCACCTTGCACCCCAT 1710
 ||||| || |||||
 Db 1 AGCCATCTAGCCACCCCTT 18
 RESULT 2058
 ABZ89370/c
 ID ABZ89370 standard; DNA; 20 BP.
 XX
 AC ABZ89370;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 4612; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or receptor, producing bronchodilation, increasing levels of adenosine or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1597 TGTATTATATAAAATT 1614
19 TGCATTTTATAAACTT 2

RESULT 2060
ABZ84798/C
ID ABZ84798 standard; DNA; 20 BP.
AC ABZ84798;
XX
XX 17-OCT-2003 (first entry)
XX Human oligonucleotide sequence.
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX Homo sapiens.
XX WO200285308-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013135.
XX 24-APR-2001; 2001US-0286137P.
XX (EPIG-) EPIGENESIS PHARM INC.
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX Claim 15; SEQ ID NO 40; 872pp; English.
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or receptor, producing bronchodilation, increasing levels of adenosine or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1956 AAGTGACCAAGAAAC 1973
18 AAGTGAGCGAGAAAC 1

RESULT 2059
ABZ90852/C
ID ABZ90852 standard; DNA; 20 BP.
AC ABZ90852;
XX
XX 17-OCT-2003 (first entry)
XX Human oligonucleotide sequence.
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX Homo sapiens.
XX WO200285308-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013135.
XX 24-APR-2001; 2001US-0286137P.
XX (EPIG-) EPIGENESIS PHARM INC.
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX Disclosure; SEQ ID NO 6094; 872pp; English.
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 1 A; 10 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1337 AGGAGGGAGAGGGGGCC 1354

Db 18 AGGAGGTAGAGGGGAC 1

RESULT 2061

ABZ85919

ID ABZ85919 standard; DNA; 20 BP.

XX AC ABZ85919;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;

XX KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

XX KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

XX KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

XX KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

XX KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX PI Miller S, Tang L, Shahabuddin S;

XX XX WPI; 2003-229219/22.

XX XX Pharmaceutical composition for treating ailments associated with impaired

XX PT respiration, has oligo(s) antisense to specific gene(s) or its

XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

XX PT ubiquinone.

XX PS Claim 15; SEQ ID NO 1161; 872pp; English.

XX XX The invention relates to a novel pharmaceutical composition, which has a

XX CC first active agent comprising an oligonucleotide antisense to the

XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 3 A; 5 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1309 TGTGAGGAGAGTTCTCC 1326

Db 1 TGGGAGGGAGGTCCTCC 18

RESULT 2062

ABZ98435

ID ABZ98435 standard; DNA; 20 BP.

XX AC ABZ98435;

XX DT 17-OCT-2003 (first entry)

XX DE Human ICAM oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;

XX KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

XX KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

XX KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

XX KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

XX KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX PI Miller S, Tang L, Shahabuddin S;

XX XX WPI; 2003-229219/22.

XX XX Pharmaceutical composition for treating ailments associated with impaired

XX PT respiration, has oligo(s) antisense to specific gene(s) or its

XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

XX PT ubiquinone.

XX PS Disclosure; SEQ ID NO 13677; 872pp; English.

XX XX The invention relates to a novel pharmaceutical composition, which has a

XX CC first active agent comprising an oligonucleotide antisense to the

XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisease gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine or receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 937 AACCTGCTATGCTGATG 954
||||| |
Db 19 AACCTGACATGCTCATG 2

RESULT 2064
ABZ88725
ID ABZ88725 standard; DNA; 20 BP.
AC ABZ88725;
XX
XX 17-OCT-2003 (first entry)
DT
DE Human oligonucleotide sequence.
XX
KW Human; antisease; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisease gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
XX WO200285308-A2.
PN
XX
XX 31-OCT-2002.
PD
XX
XX 23-APR-2002; 2002WO-US013135.
PF
XX
XX 24-APR-2001; 2001US-0286137P.
PR
XX
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
PI
XX
XX WPI; 2003-229219/22.
DR
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisease to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 3967; 872pp; English.
PS
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisease to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisease gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine or receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 262 TACCACAGCGATGACTAC 279
||||| |
Db 3 TACCACAGTGATGATGAC 20

RESULT 2063
ABZ88507/C
ID ABZ88507 standard; DNA; 20 BP.
AC ABZ88507;
XX
XX 17-OCT-2003 (first entry)
DT
DE Human oligonucleotide sequence.
XX
KW Human; antisease; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisease gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
XX WO200285308-A2.
PN
XX
XX 31-OCT-2002.
PD
XX
XX 23-APR-2002; 2002WO-US013135.
PF
XX
XX 24-APR-2001; 2001US-0286137P.
PR
XX
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
PI
XX
XX WPI; 2003-229219/22.
DR
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisease to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 3749; 872pp; English.
PS
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisease to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 7 A; 4 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 512 TCTGTACGTCATGATA 529

Db 3 TCTGTACGTCCTCAATA 20

RESULT 2065

ABZ87366/C
 ID ABZ87366 standard; DNA; 20 BP.

AC ABZ87366;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.

PN WO200295308-A2.

PD 31-OCT-2002.

PF 23-APR-2002; 2002WO-US013135.

PR 24-APR-2001; 2001US-0286137P.

PA (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

DR WPI; 2003-229219/22.

PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

PS Disclosure; SEQ ID NO 2608; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 492 GAAGTCCGAGGCATCTGG 509

Db 20 GATGTCGAGGTATCTTG 3

RESULT 2066

ABZ99185/C
 ID ABZ99185 standard; DNA; 20 BP.

AC ABZ99185;

DT 17-OCT-2003 (first entry)

DE Human PDE4C oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.

PN WO200285308-A2.

PD 31-OCT-2002.

PF 23-APR-2002; 2002WO-US013135.

PR 24-APR-2001; 2001US-0286137P.

PA (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

DR WPI; 2003-229219/22.

PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

PS Disclosure; SEQ ID NO 14427; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 20 BP; 0 A; 11 C; 0 G; 9 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1333 GAAGAGGAGGAGGAGG 1350
 Db 18 GAAGAGGAGGAGGAGAG 1

RESULT 2067
 ABZ82713/c
 ID ABZ82713 standard; DNA; 20 BP.

AC ABZ82713;
 XX 14-MAY-2003 (first entry)

DE Human HSL chimeric phosphorothioate oligonucleotide SEQ ID NO:102.
 KW Hormone-sensitive lipase; antisense oligonucleotide; inhibitor; obesity;
 KW phosphorothioate; antidiabetic; anorectic; cytostatic; antisense therapy;
 KW abnormal metabolic condition; hyperlipidaemia; type 2 diabetes; cancer;
 KW hyperproliferative disorder; human; ss.

OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate linkages"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl (2'-MOE) wing"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl (2'-MOE) wing"

XX WO2003010139-A2.

PN 06-FEB-2003.

XX 15-JUL-2002; 2002WO-US022672.

XX 26-JUL-2001; 2001US-00915814.

XX (ISIS-) ISIS PHARM INC.

XX Butler MM, Watt AT, Freier SM, Wyatt JR;

XX WPI; 2003-239411/23.

XX New antisense oligonucleotides targeted against nucleic acids encoding
 PT hormone-sensitive lipase, useful for treating abnormal metabolic
 PT condition, e.g. hyperlipidemia and obesity, or a hyperproliferative
 PT disorder, e.g. cancer.

XX Example 15; Page 89; 167pp; English.

XX The present invention describes a compound (I) 8-50 nucleobases in length
 CC targeted to a nucleic acid molecule encoding a hormone-sensitive lipase
 CC (HSL) or a splice variant of HSL. The compound specifically hybridises
 CC with and inhibits the expression of HSL or a splice variant of HSL, or
 CC specifically hybridises with at least an 8-nucleobase portion of an
 CC active site on a nucleic acid molecule encoding HSL. (I) have anorectic,
 CC antidiabetic and cytostatic activities, and can be used in antisense
 CC therapy. (I) is useful for treating an animal, particularly human,
 CC suspected of having an abnormal metabolic condition such as obesity,
 CC hyperlipidaemia, type 2 diabetes, a hyperproliferative disorder such as
 CC cancer (e.g. pituitary, colorectal, breast, testicular, pulmonary or
 CC epithelial cancer). (I) is also useful in modulating blood glucose
 CC levels, particularly plasma or serum glucose levels, in a diabetic
 CC animal. The present sequence represents a human hormone-sensitive lipase
 CC chimeric phosphorothioate antisense oligonucleotide, which is used in an
 CC example from the present invention

SQ Sequence 20 BP; 7 A; 8 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 464 ATTGGGCTGGGGCCTGC 481
 Db 20 ATTGGGCTGGGTCCTTC 3

RESULT 2068
 AAL52065/c

ID AAL52065 standard; DNA; 20 BP.

AC AAL52065;

XX 10-MAY-2003 (first entry)

XX Brassica oleracea B0GSL-ALK PCR primer #9.

XX PCR; primer; ss; ALK; ELONG; plant glucosinolate content modification.

XX Brassica oleracea.

XX WO2003004619-A2.

XX 16-JAN-2003.

XX 05-JUL-2002; 2002WO-US021408.

XX 05-JUL-2001; 2001US-0303310P.

XX (REGC) UNIV CALIFORNIA.

XX Quiros C, Li G;

XX WPI; 2003-221592/21.

XX New nucleic acid encoding an enzyme comprising ALK or ELONG gene, useful
 PT for modifying the glucosinolate content in a plant.

XX Claim 17; Page 41; 88pp; English.

XX The invention comprises the amino acid and coding sequences of Brassica
 CC oleracea ALK and ELONG genes/proteins. The DNA and proteins of the
 CC invention are useful for modifying the glucosinolate content in a plant.
 CC The present DNA sequence is used in the exemplification of the invention

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XX SQ Sequence 20 BP; 1 A; 4 C; 4 G; 11 T; 0 U; 0 Other;
Query Match      0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1405 GAAAGAGAGAGAGACCA 1422
Db 18 GAAACGACCAAGACCGA 1

RESULT 2069
ADA55758/c
ID ADA55758 standard; DNA; 20 BP.
XX AC
XX AC ADA55758;
XX DT
XX DT 20-NOV-2003 (first entry)
XX DE
XX DE Human protein-related PCR primer, SEQ ID 3326.
XX DE
XX DE Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
XX DE Gene Therapy; human; secretory protein; membrane proteins; cancer;
XX DE inflammatory disease; osteoporosis; neurological disease; PCR; primer;
XX DE ss.
XX OS Homo sapiens.
XX PN EP1293569-A2.
XX PD
XX PD 19-MAR-2003.
XX PF
XX PF 21-MAR-2002; 2002EP-00006586.
XX PR
XX PR 14-SEP-2001; 2001JP-00328381.
XX PR 24-JAN-2002; 2002US-0350435P.
XX PA (HELI-) HELIX RES INST.
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
XX PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
XX PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX PD WPI; 2003-395539/38.
XX PF
XX PF 21-MAR-2002; 2002EP-00006586.
XX PR
XX PR 14-SEP-2001; 2001JP-00328381.
XX PR 24-JAN-2002; 2002US-0350435P.
XX PA (HELI-) HELIX RES INST.
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
XX PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
XX PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX PD WPI; 2003-395539/38.
XX PF
XX PF New polynucleotides encoding full-length polypeptides, e.g. secretory
XX PT and/or membrane proteins, useful for developing medicines for diseases in
XX PT which the gene is involved, or as target molecules for gene therapy.
XX PS Example 8; Page 111; 205pp; English.
XX CC The present invention relates to novel human secretory or membrane
XX CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
XX CC ADA54071). The coding sequences are useful in the gene therapy of
XX CC diseases caused by abnormalities of the proteins, e.g. cancer,
XX CC inflammatory diseases, osteoporosis or neurological disease. The present
XX CC sequence was used in an example from the invention.
XX SQ Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match      0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1006 GAGACAGTGTGCGCCCTG 1023
Db 20 GATACACTGTGCGCCATG 3

RESULT 2070
ADA55754/c
ID ADA55754 standard; DNA; 20 BP.
XX AC
XX AC ADA55754;
XX DT
XX DT 20-NOV-2003 (first entry)
XX DE
XX DE Human protein-related PCR primer, SEQ ID 3322.
XX DE
XX DE Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
XX DE Gene Therapy; human; secretory protein; membrane proteins; cancer;
XX DE inflammatory disease; osteoporosis; neurological disease; PCR; primer;
XX DE ss.
XX OS Homo sapiens.
XX PN EP1293569-A2.
XX PD
XX PD 19-MAR-2003.
XX PF
XX PF 21-MAR-2002; 2002EP-00006586.
XX PR
XX PR 14-SEP-2001; 2001JP-00328381.
XX PR 24-JAN-2002; 2002US-0350435P.
XX PA (HELI-) HELIX RES INST.
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
XX PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
XX PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX PD WPI; 2003-395539/38.
XX PF
XX PF New polynucleotides encoding full-length polypeptides, e.g. secretory
XX PT and/or membrane proteins, useful for developing medicines for diseases in
XX PT which the gene is involved, or as target molecules for gene therapy.
XX PS Example 8; Page 111; 205pp; English.
XX CC The present invention relates to novel human secretory or membrane
XX CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
XX CC ADA54071). The coding sequences are useful in the gene therapy of
XX CC diseases caused by abnormalities of the proteins, e.g. cancer,
XX CC inflammatory diseases, osteoporosis or neurological disease. The present
XX CC sequence was used in an example from the invention.
XX SQ Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match      0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 511 TTCTGTACGTCAATGAT 528
Db 18 TTCTGTACGACCATGAT 1

RESULT 2071
ABV72413/c
ID ABV72413 standard; DNA; 20 BP.
XX AC
XX AC ABV72413;
XX DT
XX DT 29-JAN-2003 (first entry)
XX DE
XX DE PCR primer used to amplify Human Artemis gene exon 13.
XX DE
XX DE Human; Artemis gene; DNA repair factor; metallo beta-lactamase; RS-SCID;
XX DE chromosome 10; severe combined immunodeficiency; SCID1; cancer; PCR;
XX DE primer; ss.
XX OS Homo sapiens.

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XX WO200277228-A1.
XX 03-OCT-2002.
XX 22-MAR-2001; 2001WO-IB000546.
XX 22-MAR-2001; 2001WO-IB000546.
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX De Villartay J, Moshous D, Fischer A;
XX WPI; 2003-029937/02.
XX New isolated nucleic acid molecule of the Artemis gene, useful for
XX diagnosing or treating SCID or cancer.
XX Example 1; Page 67; 71pp; English.
XX PCR primers ABV72389-ABV72416 were used to amplify exons of the human
XX Artemis gene. This gene encodes a V(D)J recombination and/or DNA repair
XX factor that belongs to the metallo beta-lactamase superfamily, and whose
XX mutations give rise to the human RS-SCID condition. The gene is localised
XX to chromosome 10. The Artemis gene or its nucleic acid is useful for
XX diagnosing or treating severe combined immunodeficiencies (SCIDs) or
XX cancer
XX Sequence 20 BP; 5 A; 5 C; 1 G; 9 T; 0 U; 0 Other;
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. NO. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2070 TGTAAATAAAGTGACAT 2087
Db 18 TGTAAATAAAGTGCAAAAT 1

RESULT 2072
AAS4003/C
ID AAD54003 standard; DNA; 20 BP.
XX AAD54003;
XX 17-JUN-2003 (first entry)
XX HIV-1 tat antisense oligonucleotide #12.
XX Nucleation site; rate factor; gene therapy; antisense; phosphorothioate;
XX human immunodeficiency virus; HIV-1; tat; ss.
XX Human immunodeficiency virus 1.
XX Synthetic.
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone"
XX WO200295059-A2.
XX 28-NOV-2002.
XX 15-MAY-2002; 2002WO-US018532.
XX 17-MAY-2001; 2001US-0291737P.
XX (PUBL-) PUBLIC HEALTH RES INST NEW YORK.
XX Drlica K, Wang J;
XX WPI; 2003-140378/13.

XX Calculating a rate factor that is proportional to initial rate, for
XX predicting nucleation sites and selecting target sites for antisense
XX attack of RNA, comprises calculating the melting energy and energy gain
XX of regions of the RNA.
XX Example 6; Page 39; 59pp; English.
XX The invention relates to a method of calculating a rate factor, which is
XX proportional to initial rate, for hybridisation to an RNA molecule by a
XX given antisense nucleic acid. The method involves calculating the melting
XX energy required to convert specific regions of the RNA molecule to a
XX single-stranded state; the energy gain resulting from hybridisation of
XX the specific regions of the RNA molecule to an oligonucleotide; and the
XX rate factor. The method is useful for calculating a rate factor that is
XX proportional to a rate constant for hybridisation between complementary
XX nucleic acids. The method is particularly useful for estimating initial
XX rates, predicting nucleation sites and selecting target sites for
XX antisense attack of RNA. The invention is useful in antisense gene
XX therapy. The present sequence is an antisense oligonucleotide targetted
XX to human immunodeficiency virus type 1 (HIV-1) tat gene. This
XX oligonucleotide is used to illustrate the method of the invention
XX Sequence 20 BP; 1 A; 11 C; 1 G; 7 T; 0 U; 0 Other;
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. NO. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1334 AAGAGGAGGAGGAGGGGG 1351
Db 18 AAGAGGAGGAGGAGGCTGG 1

RESULT 2073
ABZ76926
ID ABZ76926 standard; DNA; 20 BP.
XX ABZ76926;
XX 07-MAY-2003 (first entry)
XX Bovine RPCI-41 genomic BAC library forward PCR primer 1599.
XX Acyl CoA:diacylglycerol transferase; DGAT; enzyme; chromosome 14; bovine;
XX milk; meat marbling; low fat; polymorphic; SNP;
XX single nucleotide polymorphism; PCR primer; ss.
XX Bos taurus.
XX Synthetic.
XX WO2003004630-A2.
XX 16-JAN-2003.
XX 05-JUL-2002; 2002WO-EP007520.
XX 06-JUL-2001; 2001EP-00116412.
XX 13-MAY-2002; 2002US-0379412P.
XX (ARBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUECHTER.
XX Fries H, Winter A;
XX WPI; 2003-239205/23.
XX New nucleic acid molecule comprising a sequence of an allele of a
XX polymorphic bovine acyl CoA:diacylglycerol transferase gene useful for
XX testing a mammal for its predisposition for fat content of milk and for
XX meat marbling.
XX Example 3; Page 27; 91pp; English.
```

CC The present invention describes a nucleic acid molecule (NA) (I) encoding
 CC a bovine acyl CoA-diacylglycerol transferase (DGAT) contributing to or
 CC indicative for low fat content of milk and to low meat marbling
 CC (intramuscular fat content). Human DGAT is located to chromosome 8, and
 CC bovine DGAT is located to chromosome 14. (I) is useful for testing a
 CC mammal for its predisposition for fat content of milk and/or its
 CC predisposition for meat marbling. The method comprises analysing the gene
 CC encoding DGAT for nucleotide polymorphisms (e.g. single nucleotide
 CC polymorphisms (SNPs)) which are connected with the predisposition. The
 CC nucleotide polymorphisms are located in the coding region of the DGAT
 CC gene and result in substitution, deletion and/or addition of an amino
 CC acid sequence of the polypeptide which is encoded by the gene. The
 CC nucleic acid molecule has at the position 10433 and 10434 of the DGAT
 CC gene a guanine and a cytosine residue, at position 3343 a cytosine or
 CC thymine, which correlate with a predisposition for low fat content of
 CC milk and low meat marbling. The nucleic acid molecule has at the position
 CC corresponding to position 10433 and 10434 of the DGAT gene two adenine
 CC residues which correlate with a predisposition for high content of milk
 CC and high meat marbling. The nucleotide polymorphisms are located in a
 CC region which is responsible for the regulation of the expression of the
 CC product of the gene encoding DGAT. ABZ76924 to ABZ77045 and ABP96035 to
 CC ABP96046 represent sequences used in the exemplification of the present
 CC invention

XX Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1132 GAGTACTCTGAGAGATC 1149

DB 2 GAGTACTCTGAGAGATC 19

RESULT 2074

ABZ76974

ID ABZ76974 standard; DNA; 20 BP.

AC ABZ76974;

DT 07-MAY-2003 (first entry)

XX Bovine DGAT PCR primer #10.

XX Acyl CoA:diacylglycerol transferase; DGAT; enzyme; chromosome 14; bovine;
 KW milk; meat marbling; low fat; polymorphic; SNP;
 KW single nucleotide polymorphism; PCR primer; ss.

OS Bos taurus.

OS Synthetic.

PN WO2003004630-A2.

PD 16-JAN-2003.

PF 05-JUL-2002; 2002WO-EP007520.

XX 06-JUL-2001; 2001EP-00116412.

PR 13-MAY-2002; 2002US-0379412P.

XX (ARBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUECHTER.

XX Fries H, Winter A;

DR WPI; 2003-239205/23.

XX New nucleic acid molecule comprising a sequence of an allele of a
 PT polymorphic bovine acyl CoA-diacylglycerol transferase gene useful for
 PT testing a mammal for its predisposition for fat content of milk and for
 PT meat marbling.

XX

PS Example 1; Page 36; 91pp; English.

XX The present invention describes a nucleic acid molecule (NA) (I) encoding
 CC a bovine acyl CoA-diacylglycerol transferase (DGAT) contributing to or
 CC indicative for low fat content of milk and to low meat marbling
 CC (intramuscular fat content). Human DGAT is located to chromosome 8, and
 CC bovine DGAT is located to chromosome 14. (I) is useful for testing a
 CC mammal for its predisposition for fat content of milk and/or its
 CC predisposition for meat marbling. The method comprises analysing the gene
 CC encoding DGAT for nucleotide polymorphisms (e.g. single nucleotide
 CC polymorphisms (SNPs)) which are connected with the predisposition. The
 CC nucleotide polymorphisms are located in the coding region of the DGAT
 CC gene and result in substitution, deletion and/or addition of an amino
 CC acid sequence of the polypeptide which is encoded by the gene. The
 CC nucleic acid molecule has at the position 10433 and 10434 of the DGAT
 CC gene a guanine and a cytosine residue, at position 3343 a cytosine or
 CC thymine, which correlate with a predisposition for low fat content of
 CC milk and low meat marbling. The nucleic acid molecule has at the position
 CC corresponding to position 10433 and 10434 of the DGAT gene two adenine
 CC residues which correlate with a predisposition for high content of milk
 CC and high meat marbling. The nucleotide polymorphisms are located in a
 CC region which is responsible for the regulation of the expression of the
 CC product of the gene encoding DGAT. ABZ76924 to ABZ77045 and ABP96035 to
 CC ABP96046 represent sequences used in the exemplification of the present
 CC invention

XX Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1132 GAGTACTCTGAGAGATC 1149

DB 2 GAGTACTCTGAGAGATC 19

RESULT 2075

AAL62194

ID AAL62194 standard; DNA; 20 BP.

AC AAL62194;

DT 22-SEP-2003 (first entry)

XX GAPDH gene amplifying RT-PCR primer, GAPDHR.

DE Gene expression suppression; tumour; gene therapy; GAPDH; RT-PCR; primer;

KW reverse transcription PCR; ss.

XX Unidentified.

OS WO2003048362-A2.

XX 12-JUN-2003.

PD 29-NOV-2002; 2002WO-GB005417.

XX 30-NOV-2001; 2001US-00000773.

PR (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.

XX Farrar GJ, Humphries P, Millington-Ward S, Kenna PF;

PI WPI; 2003-505296/47.

DR Suppressing the expression of a mutant allele of a gene by exposing the

XX message to a ribozyme that hybridizes with the message within or adjacent

PT to the polymorphic variation and that cleaves the message at the NUX

PT ribozyme cleavage site.

XX Example 5; Page 62; 124pp; English.

CC The invention relates to a method of suppressing the expression of a mutant allele of a gene. The method involves selecting a mutant allele that encodes a message comprising a nucleotide region comprising an NUX ribozyme cleavage site within or adjacent a polymorphic variation characteristic of the mutant allele and exposing the message to the ribozyme that hybridizes with the message within or adjacent to the polymorphic variation and that cleaves the message at the NUX ribozyme cleavage site. The method is useful for suppressing the expression of a mutant allele of a gene for treating e.g. tumour. The invention is also used in gene therapy. The present sequence is reverse transcription PCR (RT-PCR) primer used to amplify GAPDH gene. This primer is used to illustrate the method of the invention

XX Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1095 CATCAGTCTTCCCAATAT 1112
Db 1 CATGAGTCTTCCAGAT 18

RESULT 2076
ACAS8150/c
ID ACAS8150 standard; DNA; 20 BP.
XX
AC ACAS8150;
XX
XX 09-JUN-2003 (first entry)
XX Human familial bipolar affective disorder chromosome marker #98.
XX Human; genotype determination; familial bipolar affective disorder; chromosomal region linked; locus associated with resistance; D4S402; D4S424; D4S431; D4S404; D11S394; D11S29; chromosome marker; primer; ss.
XX Homo sapiens.
OS
XX US2002192655-A1.
XX 19-DEC-2002.
XX
XX 13-JUN-2001; 2001US-00881012.
XX
XX 29-MAR-1996; 96US-0014334P.
XX 20-OCT-1997; 97US-0062924P.
XX 19-OCT-1998; 98US-00175158.
XX (GINN/) GINNS E I.
XX (EGEL/) EGELAND J A.
XX (PAUL/) PAUL S M.
XX
XX Ginn EI, Egeland JA, Paul SM;
XX
XX WPI; 2003-352708/33.
XX
XX Determining a genotype associated with increased or decreased resistance to familial bipolar affective disorder in a family comprises determining the genotype of e.g., chromosomal regions D4S402 and D4S424.
XX
XX Disclosure; Page 10; 79pp; English.
XX
XX The present invention relates to a method of determining a genotype associated with increased or decreased resistance to familial bipolar affective disorder. The method comprises determining the genotype with at least one marker of at least one chromosomal region linked to a locus associated with resistance to bipolar affective disorder, where the chromosomal regions are included of and localised between D4S402 and D4S424, D4S431 and D4S404, or D11S394 and D11S29. The invention also discloses a kit for determining a genotype associated with increased or

CC decreased resistance to familial bipolar affective disorder, where the kit comprises markers for two or more of the chromosomal regions cited. The method and kit are useful for determining a genotype associated with increased or decreased resistance to familial bipolar affective disorder in a family affected by bipolar affective disorder, for determining the contribution of these chromosomal regions to bipolar affective disorder in an affected family member, and for assessing an increased or decreased risk of developing bipolar illness for a tested individual from an affected family. ACA58053-ACA58292 represent primers used in the present invention

XX Sequence 20 BP; 1 A; 4 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 325 AGCAAGCAGATGCAGAGA 342
Db 19 AACCGCAATGCAGAGA 2

RESULT 2077
ACC58924/c
ID ACC58924 standard; DNA; 20 BP.
XX
AC ACC58924;
XX
XX 11-JUL-2003 (first entry)
XX Human IL-1 receptor-associated kinase-4 antisense oligo #ISIS 156471.
XX
XX Antisense therapy; cytostatic; antimicrobial; antiinflammatory; interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer; inflammatory disease; infection; diagnostic; therapeutic; prophylaxis; ss.
XX Homo sapiens.
OS
XX Key modified_base 1..20
XX Location/Qualifiers
XX /tag= a
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages. All cytosines are 5-methylcytosine"
XX modified_base 1..5
XX /tag= b
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX modified_base 16..20
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX WO2003028636-A2.
XX
XX 10-APR-2003.
XX
XX 26-SEP-2002; 2002WO-US030574.
XX
XX 28-SEP-2001; 2001US-00966451.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett FC, Freier SM;
XX
XX WPI; 2003-363256/34.
XX
XX New antisense oligonucleotides for modulating IL-1 receptor-associated kinase-4 gene expression, particularly useful for preventing, delaying or treating e.g. cancer (e.g. renal cancer), inflammatory disease or an infection.

PS Claim 3; Page 75; 119pp; English.

CC The invention relates to a compound of 8-50 nucleobases which is targeted
 CC to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated
 CC kinase-4, specifically hybridising with the nucleic acid and inhibiting
 CC the expression of the encoded product. Also disclosed is the compound
 CC hybridising with an 8-nucleobase portion of an active site on a nucleic
 CC acid molecule encoding IL-1 receptor-associated kinase-4. The antisense
 CC oligonucleotide is useful for treating an animal having a disease or
 CC conditions associated with IL-1 receptor-associated kinase-4, e.g. cancer
 CC (particularly renal cancer), inflammatory disease or an infection. The
 CC antisense compounds are useful for diagnostics, therapeutics,
 CC prophylaxis, or as research reagents or kits. The current sequence
 CC represents a human IL-1 receptor-associated kinase-4 expression antisense
 CC inhibitor oligonucleotide

XX SQ Sequence 20 BP; 6 A; 6 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 799 TCCAAAGTAAATGAGATG 816
 Db 19 TCTCAAGTAAATGAGATG 2

RESULT 2078
 ABX95824/C
 ID ABX95824 standard; DNA; 20 BP.
 XX AC ABX95824;
 XX DT 24-JUL-2003 (first entry)
 XX DE PCR primer F2 for DNA encoding human Abl kinase.
 XX KW Human; Abl kinase domain; tyrosine kinase activity; leukaemia;
 KW N-(4-methyl-3-(4-pyridin-3-yl-pyrimidin-2-ylamino)-phenyl)-4-;
 KW (4-methyl-piperazin-1-ylmethyl)-benzamide; PCR; primer; ss.
 XX OS Homo sapiens.
 XX PN WO2003031608-A2.
 XX PD 17-APR-2003.
 XX PF 04-OCT-2002; 2002WO-EP011144.
 XX PR 05-OCT-2001; 2001US-0327389P.
 PR 12-OCT-2001; 2001US-0328740P.
 PR 11-JAN-2002; 2002US-0347351P.
 XX PA (NOVS) NOVARTIS AG.
 PA (UYBO-) UNIV BORDEAUX 2 SEGALIN VICTOR.
 PA (UYMU-) UNIV TECH MUENCHEN.
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 PA (UYHE-) UNIV HEIDELBERG.
 PA (CHRU-) CHRU LILLE.
 PA (MEDV-) MEDVET SCI PTY LTD.
 XX PI Barthe C, Branford S, Corbin A, Druker BJ, Duyster J, Hochhaus A;
 PI Hughes T, Kreil S, Leguay T, Mahon F, Marit G, Mueller M;
 PI Peschel C, Preudhomme C, Roche Lestienne C, Rudzki Z;
 XX WPI; 2003-363366/34.
 XX PT New isolated polypeptide having mutated native human Abl kinase domains,
 PT useful for screening compounds that inhibit tyrosine kinase activity and
 PT for diagnosing leukemias.
 XX PS Example 6; Page 33; 57pp; English.

CC The present invention relates to mutated human Abl kinase domains that
 CC are functional and resistant to inhibition of their tyrosine kinase
 CC activity by N-(4-methyl-3-(4-pyridin-3-yl-pyrimidin-2-ylamino)-phenyl)-4-
 CC -(4-methyl-piperazin-1-ylmethyl)-benzamide, or its salt. The mutant Abl
 CC polypeptides are useful in screening for compounds that inhibit the
 CC tyrosine kinase activity of such polypeptides. Polynucleotide sequences
 CC encoding the mutant polypeptides are useful for the production of the
 CC mutant polypeptides. The mutant polypeptides are also useful in the
 CC diagnosis of leukaemias. The present sequence represents a PCR primer
 CC used in the examples of the present invention

XX SQ Sequence 20 BP; 7 A; 1 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1554 TTCTTCCCAACCCCTC 1571
 Db 18 TTCTTCCCAACCCCTC 1

RESULT 2079
 AAD53382
 ID AAD53382 standard; DNA; 20 BP.
 XX AC AAD53382;
 XX DT 28-MAY-2003 (first entry)
 XX DE Mouse bmf DNA specific RT-PCR primer #3.
 XX KW Bcl-2 modifying factor; BMF; apoptosis; cell death; prophylaxis; cancer;
 KW autoimmune disease; cytotoxic condition; gamma-irradiation; chemotherapy;
 KW AIDS; acquired immuno deficiency syndrome; viral infection; ischaemia;
 KW myocardial infarction; cytostatic; immunosuppressive; virucide; cardiant;
 KW vasotrophic; mouse; reverse transcription; RT-PCR; primer; ss.
 XX OS Mus sp.
 XX PN WO200297094-A1.
 XX PD 05-DEC-2002.
 XX PF 30-MAY-2002; 2002WO-AU000693.
 XX PR 30-MAY-2001; 2001AU-00005351.
 XX PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 XX PI Strasser A, Puthalakath H, Villunger A, Coultas L, Beaumont J;
 PI O'reilly LA, Huang DCS;
 XX WPI; 2003-156796/15.
 XX PT Novel Bcl-2 modifying factor and polynucleotide encoding it, useful for
 PT modulating apoptosis in mammalian cells and treating cancer, autoimmune
 PT disorders, viral infections and degenerative diseases.
 XX PS Example 3; Col 90; 49pp; English.

CC The invention relates to novel Bcl-2 modifying factor (BMF) proteins and
 CC polynucleotides encoding such proteins. Sequences of the invention are
 CC useful for modulating apoptosis in a mammal in particular human and also
 CC for treating humans by modulating expression of bmf or activity of Bmf.
 CC They are useful for detecting an interactive molecule (in particular an
 CC antibody). Bmf sequences are useful as screening tools for therapeutic
 CC agents capable of modulating physiological cell death or survival and/or
 CC modulating cell cycle entry. They are also useful in screening for agents
 CC which ameliorate symptoms of diseases caused by defects in apoptosis or
 CC which specifically promote apoptosis of target cells. Increased bmf
 CC expression or Bmf activity is useful for the treatment or prophylaxis in
 CC conditions such as cancer and deletion of autoreactive lymphocytes in

CC autoimmune disease. Decreased bmf expression or Bmf activity is useful in
CC regulating inhibition or prevention of cell death or degeneration such as
CC under cytotoxic conditions during for e.g. gamma-irradiation and
CC chemotherapy or during HIV/AIDS or other viral infections, ischaemia or
CC myocardial infarction. Pharmaceutical compositions of the invention are
CC useful in therapy or prophylaxis in relation to cancer, degenerative
CC diseases, autoimmune disorders, viral infections and for germ cell
CC regulation. The present sequence is mouse bmf DNA specific RT-PCR primer.
CC This sequence is used in the exemplification of the invention
XX
SQ Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1133 AGTACCTGGAGAGATCA 1150
DB 3 ACTTCTGGAGACATCA 20
RESULT 2080
ID ABT34115 standard; DNA; 20 BP.
AC ABT34115;
XX
DT 29-MAY-2003 (first entry)
XX
DE Human pigmentation trait-related PCR primer - SEQ ID No 214.
XX
KW Human; single nucleotide polymorphism; SNP; ss; melanocortin-1 receptor;
KW genetic pigmentation trait; MC1R; agouti signaling protein; ASIP; race;
KW hair colour; eye colour; forensic tool; PCR; primer.
XX
OS Homo sapiens.
XX
PN WO200297047-A2.
XX
PD 05-DEC-2002.
XX
PF 28-MAY-2002; 2002WO-US016789.
XX
PR 25-MAY-2001; 2001US-0293560P.
PR 21-JUN-2001; 2001US-0300187P.
PR 07-AUG-2001; 2001US-0310781P.
PR 17-SEP-2001; 2001US-0323662P.
PR 26-OCT-2001; 2001US-0344418P.
PR 15-NOV-2001; 2001US-0334674P.
PR 02-JAN-2002; 2002US-0346303P.
XX
PA (DNAP-) DNAPRINT GENOMICS INC.
XX
XX Prudakis T;
XX
XX WPI; 2003-239091/23.
XX
XX Inferring genetic pigmentation trait such as hair/eye color or shade from
PT nucleic acid sample of human subject, by identifying a pigmentation-
PT related haplotype allele of a pigmentation gene in the sample.
XX
PS Example 17; Page 248; 396pp; English.
XX
SQ The invention comprises a method for inferring a genetic pigmentation
CC trait of a human. The method involves identifying a single nucleotide
CC polymorphism (SNP) in a pigmentation gene - where the pigmentation gene
CC is not melanocortin-1 receptor (MC1R) and agouti signaling protein
CC (ASIP). The method of the invention is useful for inferring a genetic
CC pigmentation trait of a human, especially for inferring the race of a
CC human subject. The method is useful for inferring a genetic pigmentation
CC trait such as hair shade or colour, or eye shade or colour of a human
CC subject. The method may be used as a forensic tool for obtaining
CC information relating to physical characteristics of a potential crime

CC victim or a perpetrator of a crime from a nucleic acid sample present at
CC a crime scene. The present PCR primer is used in the exemplification of
CC the invention
XX
SQ Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 573 GCTGTACATTCATTCGA 590
DB 18 GCTGGACAATGTCATTGA 1
RESULT 2081
ID ACD32867 standard; DNA; 20 BP.
XX
AC ACD32867;
XX
DT 02-SEP-2003 (first entry)
XX
DE Human BRCA1 (omi4) PCR primer 11C-11CF1.
XX
KW Human; ss; PCR; BRCA1 (omi4); primer; gene therapy; breast cancer; tumour;
KW protein replacement therapy; ovarian cancer.
XX
OS Homo sapiens.
XX
PN US2003027166-A1.
XX
PD 06-FEB-2003.
XX
PF 20-DEC-2001; 2001US-00022819.
XX
PR 06-MAY-1998; 98US-00074452.
XX
PA (ONCO-) ONCORMED INC.
XX
PI Allen ACP, Angelly TS, Lawrence T, Olson SJ, Rabin MB;
XX
XX WPI; 2003-492029/46.
XX
XX New BRCA1 (omi4) proteins and nucleic acids, useful in gene therapy,
PT protein replacement therapy, for treating or preventing breast and
PT ovarian cancer, and as diagnostic reagents for measuring (ab)normal
PT activity of BRCA1.
XX
PS Example 1; Page 7; 46pp; English.
XX
XX The invention relates to the BRCA1 (omi4) gene. The BRCA1 (omi4) gene is
CC useful in gene therapy. The BRCA1 (omi4) protein is useful in protein
CC replacement therapy, in the therapeutic or prophylactic treatment of
CC breast or ovarian cancer and as immunogens in generating antibodies. The
CC BRCA1 (omi4) protein, polypeptides, polynucleotides and antibodies may be
CC used as diagnostic reagents for measuring (ab)normal activity of BRCA1 at
CC the DNA, RNA or protein level, for monitoring disease progression, for
CC determining patients suited for gene and protein replacement therapy, or
CC for detecting the presence or quantifying the amount of tumour growth,
CC inhibitor following such therapy. The present sequence represents a PCR
CC primer used to amplify the the human BRCA1 (omi4) gene
XX
SQ Sequence 20 BP; 6 A; 2 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 846 TGGCTCAGACTCCCTATC 863
DB 19 TGATTGAGACTCCCTATC 2


```

RESULT 2082
ABT34180/C
ID ABT34180 standard; DNA; 20 BP.
XX
AC ABT34180;
XX
DT 12-JUN-2003 (first entry)
XX
XX Human short heterodimer partner-1 expression oligo SEQ ID No 55.
DE
DE Antiarteriosclerotic; cardiant; vasotropic; antiinfective; cytostatic;
XX antiinflammatory; inhibitor; antisense gene therapy; atherosclerosis;
XX short heterodimer partner-1; abnormal; lipid; cholesterol metabolism;
XX cardiovascular disease; infection; inflammation; tumour formation; human;
XX antisense; ds.
XX
OS Unidentified.
XX
XX WO2003012033-A2.
XX
XX 13-FEB-2003.
XX
XX 17-JUL-2002; 2002WO-US023245.
XX
XX 31-JUL-2001; 2001US-00919197.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Crooke RM, Graham MJ;
XX
XX WPI; 2003-248161/24.
XX
XX New antisense oligonucleotide targeted to a nucleic acid encoding short
XX heterodimer partner-1, useful for treating diseases involving abnormal
XX lipid or cholesterol metabolism, e.g atherosclerosis or cardiovascular
XX diseases.
XX
XX Claim 3; Page 94; 121pp; English.
XX
XX The invention relates to a novel compound of 8 - 50 nucleobases in length
XX targeted to a nucleic acid molecule encoding a short heterodimer partner-
XX 1. The novel compound specifically hybridizes with a nucleic acid
XX molecule encoding the short heterodimer partner-1, and inhibits the
XX expression of the nucleic acid molecule. The compound, and a composition
XX comprising it are useful for treating a disease or condition associated
XX with the short heterodimer partner-1, particularly a condition involving
XX abnormal lipid or cholesterol metabolism such as atherosclerosis or a
XX cardiovascular disease. They are also useful in research and diagnostics
XX for modulating the expression of short heterodimer partner-1. They can
XX also be useful prophylactically in preventing or delaying infection,
XX inflammation or tumour formation. This polynucleotide sequence represents
XX a human antisense oligo relating to the heterodimer partner-1 of the
XX invention
XX
XX Sequence 20 BP; 2 A; 10 C; 2 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1335 AGAGGAGGAGGAGGGGG 1352
XX | | | | | | | | | |
XX 19 AAAGGAGGAGGAGGGGTG 2
XX
XX Db
XX
XX RESULT 2083
XX ABT34150
XX ID ABT34150 standard; DNA; 20 BP.
XX
XX AC ABT34150;
XX
XX DT 12-JUN-2003 (first entry)
XX
XX Human short heterodimer partner-1 expression oligo SEQ ID No 55.
DE
DE Antiarteriosclerotic; cardiant; vasotropic; antiinfective; cytostatic;
XX antiinflammatory; inhibitor; antisense gene therapy; atherosclerosis;
XX short heterodimer partner-1; abnormal; lipid; cholesterol metabolism;
XX cardiovascular disease; infection; inflammation; tumour formation; human;
XX antisense; ds.
XX
OS Unidentified.
XX
XX WO2003012033-A2.
XX
XX 13-FEB-2003.
XX
XX 17-JUL-2002; 2002WO-US023245.
XX
XX 31-JUL-2001; 2001US-00919197.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Crooke RM, Graham MJ;
XX
XX WPI; 2003-248161/24.
XX
XX New antisense oligonucleotide targeted to a nucleic acid encoding short
XX heterodimer partner-1, useful for treating diseases involving abnormal
XX lipid or cholesterol metabolism, e.g atherosclerosis or cardiovascular
XX diseases.
XX
XX Claim 3; Page 94; 121pp; English.
XX
XX The invention relates to a novel compound of 8 - 50 nucleobases in length
XX targeted to a nucleic acid molecule encoding a short heterodimer partner-
XX 1. The novel compound specifically hybridizes with a nucleic acid
XX molecule encoding the short heterodimer partner-1, and inhibits the
XX expression of the nucleic acid molecule. The compound, and a composition
XX comprising it are useful for treating a disease or condition associated
XX with the short heterodimer partner-1, particularly a condition involving
XX abnormal lipid or cholesterol metabolism such as atherosclerosis or a
XX cardiovascular disease. They are also useful in research and diagnostics
XX for modulating the expression of short heterodimer partner-1. They can
XX also be useful prophylactically in preventing or delaying infection,
XX inflammation or tumour formation. This polynucleotide sequence represents
XX a human antisense oligo relating to the heterodimer partner-1 of the
XX invention
XX
XX Sequence 20 BP; 2 A; 10 C; 2 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1335 AGAGGAGGAGGAGGGGG 1352
XX | | | | | | | | | |
XX 19 AAAGGAGGAGGAGGGGTG 2
XX
XX Db
XX
XX RESULT 2084
XX ABT21302
XX ID ABT21302 standard; DNA; 20 BP.
XX
XX AC ABT21302;
XX
XX DT 16-APR-2003 (first entry)
XX
XX Multiplex group PCR primer #49.
XX
XX Racing potential; horse; grandpaternal DNA; over-represented; breeding;
XX grandmother; performance; progeny horse; PCR; primer; ss.
XX
XX Unidentified.
XX
XX

```

XX
PT An isolated polypeptide useful for screening pigs for the presence of a
PT porcine endogenous retrovirus (PERV) and providing a pig modified not to
PT express a PERV.
XX
XX Example 2; Page 24; 63pp; English.
XX
XX The present sequence is a reverse primer for the gag gene of porcine
CC endogenous retrovirus (PERV). This was used in an example from the
CC invention relating to the mapping of PERV in a non-transgenic pig. In
CC this example, DNA was extracted from porcine peripheral blood mononuclear
CC cells and used to construct cosmid and lambda libraries. The presence of
CC intact viral genes in cosmid and lambda isolates was examined by PCR
CC using primers designed to conserved sequences at the start and end of the
CC pol, gag and env open reading frames. The invention provides a method of
CC identifying PERV using polynucleotide flanking sequences (see ABZ57861-
CC 68). It also provides a pig modified not to express a selected PERV,
CC obtained by knock-out or inactivation of the PERV by homologous
CC recombination. The organs, tissues and cells of the modified pig are
CC suitable for use in xenotransplantation
XX
XX Sequence 20 BP; 5 A; 9 C; 1 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1999 TAATCTGAGGTGGAGG 2016
DB 19 TAACTTGAAGGTGGAGG 2
RESULT 2086
ABZ57870/c
ID ACC59201 standard; DNA; 20 BP.
XX
XX ACC59201;
XX 17-JUL-2003 (first entry)
XX Human hnRNP A2/B1 PCR primer #1.
XX Human; tumour; epidermal growth factor; EGF; EGFr; her-2/neu; c-myc;
KW epidermal growth factor receptor; hnRNP A2/B1; cancer; PCR; primer;
KW heterologous nuclear ribonucleoprotein A2/B1; anticancer therapy;
KW proliferative disorder; ss.
XX
XX Homo sapiens.
OS
PN WO2003028531-A2.
XX
XX 10-APR-2003.
PD
XX 26-SEP-2002; 2002WO-US030485.
XX
XX 28-SEP-2001; 2001US-00966515.
PR
XX (ONCO-) ONCOMEDX INC.
PA
XX Kopreski M;
PI
XX WPI; 2003-381575/36.
DR
XX Detecting tumor-derived or -associated RNA in the bodily fluids, useful
PT for diagnosing cancer or monitoring response to anticancer therapy, by
PT detecting e.g. epidermal growth factor RNA, EGR receptor or her-2/neu
PT RNA.
XX
XX Disclosure; Page 16; 46pp; English.
XX
XX The invention relates to a novel method for detecting tumour-derived or
CC tumour-associated RNA in the plasma or serum fraction of blood, or in a
CC body fluid, from a human or animal. The method comprises detecting an

PN WO200292851-A2.
XX
PD 21-NOV-2002.
XX
XX 15-MAY-2002; 2002WO-GB002273.
XX
XX 15-MAY-2001; 2001GB-00011886.
XX
XX (ANIM-) ANIMAL HEALTH TRUST.
PA (BRHO-) BRITISH HORSE RACING BOARD.
XX
XX Binns MM, Swinburne JB;
PI
XX WPI; 2003-129314/12.
DR
XX Determining the racing potential of a horse comprises measuring whether
PT grandpaternal or grandmaternal DNA from the selected grandmother DNA is
PT over-represented in the genome of the horse.
XX
XX Example 2; Page 23; 49pp; English.
XX
XX The invention relates to a novel method for determining racing potential
CC of a horse. The method comprises measuring: whether grandpaternal DNA is
CC over-represented in the genome of the horse; or in the case where one of
CC the grandmothers was selected for breeding on the basis of racing
CC performance, whether grandmaternal DNA from the selected grandmother is
CC over-represented in the genome of the horse which indicates that the
CC horse has good racing potential. The method of the invention is useful
CC for determining the racing potential of a horse or for obtaining a
CC progeny horse with good racing potential. This polynucleotide sequence
CC represents a PCR primer used in the detection method of over-
CC representation of DNA from male grandparents of the invention
XX
XX Sequence 20 BP; 10 A; 1 C; 8 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1401 GGATGAAAAGAGGAAGA 1418
DB 1 GGATGAAAAGAGGAAGA 18
RESULT 2085
ABZ57870/c
ID ABZ57870 standard; DNA; 20 BP.
XX
XX ABZ57870;
AC
XX
XX 14-APR-2003 (first entry)
DT
XX Porcine endogenous retrovirus gag gene reverse PCR primer.
DE
XX PERV; knockout animal; pig; xenotransplantation; organ transplant;
KW gag gene; PCR; primer; ss.
KW
XX Porcine endogenous retrovirus.
OS
XX WO2003002746-A2.
PN
XX
XX 09-JAN-2003.
PD
XX 28-JUN-2002; 2002WO-EP007159.
PF
XX 29-JUN-2001; 2001US-0302133P.
PR
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX Herring CT, Langford G, Quinn G, Scobie L;
PI
XX WPI; 2003-210279/20.
DR

CC amplified product produced from the tumour-derived or tumour-associated
 CC RNA or cDNA. The RNA is epidermal growth factor (EGF) RNA, epidermal
 CC growth factor receptor (EGFR) RNA, her-2/neu RNA, c-myc RNA, and/or
 CC heterologous nuclear ribonucleoprotein A2/B1 (hnRNP A2/B1) RNA. The
 CC method is useful for screening an animal, particularly a human, for
 CC malignancy or pre-malignancy associated with EGF RNA, EGFR RNA, her-2/neu
 CC RNA, c-myc RNA or hnRNP A2/B1 RNA. The method is useful for detecting or
 CC diagnosing a disease associated with the expression of these RNAs. The
 CC method is also useful for selecting an animal or human with cancer for a
 CC cancer-directed therapy, or for monitoring response to anticancer
 CC therapy. The method is especially useful for detecting, diagnosing,
 CC monitoring, or evaluating proliferative disorders, e.g. premalignancy,
 CC early cancer, non-invasive cancer, carcinoma-in-situ, invasive cancer,
 CC metastatic cancer, advanced cancer or benign neoplasm. The present
 CC sequence is used in the exemplification of the invention
 XX
 SQ Sequence 20 BP; 1 A; 5 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1252 GACGACGACGACCTGAC 1269
 ||||| ||||| ||||| |||||
 Db 20 GACGACGACGACCGAC 3

RESULT 2087
 AAL61455
 ID AAL61455 standard; DNA; 20 BP.
 XX
 AC AAL61455;
 XX
 DT 22-SEP-2003 (first entry)
 XX
 DE Human ATP3 antisense oligonucleotide, ISIS 185438.
 XX
 KW Human; activating transcription factor 3; ATF3; ischaemia; diabetes;
 KW liver regeneration factor-1; LRF-1; antisense therapy; CRG-5; LRG-21;
 KW TI-241; phosphorothioate backbone; antisense; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.

Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidines are 5-
 FT methylcytidines"
 FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'methoxyethyl nucleotides"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'methoxyethyl nucleotides"

WO2003040161-A2.

PD 15-MAY-2003.

PF 04-NOV-2002; 2002WO-US035331.

PR 08-NOV-2001; 2001US-00010002.

PA (ISIS-) ISIS PHARM INC.

PI Baker BF, Dobie K;

DR WPI; 2003-441517/41.

XX

PT New antisense oligonucleotide compounds, useful for diagnosing,
 PT preventing and/or treating conditions with aberrant activity of the
 PT activating transcription factor 3, such as ischemia and diabetes.
 XX

PS Example 15; Page 77; 126pp; English.

XX The invention relates to antisense compounds, compositions and methods
 CC for modulating the expression for activating transcription factor 3
 CC (ATF3). ATF3 is also known as liver regeneration factor-1 (LRF-1), CRG-5,
 CC LRG-21, and TI-241. The invention is useful for the diagnosis, prevention
 CC and/or treatment of diseases or conditions associated with aberrant
 CC expression or activity of ATF3, such as ischaemia and diabetes. The
 CC antisense compound is useful in antisense therapy. The present sequence
 CC is an antisense oligonucleotide targetted to human ATF3 DNA. This
 CC sequence is used to illustrate the method of the invention
 XX

SQ Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1967 GAAACACTGCCTGCCCTC 1984
 ||||| ||||| ||||| |||||
 Db 2 GAATCACTGCAGGCCCTC 19

RESULT 2088
 ABT13658/c
 ID ABT13658 standard; DNA; 20 BP.
 XX
 AC ABT13658;
 XX
 DT 07-FEB-2003 (first entry)
 XX
 DE Liver regeneration-related gene panel PCR primer #180.
 XX
 KW PCR; primer; ss; liver regeneration; gene panel; expression profile;
 KW drug screening; drug development; hepatitis; liver transplantation.
 XX

OS Unidentified.

XX WO200277222-A1.

PN 03-OCT-2002.

PD 13-MAR-2002; 2002WO-JP002372.

PR 13-MAR-2001; 2001JP-00070940.

XX (AJIN) AJINOMOTO CO INC.

XX Yokoya F, Okutsu T, Mori M, Takahara Y, Fukuda H, Aburatani H;
 PI Sonaka I;
 XX

DR WPI; 2003-018922/01.

XX Gene panel participating in liver regeneration, applicable in providing
 PT expression data, diagnosis and development of drugs for promoting liver
 PT regeneration e.g. after transplantation or removal of liver during
 PT cancer.
 XX

PS Example 2; Page 95; 101pp; Japanese.

XX The invention comprises a gene panel constructed from the expression
 CC profile of known genes which show a change in expression level between
 CC normal liver cells and liver cells under regeneration. The gene panel is
 CC useful for providing expression data and screening/development of drugs
 CC for liver regeneration (e.g. when treating hepatitis, after
 CC transplantation or removal of the liver during cancer or hepatitis
 CC therapy). The present DNA sequence represents a PCR primer used in the
 CC invention
 XX

SQ Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1528 TCTGGCTTCCTGCTGACT 1545
Db 20 TCTGGCTTCCTGCTGACT 3

RESULT 2089
ABX93228
ID AEX93228 standard; DNA; 20 BP.
AC AEX93228;
XX
XX 30-MAY-2003 (first entry)
DT
DE RT-PCR primer H3F used to isolate cDNA encoding cotton histone (his3).
DE
KW Cotton; (+)-delta-cadinene 8-hydroxylase; CYP706B1; cytochrome P450;
KW biosynthesis of gossypol; sesquiterpene; cotton seed; cotton cultivate;
KW sesquiterpenoid; livestock feed; reverse transcriptase-PCR; RT-PCR;
KW primer; histone; his3; ss.
XX
OS Gossypium arboreum.
XX
XX US2002187538-A1.
XX
XX 12-DEC-2002.
XX
XX 07-FEB-2002; 2002US-00067534.
XX
XX 07-FEB-2001; 2001US-0267160P.
XX
XX (ESSE/) ESSENBERG M K.
XX
XX (CHEN/) CHEN X.
XX
XX (LIJOP/) LIU P.
XX
XX (WANG/) WANG Y.
XX
XX Essenberg MK, Chen X, Luo P, Wang Y;
XX
XX WPI; 2003-341036/32.
XX
XX Novel cotton (+)-gamma-cadinene 8-hydroxylase polypeptide designated as
XX CYP706B1, useful as target for suppression of biosynthesis of gossypol
XX formation in cotton seeds.
XX
XX Example 1; Page 5; 26pp; English.
XX
XX The present invention relates to the isolation of cotton (+)-delta-
XX cadinene 8-hydroxylase (designated as CYP706B1), and the polynucleotide
XX sequence encoding it. The CYP706B1 protein is a cytochrome P450 which is
XX useful as a target for suppression of the biosynthesis of gossypol and
XX related sesquiterpenes in cotton seeds through genetic engineering
XX techniques. The polynucleotide sequence encoding CYP706B1 is useful in
XX suppression of the biosynthesis of gossypol and related sesquiterpenes in
XX cotton seeds, where the polynucleotide sequence is expressed in antisense
XX or sense orientation as a perfect match to the native gene whose
XX expression is sought to be suppressed. The polynucleotide sequence of the
XX invention is useful for producing cotton cultivars which avoid the
XX presence of sesquiterpenoids in their seeds, and for producing cotton
XX seed product which is suitable for use as a feed for both livestock and
XX humans. The present sequence represents a reverse transcriptase (RT)-PCR
XX primer used to isolate cDNA encoding cotton histone (his3) in the
XX examples of the present invention

SQ Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 153 GAAGCCTCACCAGATCCG 170
Db 1 GAAGCCTCACCAGATCCG 18

RESULT 2090
ACC45666/c
ID ACC45666 standard; DNA; 20 BP.
XX
XX ACC45666;
XX
XX 02-JUN-2003 (first entry)
DT
DE Human HBM STS marker forward primer #123.
DE
XX
KW Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;
KW gene therapy; bone density modulation; bone strength; trabecular number;
KW bone size; bone tissue connectivity; bone disease; osteoporosis; PCR;
KW osteomalacia; rickets; Paget's disease; neoplasm of the bone; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200292764-A2.
XX
XX 21-NOV-2002.
XX
XX 13-MAY-2002; 2002WO-US014876.
XX
XX 11-MAY-2001; 2001US-0290071P.
XX
XX 17-MAY-2001; 2001US-0291311P.
XX
XX 01-FEB-2002; 2002US-0353058P.
XX
XX 04-MAR-2002; 2002US-0361293P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX (AMHP) WYETH.
XX
XX Babi J P, Bex FJ, Yaworsky PJ, Bodine PV;
XX
XX WPI; 2003-129278/12.
XX
XX New transgenic animals (e.g. mice), useful as models for studying bone
XX density modulation, developing drugs for treating or preventing bone
XX diseases (e.g. osteoporosis), or diagnosing diseases characterized by
XX reduced bone density.
XX
XX Disclosure; Page 56; 603pp; English.
XX
XX The invention relates to novel transgenic animals expressing the high
XX bone mass (HBM) gene, expressing the corresponding wild type HBM gene,
XX comprising an alteration of the gene encoding LRP5 or LRP6, or expressing
XX an LRP5 that is modulated by an altered gene control sequence introduced
XX by homologous or non-homologous recombination. The transgenic animals are
XX for the study of bone density modulation or bone mass modulation. The
XX invention has osteopathic and cytostatic activity. The polynucleotides of
XX the invention may have a use in gene therapy. The transgenic animals and
XX nucleic acids are for the study of bone density modulation, where the
XX bone mass is modulated relative to non-transgenic animals of the same
XX species in more than one parameter selected from bone density, bone
XX strength, trabecular number, bone size, or bone tissue connectivity. The
XX transgenic animals, nucleic acids and methods are useful for identifying
XX molecules involved in bone development, and for developing pharmaceutical
XX compositions, which may be employed for treating or preventing bone
XX diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or
XX neoplasms of the bone. The transgenic animals and nucleic acids are also
XX useful in methods for diagnosing diseases involved in bone development, is
XX or characterised by reduced bone density or mass. The present sequence is
XX used in the exemplification of the invention

SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;

Matches	15;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
QY	1819	GCTTTGAAAGGTGCCCT	1836						
Db	18	GCTGAGGAAGGTGCTCT	1						
RESULT 2091									
ACC45427									
ID	ACC45427	standard; DNA; 20 BP.							
XX	AC	ACC45427;							
XX	AC	ACC45427;							
DT	02-JUN-2003	(first entry)							
XX	XX	Human HBM STS marker reverse primer #3.							
DE	XX	Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;							
XX	XX	gene therapy; bone density modulation; bone strength; trabecular number;							
KW	KW	bone size; bone tissue connectivity; bone disease; osteoporosis; PCR;							
KW	KW	osteomalacia; rickets; Paget's disease; neoplasm of the bone; primer; ss.							
XX	XX	Homo sapiens.							
XX	XX	WO200292764-A2.							
PN	XX	21-NOV-2002.							
XX	XX	13-MAY-2002; 2002WO-US014876.							
XX	XX	11-MAY-2001; 2001US-0290071P.							
PR	PR	17-MAY-2001; 2001US-0291311P.							
PR	PR	01-FEB-2002; 2002US-0353058P.							
PR	PR	04-MAR-2002; 2002US-0361293P.							
XX	XX	(GENO-) GENOME THERAPEUTICS CORP.							
PA	PA	(AMHP) WYETH.							
XX	XX	Babij P, Bex FJ, Yaworsky PJ, Bodine PV;							
PI	PI	WPI; 2003-129278/12.							
XX	XX	New transgenic animals (e.g. mice), useful as models for studying bone							
XX	XX	density modulation, developing drugs for treating or preventing bone							
PT	PT	diseases (e.g. osteoporosis), or diagnosing diseases characterized by							
PT	PT	reduced bone density.							
XX	XX	Disclosure; Page 54; 603pp; English.							
PS	PS	The invention relates to novel transgenic animals expressing the high							
XX	XX	bone mass (HBM) gene, expressing the corresponding wild type HBM gene,							
CC	CC	comprising an alteration of the gene encoding LRP5 or LRP6, or expressing							
CC	CC	an LRP5 that is modulated by an altered gene control sequence introduced							
CC	CC	by homologous or non-homologous recombination. The transgenic animals are							
CC	CC	for the study of bone density modulation or bone mass modulation. The							
CC	CC	invention has osteopathic and cytostatic activity. The polynucleotides of							
CC	CC	the invention may have a use in gene therapy. The transgenic animals and							
CC	CC	nucleic acids are for the study of bone density modulation, where the							
CC	CC	bone mass is modulated relative to non-transgenic animals of the same							
CC	CC	species in more than one parameter selected from bone density, bone							
CC	CC	strength, trabecular number, bone size, or bone tissue connectivity. The							
CC	CC	transgenic animals, nucleic acids and methods are useful for identifying							
CC	CC	molecules involved in bone development, and for developing pharmaceutical							
CC	CC	compositions, which may be employed for treating or preventing bone							
CC	CC	diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or							
CC	CC	neoplasms of the bone. The transgenic animals and nucleic acids are also							
CC	CC	useful in methods for diagnosing diseases involved in bone development,							
CC	CC	or characterised by reduced bone density or mass. The present sequence is							
CC	CC	used in the exemplification of the invention							
XX	XX	Sequence 20 BP; 2 A; 3 C; 7 G; 8 T; 0 U; 0 Other;							
Query Match		0.6%;	Score 13.2;	DB 1;	Length 20;				

Best Local Similarity	83.3%;	Pred. No. 1.3e+03;							
Matches	15;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
QY	2002	TTCTGCAGGTGGAGGTTG	2019						
Db	1	TTCTGCAGGTGGAGGTTG	18						
RESULT 2092									
ACC45954									
ID	ACC45954	standard; DNA; 20 BP.							
XX	XX	ACC45954;							
XX	XX	ACC45954;							
DT	02-JUN-2003	(first entry)							
XX	XX	Human HBM STS marker forward primer #267.							
DE	XX	Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;							
XX	XX	gene therapy; bone density modulation; bone strength; trabecular number;							
KW	KW	bone size; bone tissue connectivity; bone disease; osteoporosis; PCR;							
KW	KW	osteomalacia; rickets; Paget's disease; neoplasm of the bone; primer; ss.							
XX	XX	Homo sapiens.							
XX	XX	WO200292764-A2.							
PN	XX	21-NOV-2002.							
XX	XX	13-MAY-2002; 2002WO-US014876.							
XX	XX	11-MAY-2001; 2001US-0290071P.							
PR	PR	17-MAY-2001; 2001US-0291311P.							
PR	PR	01-FEB-2002; 2002US-0353058P.							
PR	PR	04-MAR-2002; 2002US-0361293P.							
XX	XX	(GENO-) GENOME THERAPEUTICS CORP.							
PA	PA	(AMHP) WYETH.							
XX	XX	Babij P, Bex FJ, Yaworsky PJ, Bodine PV;							
PI	PI	WPI; 2003-129278/12.							
XX	XX	New transgenic animals (e.g. mice), useful as models for studying bone							
XX	XX	density modulation, developing drugs for treating or preventing bone							
PT	PT	diseases (e.g. osteoporosis), or diagnosing diseases characterized by							
PT	PT	reduced bone density.							
XX	XX	Disclosure; Page 58; 603pp; English.							
PS	PS	The invention relates to novel transgenic animals expressing the high							
XX	XX	bone mass (HBM) gene, expressing the corresponding wild type HBM gene,							
CC	CC	comprising an alteration of the gene encoding LRP5 or LRP6, or expressing							
CC	CC	an LRP5 that is modulated by an altered gene control sequence introduced							
CC	CC	by homologous or non-homologous recombination. The transgenic animals are							
CC	CC	for the study of bone density modulation or bone mass modulation. The							
CC	CC	invention has osteopathic and cytostatic activity. The polynucleotides of							
CC	CC	the invention may have a use in gene therapy. The transgenic animals and							
CC	CC	nucleic acids are for the study of bone density modulation, where the							
CC	CC	bone mass is modulated relative to non-transgenic animals of the same							
CC	CC	species in more than one parameter selected from bone density, bone							
CC	CC	strength, trabecular number, bone size, or bone tissue connectivity. The							
CC	CC	transgenic animals, nucleic acids and methods are useful for identifying							
CC	CC	molecules involved in bone development, and for developing pharmaceutical							
CC	CC	compositions, which may be employed for treating or preventing bone							
CC	CC	diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or							
CC	CC	neoplasms of the bone. The transgenic animals and nucleic acids are also							
CC	CC	useful in methods for diagnosing diseases involved in bone development,							
CC	CC	or characterised by reduced bone density or mass. The present sequence is							
CC	CC	used in the exemplification of the invention							
XX	XX	Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other;							

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 35 ACTGACGGTAGGACGGG 52
DB 3 AGTGACACTAGGACGGG 20

RESULT 2093
ACC73321/c
XX ID ACC73321 standard; DNA; 20 BP.
XX AC ACC73321;
XX DT 15-JUL-2003 (first entry)
XX DE Mycobacterium vaccae specific probe VAC-01.
XX KW Microarray; probe; Mycobacterium; antibiotic-resistance; genotyping; ss.
XX OS Mycobacterium vaccae.
XX PN WO2003031654-A1.
XX PD 17-APR-2003.
XX PF 09-OCT-2002; 2002WO-KR001895.
XX PR 09-OCT-2001; 2001KR-00062125.
XX PA (SUHI-) SJ HIGHTECH CO LTD.
XX PA (KIMC/) KIM C.
XX PA (PARK/) PARK H.
XX PI Kim C, Park H, Jang H, Song E;
XX DR WPI; 2003-403109/38.
XX PT Microarray for simultaneously genotyping Mycobacteria species,
XX PT differentiating Mycobacterium tuberculosis strains and detecting
XX PT antibiotic-resistant strains, comprises specific probes on a support.
XX PS Claim 12; Page 52; 76pp; English.
XX CC The invention relates to a microarray comprising a support, a first probe
XX CC for genotyping Mycobacterium species, second probe for differentiating
XX CC Mycobacterium tuberculosis strains, and a third probe for detecting
XX CC antibiotic-resistant strains, where the probes are immobilized on the
XX CC support. This sequence represents an example of the first probe used for
XX CC genotyping Mycobacterium species. The array is useful for simultaneously
XX CC genotyping Mycobacterium species, differentiating M. tuberculosis strains
XX CC and detecting antibiotic-resistant strains
XX SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 140 AAGGCCACCAATGAAGC 157
DB 19 AAGGCCATCCACGAATC 2

RESULT 2094
ABS56187/c
XX ID ABS56187 standard; DNA; 20 BP.
XX AC ABS56187;
XX DT 30-JAN-2003 (first entry)
XX

PCR primer #1 for PKR DNA.
XX Effectiveness of interferon treatment; hepatitis C patient;
KW JAK-combined protein; C1S3; hepatocyte sample; hepatotropic;
KW antiinflammatory; virucide; JAK binding protein; PCR; primer; PKR; ss.
XX Unidentified.
XX PN JP2002125683-A.
XX PD 08-MAY-2002.
XX PF 27-OCT-2000; 2000JP-00329615.
XX PR 27-OCT-2000; 2000JP-00329615.
XX PA (TOKR-) ZH TOKYO RINSHO IGAKU SOGO KENKYUSHO.
XX PA (YABA/) YABASHI H.
XX PA (CHUS) CHUGAI PHARM CO LTD.
XX PA (SRLS-) SRL KK.
XX DR WPI; 2003-049086/05.
XX PT Estimation of effectiveness of interferon.
XX PS Example 1; Page 7; 17pp; Japanese.
XX CC The present invention relates to a method for estimating the
XX CC effectiveness of interferon treatment. The method comprises administering
XX CC interferon to a hepatitis C patient in which the expression amount of at
XX CC least one of the JAK-combined protein gene or the C1S3 gene in the
XX CC hepatocyte sample is measured. The method employs primers and probes
XX CC which are disclosed in the specification. The method is useful for
XX CC estimating the effectiveness of interferon treatment in a hepatitis C
XX CC patient. The present sequence represents a PCR primer used in the
XX CC examples of the present invention
XX SQ Sequence 20 BP; 0 A; 6 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1414 AAAGACCCAGAGGAGAG 1431
DB 18 AAAGAACCCAGAGGACAGG 1

RESULT 2095
AAD49371
XX ID AAD49371 standard; DNA; 20 BP.
XX AC AAD49371;
XX DT 07-MAR-2003 (first entry)
XX DE Mouse phospholipid scramblase I antisense oligo, ISIS #120581.
XX KW Mouse; antisense; phospholipid scramblase I; immune disorder; cancer;
XX KW inflammation; hyperproliferative; antisense therapy; phosphorothioate;
XX KW ss.
XX OS Mus musculus.
XX OS Synthetic.
XX FT Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone"
XX FT modified_base 1..5
XX FT /*tag= b
XX FT /mod_base= OTHER

```

FT modified_base /note= "2'methoxyethyl nucleotides"
FT 5
FT FT /*tag= d
FT FT /mod_base= m5c
FT modified_base 16. 20
FT FT /*tag= c
FT FT /mod_base= OTHER
FT FT /note= "2'methoxyethyl nucleotides"
FT XX
FT XX W0200281495-A1.
FT XX
FT XX 17-OCT-2002.
FT PD
FT XX
FT XX 02-APR-2002; 2002WO-US010529.
FT PF
FT XX 05-APR-2001; 2001US-00828344.
FT PR
FT XX (ISIS-) ISIS PHARM INC.
FT PA
FT XX Bennett CF, Wyatt JR;
FT PI
FT XX WPI; 2003-058495/05.
FT DR
FT XX
FT XX Novel antisense compounds targeted to nucleic acids encoding phospholipid
FT PT scramblase I, for modulating gene expression and treating inflammation,
FT PT immune disorders and hyperproliferative conditions e.g. cancer.
FT XX
FT XX Claim 3; Page 80; 131pp; English.
FT CC
FT CC The invention relates to an antisense compound targetted to a nucleic
FT CC acid molecule encoding phospholipid scramblase I and which specifically
FT CC hybridises with and inhibits the expression of phospholipid scramblase I,
FT CC or which hybridises with at least an 8-nucleobase portion of an active
FT CC site on a nucleic acid molecule encoding phospholipid scramblase I. The
FT CC invention is useful for inhibiting the expression of human phospholipid
FT CC scramblase I in cells or tissues and for treating an animal having a
FT CC disease or condition associated with phospholipid scramblase I, such as
FT CC inflammation, an immune disorder and a hyperproliferative condition, e.g.
FT CC cancer. The invention is useful for diagnostics, therapeutics and as
FT CC research reagent. The present sequence is mouse phospholipid scramblase I
FT CC antisense oligonucleotide
FT XX
FT XX Sequence 20 BP; 13 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
FT XX
FT XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
FT XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
FT XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
FT XX
FT QY 1395 AACAGAGGATGAAAGA 1412
FT Db ||||| ||||| |||||
FT 3 AACAAAGATGAAAGATA 20
FT
FT RESULT 2096
FT ABX75012
FT ID ABX75012 standard; DNA; 20 BP.
FT XX
FT AC ABX75012;
FT XX
FT DT 25-MAR-2003 (first entry)
FT XX
FT DE Human gene 216 polymorphism detection PCR primer #69.
FT XX
FT KW Human; mouse; ss; primer; gene 216; antiasthmatic; antiinflammatory;
FT KW anorectic; chromosome 20p13-p12; single nucleotide polymorphism; SNP;
FT KW gene therapy; respiratory disease; asthma; obesity; PCR;
FT KW bronchial hyper-responsiveness; chronic obstructive pulmonary disease;
FT KW adult respiratory distress syndrome; inflammatory bowel syndrome.
FT XX
FT OS Homo sapiens.
FT XX
FT PN W0200283077-A2.
FT XX

PD 24-OCT-2002.
XX
XX 15-APR-2002; 2002WO-US012063.
XX
XX 13-APR-2001; 2001US-00834597.
PR 13-APR-2001; 2001WO-US012245.
XX
XX (SCHE ) SCHERING CORP.
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Keith T, Little RD, Van Eerdewegh P, Dupuis J, Del Mastro RG;
PI Simon J, Allen K, Pandit S;
PI WPI; 2003-092960/08.
XX
XX New isolated gene 216 nucleic acids, useful for diagnosing, preventing or
FT treating a disorder, such as asthma, bronchial hyper-responsiveness,
FT chronic obstructive pulmonary disease, obesity or inflammatory bowel
FT syndrome.
FT XX
XX Example 10; Page 155; 650pp; English.
XX
XX This invention relates to a novel isolated nucleic acid, Gene 216,
CC identified from human chromosome 20p13-p12. The invention also discloses
CC regions of the 216 gene that contain single nucleotide polymorphisms
CC (SNP's) which may be used as markers for disease susceptibility or
CC severity. The nucleotides of the invention may have antiasthmatic,
CC antiinflammatory or anorectic activities and may be used in gene therapy.
CC The nucleic acids, antibodies or its fragments are useful for diagnosing,
CC preventing or treating a disorder, such as respiratory diseases (e.g.
CC asthma, bronchial hyper-responsiveness, chronic obstructive pulmonary
CC disease or adult respiratory distress syndrome), obesity, or inflammatory
CC bowel syndrome. The nucleic acids are also useful for identifying
CC increased susceptibility of a subject to the disorders mentioned. The
CC nucleic acids can also be used as primers and templates for the
CC recombinant production of disorder-associated peptides or polypeptides,
CC for chromosome and gene mapping, or for tissue distribution studies. The
CC present sequence represents a gene 216 specific PCR primer used in the
CC scope of the invention
XX
XX Sequence 20 BP; 1 A; 8 C; 1 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1545 TCCCTCACGTTTCTTCCC 1562
XX ||||| ||||| |||||
XX 2 TCTTCTCTTCTTCCC 19
XX
XX RESULT 2097
XX ABX56416
XX ID ABX56416 standard; DNA; 20 BP.
XX
XX AC ABX56416;
XX
XX DT 19-FEB-2003 (first entry)
XX
XX DE Human NOV24a PCR primer SEQ ID 202.
XX
XX NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
XX metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
XX antilipemic; cyostatic; immunomodulatory; gene therapy; dyslipidaemia;
XX cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
XX anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
XX Parkinson's disease; haematopoietic disorder; metabolic disturbance;
XX metabolic syndrome X; wasting disease; PCR; primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN W0200281625-A2.
XX

```

PD 17-OCT-2002.

03-APR-2002; 2002WO-US010366.

PR 10-APR-2001; 2001US-0282930P.
PR 12-APR-2001; 2001US-0283444P.
PR 10-APR-2001; 2001US-0283445P.

PR 12-APR-2001; 2001US-0283512P.

PR 13-APR-2001; 2001US-0283678P.

PR 17-APR-2001; 2001US-0284234P.

PR 20-APR-2001; 2001US-0285381P.

PR 25-APR-2001; 2001US-0286292P.
PR 07-JUN-2001; 2001US-0296592P.
PR 26-JUN-2001; 2001US-030083P.
PR 08-AUG-2001; 2001US-031103P.
PR 13-AUG-2001; 2001US-0311973P.
PR 16-AUG-2001; 2001US-0312901P.
PR 14-SEP-2001; 2001US-0322283P.

PR 31-DEC-2001; 2001US-0345734P.

PR 04-FEB-2002; 2002US-0354391P.

XX

[illegible]

PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;

PT Malvankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;

PT Feynman UA, Cacciatore D, Macosko S, Mazur A:
PT Mazur A:

WPT: 2003-046862/04

XX
PT
New isolated NOVX polypeptide useful for treating cardiomyopathy,

atherosclerosis, metabolic disorders, diabetes, obesity, and other disease neurodegenerative disorders. Alzheimer's disease and

PT cancer.

PS Example C; page 372; 425pp; English.

This invention describes novel polypeptides, termed NOVX which have

CC neuroprotective, antiparkinsonian, antilipaemic, cytotstatic, hootropic, CC

CC antibodies generated from it are useful in the manufacture of a

cc selected from a pathology associated with the NOVX polypeptide. Fragments

cc to map the location of NOVX genes on a chromosome, to identify

restriction fragment length polymorphism (RFLP), and are useful to

can be used in gene therapy and for treating cardiomyopathy, metabolic

CC disorders, diabetes, autoimmune disorders, Alzheimer's disease, Parkinson's
 CC anorexia, neurodegenerative disorders, haematopoietic disorders, and various
 CC disease, immune disorders, metabolic disturbances associated with obesity, metabolic
 CC dyslipidaemias, metabolic disorders associated with chronic diseases and
 CC syndrome X and wasting disorders associated with chronic diseases and
 CC various cancers. ABX56307-ABX56465 represent PCR primers and probes used
 CC for the study of the novel polynucleotide

CC represented in ABX56261-ABX56306

SQ Sequence 20 BP; 3 A; 8 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;

PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
 XX cancer.
 XX
 PS Example C; Page 372; 425pp; English.
 XX
 CC This invention describes novel polypeptides, termed NOVX which have
 CC anti-diabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
 CC neuroprotective, antiparkinsonian, antilipase, cytotonic, nootropic,
 CC cardiant and immunomodulatory activity. The polypeptide and any
 CC antibodies generated from it are useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease
 CC selected from a pathology associated with the NOVX polypeptide. Fragments
 CC and portions of the polynucleotides encoding NOVX polypeptides are useful
 CC to map the location of NOVX genes on a chromosome, to identify
 CC individuals from minute biological samples, as DNA markers for
 CC restriction fragment length polymorphism (RFLP), and are useful to
 CC prepare polymerase chain reaction primers. The products of the invention
 CC can be used in gene therapy and for treating cardiomyopathy, metabolic
 CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
 CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
 CC disease, immune disorders, haematopoietic disorders, and various
 CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
 CC syndrome X and wasting disorders associated with chronic diseases and
 CC various cancers. ABX56307-ABX56465 represent PCR primers and probes used
 CC in the amplification and detection of the NOVX polynucleotides
 CC represented in ABX56261-ABX56306
 XX
 SQ Sequence 20 BP; 3 A; 8 C; 2 G; 7 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1555 TTCTTCCCAACCCCTCA 1572
 |||||
 Db 2 TTCTTCCCAACCCCTCA 19
 RESULT 2099
 ACC47047/c
 ID ACC47047 standard; DNA; 20 BP.
 XX
 AC ACC47047;
 XX
 DT 05-JUN-2003 (first entry)
 XX
 DE Mouse phospholipase A2 antisense oligonucleotide SEQ ID NO:144.
 XX
 KW Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;
 KW phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;
 KW antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;
 KW psoriasis; diabetes; ss.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate backbone"
 FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
 XX
 PN WO200297133-A1.
 XX
 PD 05-DEC-2002.

XX 21-MAY-2002; 2002WO-US016135.
 XX
 PR 25-MAY-2001; 2001US-00865866.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Wyatt JR;
 XX
 DR WPI; 2003-140495/13.
 XX
 PT New compound that hybridizes with and inhibits the expression of
 PT phospholipase A2, group IIA, useful for preparing a composition for
 PT treating or preventing inflammation, cancer, psoriasis or diabetes.
 XX
 PS Example 15; Page 90; 135pp; English.
 XX
 CC The present invention describes a compound (I) comprising 8-50
 CC nucleobases which is targeted to a 5' untranslated region (UTR), coding,
 CC 3' UTR or intron region of a nucleic acid molecule encoding phospholipase
 CC A2, group IIA (synovial), where the compound specifically hybridizes with
 CC and inhibits the expression of phospholipase A2, group IIA (synovial).
 CC Also described: (1) a composition comprising the compound and a carrier
 CC or diluent; (2) a method of inhibiting the expression of phospholipase
 CC A2, group IIA in cells or tissues; and (3) a method of treating an animal
 CC having a disease or condition associated with phospholipase A2, group IIA
 CC (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and
 CC antipsoriatic activities, and can be used in vaccines and in gene
 CC therapy. The compound (I) can be used for preparing a composition for
 CC treating or preventing inflammation, cancer, psoriasis or diabetes. The
 CC present sequence represents a mouse phospholipase A2 group IIA (synovial)
 CC chimeric phosphorothioate antisense oligonucleotide, which is used in an
 CC example from the present invention
 XX
 SQ Sequence 20 BP; 3 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1262 ACCCTGACAGCGCATCT 1279
 |||||
 Db 18 ACCCGGACATGCGGCT 1
 RESULT 2100
 ABT43384
 ID ABT43384 standard; DNA; 20 BP.
 XX
 AC ABT43384;
 XX
 DT 22-SEP-2003 (first entry)
 XX
 DE Neuroblastoma-related DNA sequence #299.
 XX
 KW Neuroblastoma; prognosis; ds; oligonucleotide.
 XX
 OS Unidentified.
 XX
 PN WO2002103017-A1.
 PD 27-DEC-2002.
 XX
 PF 30-MAY-2002; 2002WO-JP005295.
 XX
 PR 31-MAY-2001; 2001JP-00163666.
 PR 24-AUG-2001; 2001JP-00255260.
 XX
 PA (CHIB-) CHIBA PREFECTURE.
 PA (HISM) HISAMITSU PHARM CO LTD.
 XX
 PI Nakagawara A;

CC a primer used to amplify the *Yersinia pestis* caf1, (F1)-capsular antigen
 CC gene to illustrate the method described in the invention
 XX
 SQ Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 524 ATGATATCGTCTTGCCCA 541
 DB 2 ATGACGTCGCTTGCTTA 19
 RESULT 2102
 ACC69083
 ID ACC69083 standard; DNA; 20 BP.
 XX
 AC ACC69083;
 XX 10-JUL-2003 (first entry)
 DT Human HER2 receptor PCR primer SEQ ID NO:12.
 DE
 DE
 XX Epidermal growth factor receptor; tyrosine kinase receptor inhibitor;
 KW epidermal growth factor receptor inhibitor; EGFR; mammary tumour;
 KW cytosstatic; PCR primer; ss.
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX EPI300146-A1.
 PN 09-APR-2003.
 PD
 XX 03-OCT-2001; 2001EP-00123700.
 PF
 XX 03-OCT-2001; 2001EP-00123700.
 PR
 XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 PA Hilberg F, Brandstetter I, Van Meel J, Bette P, Kleemann R;
 PI WPI; 2003-365180/35.
 XX Composition for treating mammary tumors associated with aberrant tyrosine
 PT kinase receptor activity in nonhuman animals, comprises one or more
 PT substances that inhibit the aberrant activity.
 XX Example 5; Page 22; 37pp; English.
 PS The present invention describes a composition (C) for treating mammary
 CC tumours associated with aberrant tyrosine kinase receptor activity in
 CC nonhuman animals. (C) comprises one or more substances that inhibit the
 CC aberrant tyrosine kinase receptor activity. (C) has cytostatic activity.
 CC (C) can be used as a tyrosine kinase receptor inhibitor, and an epidermal
 CC growth factor receptor (EGFR) inhibitor. (C) is especially useful for
 CC treating canine mammary tumours. The present sequence represents a PCR
 CC primer for human HER2 receptor, which is used in an example from the
 CC present invention for cloning the canine HER2 receptor
 XX Sequence 20 BP; 4 A; 1 C; 13 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1234 GAGGAGGTGGCGATGAG 1251
 DB 3 GAGGAGGTGGCGGTGAG 20
 RESULT 2103

DR WPI; 2003-167523/16.
 XX Nucleic acids isolated from neuroblastoma showing enhanced expression in
 PT human neuroblastoma with good prognosis, useful in clarifying good/poor
 PT prognosis of neuroblastoma and providing genetic data.
 XX
 PS Example 5; Page 25(1); 444pp; Japanese.
 XX The invention comprises DNA sequences that show enhanced expression in
 CC human neuroblastoma with good prognosis. The DNA sequences of the
 CC invention are useful in clarifying good/poor prognosis of neuroblastoma.
 CC The present DNA sequence was used in the exemplification of the invention
 XX
 SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1192 CCTGGGTCCAAATGCAG 1209
 DB 2 CCTGGGTCAAATCCAG 19
 RESULT 2101
 ABX13411
 ID ABX13411 standard; DNA; 20 BP.
 XX
 AC ABX13411;
 XX 15-MAY-2003 (first entry)
 DT
 DE
 DE
 XX *Yersinia pestis* caf1 detecting primer SEQ ID 11.
 KW Detection; amplification; hybridisation; infection; diagnosis;
 KW quantification; caf1; (F1)-capsular antigen; primer; ss.
 XX *Yersinia pestis*.
 OS
 XX DE10124342-A1.
 PN 28-NOV-2002.
 PD
 XX 18-MAY-2001; 2001DE-01024342.
 PF
 XX 18-MAY-2001; 2001DE-01024342.
 PR
 XX (BIOT-) BIOTECON DIAGNOSTICS GMBH.
 PA Kohlhaussen S, Grabowski R, Berghof K;
 PI WPI; 2003-240780/24.
 XX
 DR Amplification method for *Yersinia pestis* and *Yersinia pseudotuberculosis*,
 XX useful for their rapid detection and differentiation, also new primers
 PT and probes.
 PT
 XX Claim 9; Page 7; 18pp; German.
 PS This invention describes a novel amplification and hybridisation method
 CC for detecting and/or differentiating between *Yersinia pestis* and *Yersinia*
 CC *pseudotuberculosis*. The method comprises (a) treating a test sample with
 CC at least two nucleic acid primers (P1) that bind to a genomic region
 CC conserved between the two species; (b) amplification to generate at least
 CC one amplicon; (c) contacting amplicon(s) with at least one probe (P2)
 CC corresponding to a specific part of the amplified genome from at least
 CC one species and able to hybridise specifically to an amplicon and (d)
 CC detecting any hybrids formed. The method is used for (differentiation)
 CC diagnosis of infections by *Yersinia pestis* and *Y. pseudotuberculosis*. The
 CC method provides rapid (few hours) and reliable detection/differentiation
 CC of the two species and may include an amplification control to reduce the
 CC risk of false results. It is suitable for automation and makes possible
 CC quantification of the bacteria in a single step. This sequence represents

FT modified_base 1. .5
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl gapmer (2'-MOE wing)"
 FT modified_base 16. .20
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl gapmer (2'-MOE wing)"
 FT
 FT WO200295053-A2.
 FT
 FT 28-NOV-2002.
 FT
 FT 16-MAY-2002; 2002WO-US015684.
 FT
 FT 18-MAY-2001; 2001US-00860473.
 FT
 FT (ISIS-) ISIS PHARM INC.
 FT Bennett FC, Watt AT;
 FT
 FT WPI; 2003-120806/11.
 FT
 FT New antisense oligonucleotides targeted to nucleic acids encoding src-c,
 FT useful for diagnosing, treating or preventing diseases associated with
 FT the expression of src-c, e.g. cancer or inflammation, and in research
 FT applications.
 FT
 FT Example 15; Page 89; 137pp; English.
 FT
 FT The present invention describes a compound (I) that is 8-50 nucleobases
 FT in length targeted to a nucleic acid molecule encoding a 5'UTR, 3'UTR,
 FT coding region, intron region, exon region, stop codon, intron:exon
 FT junction, exon:exon junction, or 5' mRNA variant of src-c, and which
 FT specifically hybridizes with and inhibits the expression of src-c. (I)
 FT have cytosolic, antiinflammatory, osteopathic and antibacterial
 FT activities, and can be used in antisense therapy and in vaccines. The
 FT antisense compounds (I) can be used for modulating the expression of src-
 FT c and for treating diseases or conditions associated with expression of
 FT src-c, e.g. aberrant bone remodeling or hyperproliferative disorders,
 FT particularly cancer, such as breast cancer, pancreatic cancer, lung
 FT cancer, ovarian cancer, esophageal cancer, neuroblastoma, retinoblastoma
 FT or Kaposi's sarcoma. (I) are also useful for diagnostics, therapeutics,
 FT prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
 FT formation, as research reagents and kits, and in distinguishing between
 FT functions of various members of a biological pathway. The present
 FT sequence represents a human src-c antisense chimeric phosphorothioate
 FT oligonucleotide, which is used in an example from the present invention
 FT
 FT Sequence 20 BP; 1 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
 FT
 FT Query Match 0.6%; Score 13.2; DB 1; Length 20;
 FT Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 FT Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 64 ATGGCGCAGACGACGGC 81
 Db 18 AAGCGCGACACTCAGGGC 1
 RESULT 2106
 ID ABZ74902
 ID ABZ74902 standard; DNA; 20 BP.
 XX
 AC ABZ74902;
 XX
 DT 10-MAY-2003 (first entry)
 DE Human acyl coenzyme A cholesterol acyltransferase-1 antisense oligo #22.
 DE
 XX Human; acyl coenzyme A cholesterol acyltransferase-1; ACAT; liver;
 XX chromosome 1q25; chromosome 1; chromosome 7; cholesterol metabolism;
 XX free sterol regulation; cholesterol metabolism disorder;
 KW

KW lipid metabolism disorder; atherosclerosis; cardiovascular disease;
 KW cardiant; expression inhibition; phosphorothioate;
 XX antisense oligonucleotide; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT modified_base 1. .20
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate linkages"
 FT modified_base 1. .5
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
 FT cytosines are 5-methylcytosine"
 FT modified_base 16. .20
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
 FT cytosines are 5-methylcytosine"
 FT
 FT WO2003012144-A1.
 FT
 FT 13-FEB-2003.
 FT
 FT 17-JUL-2002; 2002WO-US022696.
 FT
 FT 01-AUG-2001; 2001US-00920394.
 FT
 FT (ISIS-) ISIS PHARM INC.
 FT Crooke RM, Graham MJ, Lemonidis KM;
 FT WPI; 2003-239532/23.
 FT
 FT New antisense oligonucleotides targeted to a nucleic acid encoding acyl
 FT coenzyme A cholesterol acyltransferase-1, useful for treating a
 FT disease/condition involving abnormal lipid or cholesterol metabolism,
 FT e.g. atherosclerosis.
 FT
 FT Claim 3; Page 91; 117pp; English.
 FT
 FT Sequences ABZ74897-ABZ74942 represent antisense oligonucleotides targeted
 FT to the human or murine acyl coenzyme A cholesterol acyltransferase-1
 FT gene, which inhibit its expression. The antisense oligonucleotides were
 FT designed to target different regions of the human or murine acyl coenzyme
 FT A cholesterol acyltransferase-1 RNA, and were analysed for their effect
 FT on acyl coenzyme A cholesterol acyltransferase-1 mRNA levels by
 FT quantitative real-time PCR. Acyl coenzyme A cholesterol acyltransferase
 FT (ACAT) enzymes catalyse the synthesis of cholesterol esters from free
 FT cholesterol and fatty acyl-CoA, and are also involved in regulating the
 FT concentration of cellular free sterols. The human acyl coenzyme A
 FT cholesterol acyltransferase-1 is the predominant ACAT isoform in the
 FT liver, and the gene encoding it is located on chromosome 1q25, although a
 FT subsequent study has indicated that one acyl coenzyme A cholesterol
 FT acyltransferase-1 mRNA is produced from genes on two different
 FT chromosomes (chromosomes 1 and 7) by a novel RNA recombination mechanism
 FT involving trans-splicing of the two discontinuous precursor mRNAs. The
 FT oligonucleotides of the invention are useful for the prevention and
 FT treatment of conditions associated with acyl coenzyme A cholesterol
 FT acyltransferase-1, such as disorders involving abnormal lipid or
 FT cholesterol metabolism, e.g., atherosclerosis or cardiovascular disease.
 FT They are also useful in research and diagnostics for modulating the
 FT expression of acyl coenzyme A cholesterol acyltransferase-1
 FT
 FT Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
 FT
 FT Query Match 0.6%; Score 13.2; DB 1; Length 20;
 FT Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 FT Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 551 TGCTAAGTATCACCAGA 568

```

Db      ||||| ||| ||| ||| ||| |||
3 TGCTGAAGATCCCGAGA 20

RESULT 2107
ABZ74929
ID ABZ74929 standard; DNA; 20 BP.
XX
AC ABZ74929;
XX
DT 10-MAY-2003 (first entry)
XX
DE Mouse acyl coenzyme A cholesterol acyltransferase-1 antisense oligo #49.
XX
KW Mouse; murine; acyl coenzyme A cholesterol acyltransferase-1; ACAT;
KW chromosome 1; cholesterol metabolism; free sterol regulation;
KW cholesterol metabolism disorder; lipid metabolism disorder;
KW atherosclerosis; cardiovascular disease; cardiac; expression inhibition;
KW phosphorothioate; antisense oligonucleotide; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /*note= "Phosphorothioate linkages"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /*note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT cytosines are 5-methylcytosine"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /*note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT cytosines are 5-methylcytosine"
FT
FT WO2003012144-A1.
PN
XX
XX 13-FEB-2003.
PD
XX
XX 17-JUL-2002; 2002WO-US022696.
PF
XX
XX 01-AUG-2001; 2001US-00920394.
PR
XX
PA (ISIS-) ISIS PHARM INC.
XX
XX Crooke RM, Graham MJ, Lemonidis KM;
XX
XX WPI; 2003-239532/23.
DR
XX
XX New antisense oligonucleotides targeted to a nucleic acid encoding acyl
XX coenzyme A cholesterol acyltransferase-1, useful for treating a
XX disease/condition involving abnormal lipid or cholesterol metabolism,
XX e.g. atherosclerosis.
XX
XX Claim 3; Page 92; 117pp; English.
PS
XX
XX Sequences ABZ74897-ABZ74942 represent antisense oligonucleotides targeted
XX to the human or murine acyl coenzyme A cholesterol acyltransferase-1
XX gene, which inhibit its expression. The antisense oligonucleotides were
XX designed to target different regions of the human or murine acyl coenzyme
XX A cholesterol acyltransferase-1 RNA, and were analysed for their effect
XX on acyl coenzyme A cholesterol acyltransferase-1 mRNA levels by
XX quantitative real-time PCR. Acyl coenzyme A cholesterol acyltransferase
XX (ACAT) enzymes catalyse the synthesis of cholesterol esters from free
XX cholesterol and fatty acyl-CoA, and are also involved in regulating the
XX concentration of cellular free sterols. The murine acyl coenzyme A
XX cholesterol acyltransferase-1 gene is located on chromosome 1. The
XX oligonucleotides of the invention are useful for the prevention and
XX treatment of conditions associated with acyl coenzyme A cholesterol
XX acyltransferase-1, such as disorders involving abnormal lipid or
CC
CC cholesterol metabolism, e.g., atherosclerosis or cardiovascular disease.
CC They are also useful in research and diagnostics for modulating the
CC expression of acyl coenzyme A cholesterol acyltransferase-1
XX
SQ Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 551 TGCTAAAGTATCACCAGA 568
Db 2 TGCTGAAGATCCCGAGA 19

RESULT 2108
ACC86764/c
ID ACC86764 standard; DNA; 20 BP.
XX
AC ACC86764;
XX
XX 04-AUG-2003 (first entry)
DT
XX
XX Human VEGFR-1 chimeric phosphorothioate oligonucleotide SEQ ID NO:59.
XX
DE Vascular endothelial growth factor receptor 1; VEGF receptor; VEGFR;
XX inhibitor; cytostatic; antirheumatic; antiarthritic; antiangiogenic;
KW antiinflammatory; antisense gene therapy; hyperproliferative disorder;
KW cancer; rheumatoid arthritis; angiogenesis; infection; inflammation;
KW tumour formation; phosphorothioate; 2'-O-methoxyethyl; 2'-MOE; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /*note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-O-methoxyethyl (2'-MOE) wings at the 5',
FT and 3' ends, which are 5 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
FT
FT WO2003022227-A2.
PN
XX
XX 20-MAR-2003.
PD
XX
XX 12-SEP-2002; 2002WO-US029148.
PF
XX
XX 13-SEP-2001; 2001US-00953318.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Bennett CF, Watt AT;
PI
XX
XX WPI; 2003-301004/29.
DR
XX
XX New antisense oligonucleotide targeted to a nucleic acid encoding
XX vascular endothelial growth factor receptor-1, useful for diagnosing or
XX involving angiogenesis.
XX
XX Claim 3; Page 83; 150pp; English.
PS
XX
XX The present invention describes a compound (C) 8-50 nucleobases in length
XX targeted to a nucleic acid molecule encoding vascular endothelial growth
XX factor receptor-1 (VEGFR-1), where the compound inhibits the expression
XX of VEGFR-1 and specifically hybridises with the nucleic acid encoding
XX VEGFR-1 or with an 8-nucleobase portion of an active site on the nucleic
XX acid molecule encoding VEGFR-1. Also described: (1) a composition
XX comprising (C) and a carrier or diluent; (2) inhibiting the expression of
XX VEGFR-1 in cells or tissues by contacting the cells or tissues with (C)
XX so that the expression of VEGFR-1 is inhibited; and (3) treating an

```

CC animal having a disease or condition associated with VEGFR-1 by
 CC administering (C) to the animal so that the expression of VEGFR-1 is
 CC inhibited. (C) has antiangiogenic, antirheumatic, antiarthritic,
 CC cytostatic and antiinflammatory activities, and can be used in antisense
 CC gene therapy. The antisense compounds are useful for modulating the
 CC expression of VEGFR-1 and for treating diseases or conditions associated
 CC with the expression of VEGFR-1, such as hyperproliferative disorders
 CC (e.g. cancer), rheumatoid arthritis, or diseases or conditions involving
 CC angiogenesis. The antisense compounds are also useful for diagnostics,
 CC therapeutics, prophylaxis, e.g. to prevent or delay infection,
 CC inflammation or tumour formation, as research reagents and kits, and in
 CC distinguishing between functions of various members of a biological
 CC pathway. The present sequence represents a human VEGFR-2 chimeric
 CC phosphorothioate antisense oligonucleotide, which is used in an example
 CC from the present invention

XX
 SQ Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1433 AAGAAGTCACGAGAGG 1450
 Db 18 AAAGAGTCACGAGAGG 1

RESULT 2109
 ACC86804
 ID ACC86804 standard; DNA; 20 BP.
 AC ACC86804;
 AC ACC86804;
 DT 04-AUG-2003 (first entry)
 DE Human VEGFR-1 chimeric phosphorothioate oligonucleotide SEQ ID NO:99.
 KW Vascular endothelial growth factor receptor 1; VEGF receptor; VEGFR;
 KW inhibitor; cytostatic; antirheumatic; antiarthritic; antiangiogenic;
 KW antiinflammatory; antisense gene therapy; hyperproliferative disorder;
 KW cancer; rheumatoid arthritis; angiogenesis; infection; inflammation;
 KW tumour formation; phosphorothioate; 2'-O-methoxyethyl; 2'-MOE; ss.
 OS Homo sapiens.
 OS Synthetic.

Key Location/Qualifiers
 modified_base 1..20
 /tag= a
 /mod_base= OTHER
 /note= "This oligonucleotide has a phosphorothioate
 backbone and 2'-O-methoxyethyl (2'-MOE) wings at the 5',
 and 3' ends, which are 5 nucleotides in length. Also all
 cytidine residues are 5-methylcytidines"

XX
 PN WO2003022227-A2.
 XX
 XX
 PD 20-MAR-2003.
 XX
 PF 12-SEP-2002; 2002WO-US029148.
 XX
 PR 13-SEP-2001; 2001US-00953318.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 XX Bennett CF, Watt AT;
 PI
 XX WPI; 2003-301004/29.
 DR
 XX New antisense oligonucleotide targeted to a nucleic acid encoding
 PT vascular endothelial growth factor receptor-1, useful for diagnosing or
 PT treating cancer, rheumatoid arthritis, or diseases or conditions
 PT involving angiogenesis.

XX Claim 3; Page 84; 150pp; English.
 XX
 CC The present invention describes a compound (C) 8-50 nucleobases in length
 CC targeted to a nucleic acid molecule encoding vascular endothelial growth
 CC factor receptor-1 (VEGFR-1), where the compound inhibits the expression
 CC of VEGFR-1 and specifically hybridises with the nucleic acid encoding
 CC VEGFR-1 or with an 8-nucleobase portion of an active site on the nucleic
 CC acid molecule encoding VEGFR-1. Also described: (1) a composition
 CC comprising (C) and a carrier or diluent; (2) inhibiting the expression of
 CC VEGFR-1 in cells or tissues by contacting the cells or tissues with (C)
 CC so that the expression of VEGFR-1 is inhibited; and (3) treating an
 CC animal having a disease or condition associated with VEGFR-1 by
 CC administering (C) to the animal so that the expression of VEGFR-1 is
 CC inhibited. (C) has antiangiogenic, antirheumatic, antiarthritic,
 CC cytostatic and antiinflammatory activities, and can be used in antisense
 CC gene therapy. The antisense compounds are useful for modulating the
 CC expression of VEGFR-1 and for treating diseases or conditions associated
 CC with the expression of VEGFR-1, such as hyperproliferative disorders
 CC (e.g. cancer), rheumatoid arthritis, or diseases or conditions involving
 CC angiogenesis. The antisense compounds are also useful for diagnostics,
 CC therapeutics, prophylaxis, e.g. to prevent or delay infection,
 CC inflammation or tumour formation, as research reagents and kits, and in
 CC distinguishing between functions of various members of a biological
 CC pathway. The present sequence represents a human VEGFR-2 chimeric
 CC phosphorothioate antisense oligonucleotide, which is used in an example
 CC from the present invention

XX
 SQ Sequence 20 BP; 5 A; 3 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1307 CCTGTGAGGAGAGTTCT 1324
 Db 1 CCGATGAGTAGAGTTCT 18

RESULT 2110
 ABT43599/c
 ID ABT43599 standard; DNA; 20 BP.
 XX
 AC ABT43599;
 XX
 XX 17-OCT-2003 (first entry)
 DT
 XX
 DE MA10 PCR primer related to the class II cytokine receptor SU2368.
 XX
 KW Class II cytokine receptor; SU2368; autoimmune; inflammatory; cytostatic;
 KW allergic disease; septicemia; tumour; immunosuppressive; antiallergic;
 KW antiinflammatory; ss; PCR; primer.
 XX
 OS Unidentified.
 XX
 PN WO2003031620-A1.
 XX
 XX
 PD 17-APR-2003.
 XX
 PF 02-OCT-2002; 2002WO-JP010280.
 XX
 PR 02-OCT-2001; 2001JP-00306851.
 PR 12-JUL-2002; 2002JP-00204385.
 XX
 XX (MOCH) MOCHIDA PHARM CO LTD.
 PA (KAZU-) KAZUDA DNA RES INST.
 XX
 XX Ohara O, Nagase T, Katou Y, Takahashi T, Ohkawa K, Shirakawa K;
 PI WPI; 2003-381719/36.
 XX
 DR Class II cytokine receptor SU2368 and regulators of its activity and
 XX expression for treatment and diagnosis of autoimmune, inflammatory and
 PT

```
PT allergic diseases and tumours.
XX
XX Example 7; Page 89; 188pp; Japanese.
XX
CC This invention relates to the class II cytokine receptor gene SJ2368 and
CC the encoded protein, derived from either a mouse or human origin.
CC Agonists or antagonists of the cytokine receptor SJ2368 can be used for
CC the treatment and diagnosis of autoimmune, inflammatory and allergic
CC diseases, as well as for treating the effects of septicemia and for
CC tumours. Accordingly, they can be described as having immunosuppressive,
CC antiinflammatory, antiallergic and/ or cytostatic activity. This
CC oligonucleotide sequence is a PCR primer related to the class II cytokine
CC receptor SJ2368 cDNA of the invention
XX
XX Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match      0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1253 ACGAAGACGACCTGACA 1270
Db      ||||| ||||| |||||
      18 ACGATGACGACGGTGACA 1

RESULT 2111
AAD47557/c
ID AAD47557 standard; DNA; 20 BP.
XX
XX AAD47557;
XX
XX 24-FEB-2003 (first entry)
XX
XX Human Artemis exon 13 amplifying PCR primer, Ex13F1.
XX
XX Human; ARTEMIS protein; V(D)J recombination; DNA repair; gene therapy;
XX severe combined immunodeficiency; SCID; cancer; exon 13; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200277026-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-IB001737.
XX
XX 22-MAR-2001; 2001WO-IB000546.
XX
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX De Villartay J, Moshous D, Fischer A;
XX
XX WPI; 2003-018886/01.
XX
XX New ARTEMIS nucleic acid coding for a protein involved in V(D)J
XX recombination and/or DNA repair, useful for treating and diagnosing
XX severe combined immunodeficiencies (SCID) or cancer.
XX
XX Example 1; Page 70; 71pp; English.
XX
XX The invention relates to an Artemis nucleic acid coding for a protein
XX involved in V(D)J recombination and/or DNA repair. Sequences of the
XX invention are useful for treating severe combined immunodeficiencies
XX (SCID) or cancer. They are also useful for diagnosing a patient,
XX including a prenatal diagnosis with SCID, a predisposition to cancer, an
XX immune deficiency or a carriage of a mutation increasing the risk of
XX progeny to have such a disease. Peptides of the invention are used for
XX preparing antibodies. The invention is useful in gene therapy. The
XX present sequence is a PCR primer used to amplify human Artemis exon 13
XX DNA
XX
XX Sequence 20 BP; 5 A; 5 C; 1 G; 9 T; 0 U; 0 Other;

PT allergic diseases and tumours.
XX
XX Example 7; Page 89; 188pp; Japanese.
XX
CC This invention relates to the class II cytokine receptor gene SJ2368 and
CC the encoded protein, derived from either a mouse or human origin.
CC Agonists or antagonists of the cytokine receptor SJ2368 can be used for
CC the treatment and diagnosis of autoimmune, inflammatory and allergic
CC diseases, as well as for treating the effects of septicemia and for
CC tumours. Accordingly, they can be described as having immunosuppressive,
CC antiinflammatory, antiallergic and/ or cytostatic activity. This
CC oligonucleotide sequence is a PCR primer related to the class II cytokine
CC receptor SJ2368 cDNA of the invention
XX
XX Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match      0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1253 ACGAAGACGACCTGACA 1270
Db      ||||| ||||| |||||
      18 ACGATGACGACGGTGACA 1

RESULT 2111
AAD47557/c
ID AAD47557 standard; DNA; 20 BP.
XX
XX AAD47557;
XX
XX 24-FEB-2003 (first entry)
XX
XX Human Artemis exon 13 amplifying PCR primer, Ex13F1.
XX
XX Human; ARTEMIS protein; V(D)J recombination; DNA repair; gene therapy;
XX severe combined immunodeficiency; SCID; cancer; exon 13; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200277026-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-IB001737.
XX
XX 22-MAR-2001; 2001WO-IB000546.
XX
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX De Villartay J, Moshous D, Fischer A;
XX
XX WPI; 2003-018886/01.
XX
XX New ARTEMIS nucleic acid coding for a protein involved in V(D)J
XX recombination and/or DNA repair, useful for treating and diagnosing
XX severe combined immunodeficiencies (SCID) or cancer.
XX
XX Example 1; Page 70; 71pp; English.
XX
XX The invention relates to an Artemis nucleic acid coding for a protein
XX involved in V(D)J recombination and/or DNA repair. Sequences of the
XX invention are useful for treating severe combined immunodeficiencies
XX (SCID) or cancer. They are also useful for diagnosing a patient,
XX including a prenatal diagnosis with SCID, a predisposition to cancer, an
XX immune deficiency or a carriage of a mutation increasing the risk of
XX progeny to have such a disease. Peptides of the invention are used for
XX preparing antibodies. The invention is useful in gene therapy. The
XX present sequence is a PCR primer used to amplify human Artemis exon 13
XX DNA
XX
XX Sequence 20 BP; 5 A; 5 C; 1 G; 9 T; 0 U; 0 Other;

Query Match      0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1217 CTGAGGACGCCATCCCTG 1234
Db      ||||| ||||| |||||
      1 CTCAGGCCGCCCTCCCTG 18

RESULT 2113
ABQ84125
ID ABQ84125 standard; DNA; 20 BP.
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XX AC ABQ84125;
XX DT 27-OCT-2003 (revised)
XX DT 18-FEB-2003 (first entry)
XX DE HIV-1 amplification and detection third PCR primer SEQ ID NO:28.
XX KW HIV-1; amplification; detection; PCR primer; ss.
XX OS Human immunodeficiency virus 1.
XX PN EPI253206-A2.
XX 30-OCT-2002.
XX 26-APR-2002; 2002EP-00009618.
XX 26-APR-2001; 2001JP-00129210.
XX (TOYJ) TOSOH CORP.
XX Ishizuka T, Yasukawa K, Ishiguro T;
XX WPI; 2003-077620/08.
XX Amplifying RNA of human immunodeficiency virus-1, by synthesizing cDNA by
XX polymerase, denuding cDNA to single-stranded DNA, forming and
XX transcribing the double-stranded DNA into RNA transcript, and
XX synthesizing cDNA.
XX Claim 6; Page 16; 24pp; English.
XX The present invention describes a method (M1) for amplifying human
XX immunodeficiency virus (HIV)-1 RNA, comprising synthesizing a cDNA by RNA
XX dependent DNA polymerase using a primer, denuding cDNA to a single-
XX stranded DNA by degrading the RNA in the resulting RNA-DNA double strand,
XX forming a double-stranded DNA having a promoter sequence transcribed into
XX RNA, transcribing a strand of double-stranded DNA into an RNA transcript,
XX and synthesizing a cDNA. Also described is a method (M2) for detecting
XX HIV-1. M1 is useful for amplifying RNA of HIV-1, and M2 is useful for
XX detecting HIV-1. Oligonucleotides (ABQ84098 to ABQ84132) from the present
XX invention can be used for the amplification and detection of HIV-1 RNA in
XX a sample. (Updated on 27-OCT-2003 to standardise OS field)
XX Sequence 20 BP; 2 A; 6 C; 0 G; 12 T; 0 U; 0 Other;
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1577 TTATATTTTCATTTCCTC 1594
XX 1 TTATATTTTCATTTCCTC 18
XX
XX RESULT 2114
XX ABT32496
XX ID ABT32496 standard; DNA; 20 BP.
XX AC ABT32496;
XX 08-MAY-2003 (first entry)
XX DE Neuroblastoma-related oligonucleotide #273.
XX KW Neuroblastoma; prognosis; spontaneous regression; primer; probe; ds;
XX high malignancy.
XX Unidentified.
XX OS WO200297093-A1.
XX PN
XX

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PD 05-DEC-2002.
XX 30-MAY-2002; 2002WO-JP005294.
XX 30-MAY-2001; 2001JP-00162775.
XX 24-AUG-2001; 2001JP-00255226.
XX (CHIB-) CHIBA PREFECTURE.
XX PA (HISM) HISAMITSU PHARM CO LTD.
XX XX
XX Nakagawara A;
XX WPI; 2003-140476/13.
XX Nucleic acids having higher expression in human neuroblastoma with poor
XX prognosis for diagnostic prediction of neuroblastoma prognosis.
XX Example 5; Page 28; 111pp; Japanese.
XX The invention comprises nucleic acids that show increased expression in
XX human neuroblastomas with poor prognosis over those with a good
XX prognosis. The nucleic acids of the invention are useful as a tool for
XX distinguishing neuroblastomas with a favourable prognosis (spontaneous
XX regression) from neuroblastomas with a poor prognosis (high malignancy).
XX The DNA sequences ABT32224 - ABT32571 represent oligonucleotides used in
XX an example of the invention
XX Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1192 CCTGGGTCCAAATGCAG 1209
XX 2 CCTGTGTCAAATCCAG 19
XX
XX RESULT 2115
XX ADA20862
XX ID ADA20862 standard; DNA; 20 BP.
XX AC ADA20862;
XX 20-NOV-2003 (first entry)
XX Human BAX chimeric phosphorothioate oligonucleotide SEQ ID NO:35.
XX BCL2-associated X; BAX; neurotropic; neuroprotective; antiparkinsonian;
XX anticonvulsant; ophthalmological; antidiabetic; virucide;
XX antisense therapy; BAX antagonist; BAX inhibitor;
XX familial amyotrophic lateral sclerosis; Alzheimer's disease;
XX Parkinson's disease; Hodgkin's disease; cartilage-hair hyperplasia;
XX diabetes-associated ocular disorder; scrapie infection;
XX aberrant apoptosis; human; phosphorothioate; ss.
XX Synthetic.
XX OS Homo sapiens.
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages, and all cytidine
XX residues are 5-methylcytidines"
XX modified_base 1..5
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX modified_base 16..20
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"

```


Db 2 AACCTGAAGCAAAAGG 19

RESULT 2117

ACA92346

ID ACA92346 standard; DNA; 20 BP.

XX AC

XX ACA92346;

XX 16-JUL-2003 (first entry)

XX AC

XX Lawsonia intracellularis DNA PCR primer #23.

XX AC

XX Primer; ss; antibacterial; HtrA; PonA; HycP; Lyss; YcfW; ABC1; Omp100;

XX KW Lawsonia intracellularis infection; Orf1; pig; PCR.

XX KW

XX Lawsonia intracellularis.

XX OS

XX US2003021802-A1.

XX PN

XX 30-JAN-2003.

XX PD

XX 01-AUG-2002; 2002US-00210296.

XX PF

XX 22-OCT-1999; 99US-0160922P.

XX PR

XX 05-NOV-1999; 99US-0163858P.

XX PR

XX 12-OCT-2000; 2000US-00689065.

XX PR

XX (ROSE/) ROSEY E L.

XX PA

XX Rosey EL;

XX PI

XX WPI; 2003-416977/39.

XX DR

XX New isolated Lawsonia intracellularis polynucleotide and polypeptide,

XX PT useful for the prevention and diagnosis of Lawsonia infections in

XX PT susceptible animals, such as pigs.

XX PT

XX Example 1; Page 44; 64pp; English.

XX PS

XX The invention relates to an isolated polynucleotide molecule comprising a

XX CC sequence encoding Lawsonia intracellularis HtrA, PonA, HycP, Lyss, YcfW,

XX CC ABC1 or Omp100 protein. The invention also relates to a genetic construct

XX CC comprising a polynucleotide molecule that can be used to alter a Lawsonia

XX CC gene, comprising a polynucleotide molecule comprising a sequence that is

XX CC otherwise the same as a nucleotide sequence of a htrA, ponA, hycP, lyss,

XX CC ycfW, abc1 or omp100 gene, or its homologue, a substantial portion, or

XX CC mutations capable of altering the above mentioned genes or a

XX CC polynucleotide molecule comprising a sequence that naturally flanks in

XX CC situ the ORF of the htrA, ponA, hycP, lyss, ycfW, abc1 or omp100 gene or

XX CC its homologue. The invention also relates to a fusion protein of a

XX CC polypeptide of the invention fused to another polypeptide or an analogue

XX CC or derivative. The invention further relates to a substantially pure

XX CC polypeptide comprising an epitope of HtrA, PonA, HycP, Lyss, YcfW, ABC1

XX CC or Omp100 protein that is specifically reactive with anti-Lawsonia

XX CC antibodies. The methods and compositions of the present invention are

XX CC useful for the prevention and diagnosis of L. intracellularis infections

XX CC in susceptible animals, such as pigs. Sequences ACA92324-ACA92415

XX CC represent PCR primers used to amplify DNA encoding L. intracellularis

XX CC proteins of the invention

XX SQ

Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 1.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1083 TTTCAGCTCCATCAG 1100

|||||

Db 3 TTTCAGATCTACTTCAG 20

|||||

RESULT 2118

ADA26271

ID ADA26271 standard; DNA; 20 BP.

XX AC

XX ADA26271;

XX 20-NOV-2003 (first entry)

XX DT

XX Chicken Sonic hedgehog (Shh) oligonucleotide #8.

XX DE

XX Chicken; ss; Sonic hedgehog; neuronal cell; skeletogenesis;

XX KW chondrogenesis; osteogenesis; degenerative disorder; nervous system;

XX KW neuronal cell death; neural cell; neuromuscular disorder;

XX KW autonomic disorder; central nervous system disorder; anoxia; ischaemia;

XX KW peripheral nervous system disorder; tachycardia;

XX KW atrial cardiac arrhythmia; striated heart; stem cell development;

XX KW digestive tract; liver; multiple sclerosis; Shh.

XX KW

XX Synthetic.

XX OS

XX Gallus gallus.

XX OS

XX US2003054437-A1.

XX PN

XX 20-MAR-2003.

XX PD

XX 20-OCT-1997; 97US-00954771.

XX PF

XX 30-DEC-1993; 93US-00176427.

XX PR

XX 14-DEC-1994; 94US-00356060.

XX PR

XX 04-MAY-1995; 95US-00435093.

XX PR

XX 05-JUN-1995; 95US-00462386.

XX PR

XX (INGH/) INGHAM P W.

XX PA

XX (MCMA/) MCMANON A P.

XX PA

XX (TAB1/) TABIN C J.

XX XX

XX Ingham PW, Mcmahon AP, Tabin CJ;

XX PI

XX WPI; 2003-555377/52.

XX DR

XX Modulating growth, differentiation or survival of a cell, useful for

XX PT treating a degenerative disorder of the nervous system characterized by

XX PT neuronal cell death, comprises contacting the cell with a hedgehog

XX PT polypeptide.

XX PS

XX Example 2; Page 39; 121pp; English.

XX CC The invention relates to a method for modulating growth, differentiation

XX CC or survival of a cell, comprising contacting the cell with a hedgehog

XX CC polypeptide. The invention also relates to methods for inducing a cell to

XX CC differentiate to a neuronal cell phenotype comprising contacting the cell

XX CC with a hedgehog polypeptide, modulating skeletogenesis by contacting a

XX CC target tissue of a hedgehog polypeptide to cause chondrogenesis and/or

XX CC osteogenesis in the target tissue and treating a degenerative disorder of

XX CC the nervous system characterised by neuronal cell death, comprising

XX CC administering a hedgehog polypeptide causing prolonged survival of neural

XX CC cells in the patient, relative to the absence of hedgehog treatment. The

XX CC hedgehog polypeptides are useful for treating a degenerative disorder of

XX CC the nervous system characterised by neuronal cell death, including

XX CC neuromuscular, autonomic or central nervous system disorders,

XX CC specifically Alzheimer's disease, Parkinson's disease, amyotrophic

XX CC lateral sclerosis, Pick's disease, Huntington's disease, multiple

XX CC sclerosis, neuronal damage resulting from anoxia, ischaemia or trauma and

XX CC neuronal degeneration associated with a natural aging process. The

XX CC polypeptides may also be used for treating peripheral nervous system

XX CC disorders including disorders affecting innervation of smooth muscle and

XX CC endocrine tissue, such as tachycardia or atrial cardiac arrhythmias which

XX CC may arise from a degenerative condition whereby the nerves innervate the

XX CC striated muscle of the heart, in nerve prostheses for repairing central

XX CC and peripheral nerve damage, for treating neoplastic or hyperplastic

XX CC transformations and in controlling the development of stem cells

XX CC responsible for the formation of the digestive tract, liver and other

XX CC organs. This sequence represents a chicken Sonic hedgehog (Shh)

XX CC oligonucleotide, used in the method of the invention.

XX SQ Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1436 AAGTCACCGAGAGGAGA 1453
||||| |
Db 1 AAGTCAGCCAGAGGAGA 18
RESULT 2119
AAD57580
ID AAD57580 standard; DNA; 20 BP.
XX AC AAD57580;
XX DT 20-NOV-2003 (first entry)
XX DE Human PLSCR3 antisense oligonucleotide, ISIS #196392.
XX KW Human; phospholipid scramblase 3; gene therapy; HuPLSCR3; MuPLSCR3;
KW PLSCR3; neurodegenerative disease; hyperproliferative disorder;
KW autoimmune disorder; neuroprotective; immunosuppressive; antisense;
KW phosphorothioate backbone; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1. .5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotides"
FT modified_base 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotides"
XX PN WO2003048324-A2.
XX PD 12-JUN-2003.
XX PF 04-DEC-2002; 2002WO-US038521.
XX PR 04-DEC-2001; 2001US-00006972.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Dobie KW;
XX DR WPI; 2003-569053/53.
XX PT New compound, useful for preparing a composition for treating
PT hyperproliferative or autoimmune disorders, comprises a sequence targeted
PT to a nucleic acid encoding human phospholipid scramblase 3.
XX PS Example 15; Page 78; 107pp; English.
XX CC The present invention is directed to compounds, particularly antisense
CC oligonucleotides, which are targeted to a nucleic acid encoding human
CC phospholipid scramblase 3 (also known as PLSCR3, HuPLSCR3 and MuPLSCR3)
CC and which modulates the expression of phospholipid scramblase 3. The
CC compounds of the invention are useful for preparing compositions for
CC treating neurodegenerative diseases e.g. hyperproliferative or autoimmune
CC disorders. The invention is also used in gene therapy. The present
CC sequence is an antisense oligonucleotide targeted to human PLSCR3 DNA

XX SQ Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 753 CGGATTGATCAGGAGTC 770
||||| |
Db 3 CGGATTTCATCCGAGTC 20
RESULT 2120
AAL61824
ID AAL61824 standard; DNA; 20 BP.
XX AC AAL61824;
XX DT 22-SEP-2003 (first entry)
XX DE Human ETBR-LP-2 antisense oligonucleotide ISIS #204250.
XX KW Human; G protein-coupled receptor; hyperproliferative disorder; GPR37L1;
KW endothelin type b receptor-like protein-2; cerebral vascular disease;
KW antisense; endothelin-binding receptor-like protein-2; atherosclerosis;
KW cardiovascular disease; ETBR-LP-2; G-protein coupled receptor 37 like 1;
KW acute proliferative nephropathy; ETBR-like protein 2; cancer; stroke;
KW angiogenesis; hypertension; phosphorothioate; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1. .5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX PN WO2003050244-A2.
XX PD 19-JUN-2003.
XX PF 04-DEC-2002; 2002WO-US038520.
XX PR 06-DEC-2001; 2001US-00003126.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM;
XX DR WPI; 2003-558997/52.
XX PT New oligonucleotides which bind the nucleic acid encoding the G protein
PT coupled receptor ETBR-LP-2 (endothelin type b receptor-like protein-2
PT receptor), useful for treating e.g. cancer and cardiovascular diseases.
XX PS Claim 3; Page 79; 106pp; English.
XX CC The invention relates to antisense compounds targeted to the nucleic
CC acid encoding the G protein-coupled receptor ETBR-LP-2 (endothelin type b
CC receptor-like protein-2) to inhibit its expression. ETBR-LP-2 is also
CC known as endothelin-binding receptor-like protein-2, ETBR-like protein 2
CC and G-protein coupled receptor 37 like 1 (GPR37L1). Antisense compounds
CC of the invention are useful for treating hyperproliferative disorders

CC (especially cancer) and cardiovascular diseases especially angiogenesis,
CC atherosclerosis, hypertension, cerebral vascular disease, stroke and
CC acute proliferative nephropathy. The present sequence is an antisense
CC oligonucleotide targeted to human ETBR-LP-2 DNA
XX
SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1500 CAAGTGGCTGATGGA 1517
DB 2 CAAGTGGCTGATGGA 19
RESULT 2121
ADA45335/c
ID ADA45335 standard; DNA; 20 BP.
XX
AC ADA45335;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human BRAC1 gene sequencing primer #21.
XX
KW Functional allele profile; genetic inheritance; haplotype; population;
KW disease; pharmacogenetic application; selective pressure; human; MSH2;
KW MLH1; BRCA1; BRCA2; PTEN; BAP1; BARD1; p53; sequencing; primer; ss.
XX
OS Homo sapiens.
XX
XX US2003096236-A1.
PN
XX 22-MAY-2003.
PD
XX 08-AUG-2001; 2001US-00923327.
PF
XX 12-FEB-1996; 96US-00598591.
PR
XX 04-AUG-1997; 97US-00798691.
PR
XX 04-AUG-1997; 97US-00905772.
PR
XX 22-MAY-1998; 98US-00084471.
PR
XX 04-AUG-1998; 98US-00129134.
PR
XX 14-MAR-2000; 2000US-00524794.
XX
XX (ONCO-) ONCORMED INC.
PA
XX Murphy PD;
PI
XX WPI; 2003-576875/54.
DR
XX
XX Determining a functional allele profile of a gene in a population by
PT identifying the nucleotide sequence of a gene of genomic DNA from each of
PT the individuals with a family history of functional alleles of the gene
PT of interest.
XX
XX Example 3; Page 11; 28pp; English.
PS
XX The present invention relates to a method for determining a functional
XX allele profile of a gene in a population. The method comprises
CC identifying the nucleotide sequence of a gene of interest out of genomic
CC DNA from each of a population of individuals identified as having a
CC family history which indicates inheritance of functional alleles of the
CC gene of interest, and rank ordering the frequency of occurrence of each
CC haplotype, where the identity of the alleles containing each haplotype
CC and the determination of their relative frequencies constitutes the
CC functional allele profile of the gene of interest in the population. The
CC method is useful for determining functional allele profiles which are
CC useful in the treatment and diagnosis of diseases, for genetic and
CC pharmacogenetic applications, and for evaluating the degree to which the
CC gene(s) are under selective pressure. The present sequence represents a
CC sequencing primer used in the method of the invention.
XX

SQ Sequence 20 BP; 6 A; 2 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 846 TGGCTCAGACTCCCTATC 863
DB 19 TGATTCAGACTCCCTATC 2
RESULT 2122
ACC99645/c
ID ACC99645 standard; DNA; 20 BP.
XX
AC ACC99645;
XX
DT 02-SEP-2003 (first entry)
XX
DE PECAM PCR primer SEQ ID NO:26.
XX
KW Multiplex real-time quantitative PCR; PCR primer; copy number;
KW Alzheimer's disease; ss.
XX
OS Synthetic.
XX
XX WO2003048377-A2.
PN
XX 12-JUN-2003.
PD
XX 02-DEC-2002; 2002WO-US038806.
PF
XX 30-NOV-2001; 2001US-0336095P.
PR
XX 19-JUL-2002; 2002US-0397475P.
PR
XX (UYVP) UNIV ROCHESTER.
PA (THER/) THERIANOS S.
XX
XX Zhu M, Coleman P;
PI
XX WPI; 2003-532841/50.
DR
XX
XX Determining the relative copy number of a group of target nucleic acid
PT molecules present in a sample by performing a first or second PCR in a
PT PCR mixture and quantifying the number of copies of the second target
PT nucleic acid product.
XX
XX Example 1; Fig 8; 118pp; English.
PS
XX The present invention describes a multiplex real-time quantitative PCR
XX method for determining the relative copy number of a group of target
CC nucleic acid molecules present in a sample. The method comprises: (1)
CC performing a first PCR in a PCR mixture; (2) performing a second PCR in a
CC PCR mixture; and (3) quantifying the number of copies of the second
CC target nucleic acid product present in the sample containing the target
CC nucleic acid molecule. Also described: (1) quantifying the copy number of
CC a group of target nucleic acids in a sample; and (2) determining whether
CC a subject is at risk of acquiring Alzheimer's disease. The method is
CC useful for determining the relative copy number of a group of target
CC nucleic acid molecules present in a sample for determining whether a
CC subject is at risk of acquiring Alzheimer's disease. ACC99620 to ACC99730
CC represent PCR primer used in the exemplification of the present invention
XX
SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 373 GATGGCTGTTTTCAGTTC 390
DB 20 GATGCCCACTTTGAGGTC 3

```

RESULT 2123
ADA37216/c
ID ADA37216 standard; DNA; 20 BP.
XX
XX
AC ADA37216;
XX
DT 20-NOV-2003 (first entry)
XX
DE ATP synthase PCR primer SEQ ID NO:20.
XX
XX mitochondrial disease; central nervous system; CNS; cerebroprotective;
KW neuroprotective; anticonvulsant; antiparkinsonian; nootropic;
KW gastrointestinal; ophthalmological; antidiabetic;
KW mitochondrial encephalomyopathy; lactic acidosis; MELAS;
KW Leigh's syndrome; Huntington's disease; Parkinson's disease;
KW Alzheimer's disease; neurogastrointestinal encephalomyopathy;
KW chronic progressive external ophthalmoplegia; myoclonus epilepsy;
KW diabetes; PCR primer; ATP synthase; ss.
XX
OS Synthetic.
XX
XX WO2003068215-A1.
XX
PN 21-AUG-2003.
XX
PD 13-FEB-2003; 2003WO-JP001462.
XX
XX 14-FEB-2002; 2002JP-00036468.
XX
XX (AJIN) AJINOMOTO CO INC.
XX
XX Mori M, Takahara Y, Ishizaki S, Sonaka I;
XX WPI; 2003-689611/65.
XX
XX Agents for treating mitochondrial diseases comprise alanine compound.
XX
XX Example 1; Page 9; 29pp; Japanese.
XX
XX The present invention describes agents for treating, preventing or
CC ameliorating mitochondrial diseases, where the agents comprise an alanine
CC compound. The agents have central nervous system (CNS),
CC cerebroprotective, neuroprotective, anticonvulsant, antiparkinsonian,
CC nootropic, gastrointestinal, ophthalmological and antidiabetic
CC activities. The agents can be used for treating, preventing or
CC ameliorating mitochondrial diseases such as mitochondrial
CC encephalomyopathy, lactic acidosis, and stroke-like episodes (MELAS),
CC Leigh's syndrome, Huntington's disease, Parkinson's disease, Alzheimer's
CC disease, neurogastrointestinal encephalomyopathy (MNGIE), chronic
CC progressive external ophthalmoplegia (CPEO), myoclonus epilepsy
CC associated with ragged-red fibre disease syndrome, reba disease and
CC diabetes. The present sequence represents a PCR primer for ATP synthase
CC H+ transporting mitochondrial F0 complex subunit c (subunit 9) isoform 1,
CC which is used in an example from the present invention.
XX
SQ Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1528 TCTGGCTTCTCTGGTGA CT 1545
||| ||| ||| ||| |||
Db 20 TCTGCTCTCTCTGGTGA CT 3
RESULT 2124
ADA15243/c
ID ADA15243 standard; DNA; 20 BP.
XX
XX ADA15243;
AC
XX

```

```

DT XX 06-NOV-2003 (first entry)
DE XX Mouse HYPLIPI locus PCR primer #183.
XX
KW KW Mouse; PCR; primer; ss; HYPLIPI; FCHL1; variation; lipid disorder;
KW allele; anti-lipid disorder; anti-cancer therapy; gene therapy;
KW familial combined hyperlipidaemia; coronary artery disease;
KW atherogenic lipoprotein phenotype; hyperapobetalipoproteinaemia;
KW hypertriglyceridaemia; low density lipoprotein subclass B; LDL;
KW familial dyslipidemic hypertension; syndrome X; hypercholesterolaemia;
KW obesity; insulin resistance; cancer; cytostatic; antilipemic;
KW hypotensive; anorectic.
XX
OS Mus sp.
XX
XX US2003064372-A1.
XX
PD 03-APR-2003.
XX
XX 07-SEP-2001; 2001US-00949428.
XX
XX 22-JUN-2000; 2000US-0213322P.
XX
XX (BODN/) BODNAR J S.
XX (CAST/) CASTELLANI L W.
XX (CHAT/) CHATTERJEE A.
XX (JONG/) JONG P D.
XX (LUSI/) LUSIS A J.
XX (OHME/) OHMEN J.
XX (ROSS/) ROSS D.
XX (TAFU/) TAFURI S.
XX (WUCC/) WU C.
XX
XX Bodnar JS, Castellani LW, Chatterjee A, Jong PD, Lusis AJ;
XX Ohmen J, Ross D, Tafuri S, Wu C;
XX WPI; 2003-540780/51.
XX
XX Novel isolated polynucleotide comprising a mouse or human familial
PT combined hyperlipidaemia 1 gene having a variation that is associated with
PT a lipid disorder, useful for identifying susceptibility to the lipid
PT disorder.
XX
XX Claim 11; Page 39; 63pp; English.
XX
XX The invention discloses isolated polynucleotides comprising mouse HYPLIPI
CC cDNA sequence, mouse HYPLIPI genomic DNA, or the homologous human
CC familial combined hyperlipidaemia 1 (FCHL1) gene, where a variation in
CC the sequence is associated with a lipid disorder. Also claimed is an
CC isolated polypeptide comprising a variant form of the mouse HYPLIPI amino
CC acid sequence, or a variant form of a fully defined human FCHL1 amino
CC acid sequence, where the variant is associated with the lipid disorder,
CC an isolated polynucleotide having at least 12 contiguous nucleotides of
CC the isolated polynucleotides, where the 12 contiguous nucleotides span
CC the variation position, an isolated polypeptide comprising 4 contiguous
CC amino acids of the encode polypeptides, where the 4 contiguous amino
CC acids span the variation position, a kit for the detection of the FCHL1
CC locus comprising, an isolated antibody, identifying susceptibility to a
CC lipid disorder which comprises comparing the nucleotide sequence of the
CC suspected FCHL1 allele with a wild-type FCHL1 nucleotide sequence, where
CC the difference between the suspected allele and the wild-type sequence
CC identifies a sequence variation of FCHL1 nucleotide sequence and a
CC pharmaceutical composition. Also disclosed is a transgenic animal which
CC carries an altered HYPLIPI or FCHL1 allele and a method for screening
CC drugs for inhibition or restoration of FCHL1 gene function as an anti-
CC lipid disorder or anti-cancer therapy. The polynucleotides, polypeptides
CC and antibodies are useful for treating or preventing (e.g. gene therapy)
CC a lipid disorder associated with expression of FCHL1, for diagnosis or
CC prognosis of predisposition to lipid disorder, and cancer and for
CC treating a lipid disorder such as familial combined hyperlipidaemia,
CC coronary artery disease, atherogenic lipoprotein phenotype,
CC hyperapobetalipoproteinaemia, hypertriglyceridaemia, low density
CC lipoprotein (LDL) subclass B, familial dyslipidemic hypertension,

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CC syndrome X, hypercholesterolaemia, obesity, insulin resistance and
CC cancer. The sequence presented is a PCR primer which was used to amplify
CC part of the mouse Hylp1 locus.
XX
SQ Sequence 20 BP; 8 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1522 TCCAGCTCTGGCTTCG 1539
DB 19 TCCACCTCTGTTCTCG 2

RESULT 2125
ADB25698
ID ADB25698 standard; DNA; 20 BP.
XX
AC ADB25698;
XX
XX 20-NOV-2003 (first entry)
XX Human connective tissue growth factor antisense oligo DNA (SeqID 91).
DE antisense; human; ss; connective tissue growth factor; CTGF;
XX chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;
KW fisp-12; NOV2;
KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
KW scleroderma; atherosclerosis; cytostatic; dermatological;
KW antiarteriosclerotic.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
XX WO2003053340-A2.
XX
XX PD 03-JUL-2003.
XX
XX PF 09-DEC-2002; 2002WO-US038618.
XX
XX PR 10-DEC-2001; 2001US-00006191.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Gaarde WA, Watt AT;
XX
XX DR WPI; 2003-559091/52.
XX
XX New antisense oligonucleotides for modulating connective tissue growth
PT factor expression, particularly useful for treating cancers (e.g. breast
PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or
PT atherosclerosis.
XX
XX Claim 3; Page 86; 139pp; English.
XX
XX This invention relates to novel methods for modulating the expression of
CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
CC as ctgofact, fibroblast inducible secreted protein, fisp-12, NOV2,
CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
CC promote chemotaxis of fibroblasts, however, it is also upregulated in
CC acute lymphoblastic leukaemia and in tumour or endothelial cells

CC associated with the vasculature. Accordingly, antisense oligonucleotides
CC that inhibit the expression of CTGF in cells or tissues can be used in
CC gene therapy to treat various conditions including hyperproliferative
CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),
CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
CC such, the present invention describes these antisense oligos as having
CC cytostatic, dermatological and antiarteriosclerotic activities. This
CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
CC human CTGF of the invention.
XX
SQ Sequence 20 BP; 2 A; 8 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1519 CTCCTCCAGCTCTGGCTTC 1536
DB 2 CTCCTCCTCTGGCTTC 19

RESULT 2126
ADB25712
ID ADB25712 standard; DNA; 20 BP.
XX
AC ADB25712;
XX
XX 20-NOV-2003 (first entry)
XX Mouse connective tissue growth factor antisense oligo DNA (SeqID 105).
DE antisense; mouse; murine; ss; connective tissue growth factor; CTGF;
XX chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;
KW fisp-12; NOV2;
KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
KW scleroderma; atherosclerosis; cytostatic; dermatological;
KW antiarteriosclerotic.
XX Mus sp.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
XX WO2003053340-A2.
XX
XX PD 03-JUL-2003.
XX
XX PF 09-DEC-2002; 2002WO-US038618.
XX
XX PR 10-DEC-2001; 2001US-00006191.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Gaarde WA, Watt AT;
XX
XX DR WPI; 2003-559091/52.
XX
XX New antisense oligonucleotides for modulating connective tissue growth
PT factor expression, particularly useful for treating cancers (e.g. breast
PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or
PT atherosclerosis.
XX
XX Example 16; Page 88; 139pp; English.
XX This invention relates to novel methods for modulating the expression of

CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
 CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
 CC as ctgofact, fibroblast inducible secreted protein, fisp-12, NOV2.
 CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
 CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
 CC promote chemotaxis of fibroblasts, however, it is also upregulated in
 CC acute lymphoblastic leukaemia and in tumour or endothelial cells
 CC associated with the vasculature. Accordingly, antisense oligonucleotides
 CC that inhibit the expression of CTGF in cells or tissues can be used in
 CC gene therapy to treat various conditions including hyperproliferative
 CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),
 CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
 CC such, the present invention describes these antisense oligos as having
 CC cytosstatic, dermatological and antiarteriosclerotic activities. This
 CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
 CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
 CC mouse CTGF of the invention.

XX
 SQ Sequence 20 BP; 5 A; 4 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 GAGCGGAGCAAGATGGCG 69
 |||||
 Db 1 GAGCGGAGCATGTCGGG 18

RESULT 2127

AA6009/C

ID AAL60009 standard; DNA; 20 BP.

XX

AC AAL60009;

XX

DT 27-AUG-2003 (first entry)

XX

DE Human GH-1 gene amplifying PCR primer, CRV156.1t1.

XX

KW Human; growth hormone 1; GH-1; single nucleotide polymorphism; SNP;

KW gene therapy; PCR; primer; ss.

XX

OS Homo sapiens.

XX

PN WO2003042226-A2.

XX

PD 22-MAY-2003.

XX

PF 07-NOV-2002; 2002WO-US035719.

XX

PR 09-NOV-2001; 2001US-0347448P.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Wood LS, Wagner S, Parodi LA;

XX

DR WPI; 2003-449555/42.

XX

PT New growth hormone 1 (GH-1) diagnostic polynucleotide, useful as markers
 PT for the analysis of a disease, or of susceptibility to drug treatment for
 PT GH-1 dysfunction or other diseases.

XX

PS Example 2; Page 30; 74pp; English.

XX

CC The invention relates to growth hormone 1 (GH-1) gene including single
 CC nucleotide polymorphisms (SNP). The GH-1 diagnostic polynucleotide is
 CC useful as markers for the analysis of a disease, of susceptibility to
 CC drug treatment for GH-1 dysfunction or other diseases, or may be included
 CC in any complete or partial genetic map of the human genome. GH-1 mutant
 CC polypeptides are useful as antagonists of GH-1 hormone action.

CC Polynucleotides encoding these polypeptides are useful in gene therapy.

CC The present sequence is a PCR primer used for amplifying human GH-1 gene

XX

SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1330 TCTCAAGAGGAGGAGAG 1347
 |||||
 Db 18 TCTGAAAGGAGGAGGAG 1

RESULT 2128

ACD07260/C

ID ACD07260 standard; DNA; 20 BP.

XX

AC ACD07260;

XX

DT 07-AUG-2003 (first entry)

XX

DE Human BRCA1 gene forward PCR primer for exon 11C.

XX

KW Human; ss; PCR; primer; BRCA1; omi1; omi2; omi3; gene therapy; tumour;

KW breast cancer; ovarian cancer; prostate cancer; colon cancer.

XX

OS Homo sapiens.

XX

PN US2003022184-A1.

XX

PD 30-JAN-2003.

XX

PF 22-OCT-2001; 2001US-00982828.

XX

PR 12-FEB-1996; 96US-00598591.

PR

PR 12-FEB-1997; 97US-00798691.

PR

PR 06-MAY-1998; 98US-00074453.

XX

PA (ONCO-) ONCORMED INC.

XX

PI Murphy PD, Allen ACP, Alvares CP, Critz BS, Olson SJ, Thurber D;

PI Zeng B;

XX

DR WPI; 2003-456286/43.

XX

PT New protein sequence comprising an amino acid sequence derived from the
 PT BRCA1 omi1, omi2 or omi3 sequence useful in performing gene therapy for
 PT treating patients suspected of having tumor, e.g. breast, ovarian,
 PT prostate or colon cancer.

XX

PS Example 1; Page 11; 60pp; English.

XX

CC The invention relates to a protein sequence comprising an amino acid
 CC sequence derived from the human BRCA1 omi1, omi2 or omi3 sequences
 CC appearing as ABU61603 ABU61605. Also included are determining the
 CC consensus genomic sequence or consensus coding sequence for a target
 CC gene, oligonucleotide probes (each capable of hybridising to a target
 CC BRCA1 omi gene/cDNA appearing as ACA6132-ACA6134) or their complements,
 CC a chip array having n elements for performing allele specific sequence-
 CC based techniques comprising a solid phase chip and oligonucleotides
 CC having n different nucleotide sequences (where n is an integer greater
 CC than or equal to 7, where the oligonucleotides are bound to the solid
 CC phase chip in a manner that permits the oligonucleotides to effectively
 CC hybridise to complementary oligonucleotides or polynucleotides, and the
 CC oligonucleotides having different nucleotide sequence are bound to the
 CC solid phase chip at different locations so that a particular location on
 CC the solid phase chip exclusively binds oligonucleotides having a specific
 CC nucleotide sequence, and the oligonucleotides are capable of specifically
 CC hybridising to the BRCA1 omi DNA), performing gene therapy on a patient,
 CC treating a patient suspected of having a tumour, a expression/cloning
 CC vector comprising the BRCA1 DNA sequence (or fragments), preventing the
 CC formation or growth of a tumour, a host cell transformed with the vector
 CC and an anti-BRCA1 antibody. The protein sequences are useful in
 CC performing gene therapy for treating patients suspected of having a
 CC tumour, e.g. breast cancer, ovarian cancer, prostate cancer or colon

CC cancer. The antibody is useful as an immunogen. The present sequence is a
CC PCR primer used to amplify/sequence an exon of the BRCA1 gene
XX
SQ Sequence 20 BP; 6 A; 2 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 846 TGGCTCAGACCTCCCTATC 863
DB 19 TGATTCAGACTCCCATC 2
RESULT 2129
AAL62409
ID AAL62409 standard; DNA; 20 BP.
AC
AC AAL62409;
DT 06-OCT-2003 (first entry)
XX Human ABC transporter MHC I antisense oligonucleotide, ISIS 206590.
DE ABC transporter; ABCT; major histocompatibility complex; MHC; cytostatic;
XX hyperproliferative; autoimmune disorder; antisense gene therapy;
KW inflammation; tumour formation; immunosuppressive; antimicrobial; human;
KW phosphorothioate backbone; antisense; ss.
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-methylcytidines"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
XX WO2003051309-A2.
XX
XX 26-JUN-2003.
XX
XX 12-DEC-2002; 2002WO-US040101.
XX
XX 17-DEC-2001; 2001US-00024369.
XX (ISIS-) ISIS PHARM INC.
XX Borchers AH, Ward DT, Freier SM;
XX WPI; 2003-577305/54.
XX
XX New antisense compound that hybridizes and inhibits the nucleic acid
PT encoding ABC transporter major histocompatibility complex 1, for treating
PT diseases or conditions such as a hyperproliferative or autoimmune
PT disorder.
XX
XX Claim 3; Page 80; 112pp; English.
XX
XX The invention relates to a compound targetted to a nucleic acid molecule
CC encoding ABC transporter (ABCT) major histocompatibility complex (MHC) 1
CC where the compound specifically hybridises with the nucleic acid molecule
CC and inhibits expression of ATM or specifically hybridises with at least a
CC portion of an active site on the nucleic acid molecule. The invention is

CC useful for inhibiting the expression of ATM in cells or tissues. The
CC invention is useful for treating an animal with hyperproliferative or
CC autoimmune disorder. The invention is useful for diagnostics,
CC therapeutics, prophylaxis, as research reagents and kits, for
CC distinguishing functions of various members of a biological pathway and
CC in antisense gene therapy. The invention is also useful prophylactically
CC e.g., to prevent or delay infection, inflammation or tumour formation.
CC The present sequence is an antisense oligo targetted to human ABC
CC transporter MHC I DNA. This sequence is used to illustrate the method of
CC the invention
XX
XX Sequence 20 BP; 8 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 256 ACCAAGTACCACAGCAT 273
DB 3 ACCAGTACCACAGCAT 20
RESULT 2130
ACD05059
ID ACD05059 standard; DNA; 20 BP.
XX
AC ACD05059;
XX
DT 05-AUG-2003 (first entry)
XX
DE Tumour necrosis factor alpha antisense oligonucleotide #64.
XX
XX Tumour necrosis factor alpha; TNF-alpha; antiinflammatory; antirheumatic;
KW antiarthritic; antidiabetic; dermatological; hepatotropic; antiasthmatic;
KW inflammatory disorder; inflammatory bowel disease; Crohn's disease;
KW colitis; rheumatoid arthritis; diabetes; pancreatitis;
KW multiple sclerosis; atopic dermatitis; asthma; hepatitis;
KW antisense technology; ss.
XX
OS Synthetic.
XX
XX US2003022848-A1.
XX
XX 30-JAN-2003.
XX
XX 02-APR-2001; 2001US-00824322.
XX
XX 05-OCT-1998; 98US-00166186.
XX 18-MAY-1999; 99US-00313932.
XX
XX (BAKE/) BAKER B F.
XX (BENN/) BENNETT C F.
XX (BUTL/) BUTLER M M.
XX (SHAN/) SHANAHAN W R.
XX
XX Baker BF, Bennett CF, Butler MM, Shanahan WR;
XX WPI; 2003-447433/42.
XX
XX Treating inflammatory disorders such as inflammatory bowel disease,
XX Crohn's disease or rheumatoid arthritis, in a subject, by administering
XX oligonucleotide which inhibits expression of human tumor necrosis factor
XX alpha.
XX
XX Example 6; Page 18; 142pp; English.
XX
XX The invention describes a method of treating an inflammatory disorder in
XX an individual, comprising administering to the individual an
XX oligonucleotide upto 30 nucleotides in length complementary to a nucleic
XX acid molecule encoding human tumor necrosis factor (TNF)-alpha. The
XX method is useful for treating an inflammatory disorder such as
XX inflammatory bowel disease, Crohn's disease, colitis or rheumatoid
XX arthritis, in an individual. The method is also useful for treating

CC diabetes, pancreatitis, multiple sclerosis, atopic dermatitis, asthma,
CC and hepatitis in an individual. This sequence represents an antisense
CC oligonucleotide used to modulate expression of tumour necrosis factor
CC alpha (TNF-alpha)
XX
SQ Sequence 20 BP; 3 A; 6 C; 2 G; 9 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1585 TCTATTCTCTGTGTATT 1602
Db 2 TCCATTCTCTGTGTATT 19
RESULT 2131
ACD05306/C
ID ACD05306 standard; DNA; 20 BP.
XX
AC ACD05306;
XX
DT 05-AUG-2003 (first entry)
XX
DE Tumour necrosis factor alpha antisense oligonucleotide #309.
XX
KW Tumour necrosis factor alpha; TNF-alpha; antiinflammatory; antirheumatic;
KW antiarthritic; antidiabetic; dermatological; hepatotropic; antiasthmatic;
KW inflammatory disorder; inflammatory bowel disease; Crohn's disease;
KW colitis; rheumatoid arthritis; diabetes; pancreatitis;
KW multiple sclerosis; atopic dermatitis; asthma; hepatitis;
KW antisense technology; ss.
XX
OS Synthetic.
XX
PN US2003022848-A1.
XX
PD 30-JAN-2003.
XX
PF 02-APR-2001; 2001US-00824322.
XX
PR 05-OCT-1998; 98US-00166186.
PR 18-MAY-1999; 99US-00313932.
XX
PI (BAKE/) BAKER B F.
PA (BENN/) BENNETT C F.
PA (BUTL/) BUTLER M M.
PA (SHAN/) SHANAHAN W R.
XX
PI Baker BF, Bennett CF, Butler MM, Shanahan WR;
PI WPI; 2003-447433/42.
XX
PT Treating inflammatory disorders such as inflammatory bowel disease,
PT Crohn's disease or rheumatoid arthritis, in a subject, by administering
PT oligonucleotide which inhibits expression of human tumor necrosis factor
PT alpha.
XX
PS Example 24; Page 38; 142pp; English.
XX
CC The invention describes a method of treating an inflammatory disorder in
CC an individual, comprising administering to the individual an
CC oligonucleotide upto 30 nucleotides in length complementary to a nucleic
CC acid molecule encoding human tumor necrosis factor (TNF)-alpha. The
CC method is useful for treating an inflammatory disorder such as
CC inflammatory bowel disease, Crohn's disease, colitis or rheumatoid
CC arthritis, in an individual. The method is also useful for treating
CC diabetes, pancreatitis, multiple sclerosis, atopic dermatitis, asthma,
CC and hepatitis in an individual. This sequence represents an antisense
CC oligonucleotide used to modulate expression of tumour necrosis factor
CC alpha (TNF-alpha)
XX
SQ Sequence 20 BP; 5 A; 8 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1674 CTGGGTGAGCTCTTCCAG 1691
Db 20 CTGGGAGGGTCTTCCAG 3
RESULT 2132
ACD05070
ID ACD05070 standard; DNA; 20 BP.
XX
AC ACD05070;
XX
DT 05-AUG-2003 (first entry)
XX
DE Tumour necrosis factor alpha antisense oligonucleotide #75.
XX
KW Tumour necrosis factor alpha; TNF-alpha; antiinflammatory; antirheumatic;
KW antiarthritic; antidiabetic; dermatological; hepatotropic; antiasthmatic;
KW inflammatory disorder; inflammatory bowel disease; Crohn's disease;
KW colitis; rheumatoid arthritis; diabetes; pancreatitis;
KW multiple sclerosis; atopic dermatitis; asthma; hepatitis;
KW antisense technology; ss.
XX
OS Synthetic.
XX
PN US2003022848-A1.
XX
PD 30-JAN-2003.
XX
PF 02-APR-2001; 2001US-00824322.
XX
PR 05-OCT-1998; 98US-00166186.
PR 18-MAY-1999; 99US-00313932.
XX
PI (BAKE/) BAKER B F.
PA (BENN/) BENNETT C F.
PA (BUTL/) BUTLER M M.
PA (SHAN/) SHANAHAN W R.
XX
PI Baker BF, Bennett CF, Butler MM, Shanahan WR;
PI WPI; 2003-447433/42.
XX
PT Treating inflammatory disorders such as inflammatory bowel disease,
PT Crohn's disease or rheumatoid arthritis, in a subject, by administering
PT oligonucleotide which inhibits expression of human tumor necrosis factor
PT alpha.
XX
PS Example 6; Page 18; 142pp; English.
XX
CC The invention describes a method of treating an inflammatory disorder in
CC an individual, comprising administering to the individual an
CC oligonucleotide upto 30 nucleotides in length complementary to a nucleic
CC acid molecule encoding human tumor necrosis factor (TNF)-alpha. The
CC method is useful for treating an inflammatory disorder such as
CC inflammatory bowel disease, Crohn's disease, colitis or rheumatoid
CC arthritis, in an individual. The method is also useful for treating
CC diabetes, pancreatitis, multiple sclerosis, atopic dermatitis, asthma,
CC and hepatitis in an individual. This sequence represents an antisense
CC oligonucleotide used to modulate expression of tumour necrosis factor
CC alpha (TNF-alpha)
XX
SQ Sequence 20 BP; 1 A; 8 C; 3 G; 8 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1978 TGCCCTCTGTCTCTTC 1995

XX WPI; 2003-129214/12.

XX New nucleic acid comprising a mutation in LRP5 or LRP6, useful for

XX diagnosing a HBM-like phenotype in a subject and for preparing a

PT composition for modulating bone mass and/or lipid levels in a subject

PT suffering from e.g. osteoporosis.

XX Example 2; Page 65; 629pp; English.

XX The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and

CC LRP6 mutants, which results in a HBM-like phenotype when expressed in a

CC cell. The HBM-like phenotype results in bone mass modulation and/or lipid

CC level modulation. The invention is useful for diagnosing a HBM-like

CC phenotype in a subject and for preparing a composition for modulating

CC bone mass and/or lipid levels in a subject suffering from e.g.

CC osteoporosis. The present sequence is a sequence Tagged Site (STS)

CC marker, which was used to prepare a physical map of the Zmax1 (LRP5) gene

CC region.

XX Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other;

SQ

Query Match 0.6%; Score 13.2; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 1.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 35 ACTGACGGTAGGGACGGG 52

Db 3 AGTGACACTAGGGACGGG 20

|||||

RESULT 2138

ADB81447/c

ID ADB81447 standard; DNA; 20 BP.

XX ADB81447;

AC

XX 04-DEC-2003 (first entry)

DT

XX Human oestrogen receptor alpha antisense oligonucleotide DNA (SeqID 67).

DE

XX antisense; human; ss; oestrogen receptor alpha; ESR-alpha;

KW oestrogen receptor 1; ESR1; NR3A1; bone maintenance;

KW cardiovascular system; cancer; gene therapy; hyperproliferative disease;

KW inflammation; tumour formation; infection; cytostatic; antiinflammatory;

KW antimicrobial.

XX Homo sapiens.

OS

XX

PH Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /mod_base= OTHER

FT /note= "OTHER= phosphorothioate backbone, where 1-5 and

FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are

FT 5-methylcytidines"

XX

XX WO2003052072-A2.

PN

XX 26-JUN-2003.

PD

XX 13-DEC-2002; 2002WO-US040083.

PF

XX 18-DEC-2001; 2001US-00027983.

PR

XX (ISIS-) ISIS PHARM INC.

PA

XX Dobie KW, Roach MP;

PI

XX WPI; 2003-577322/54.

DR

XX New antisense compound targeted to nucleic acid encoding estrogen

PT receptor alpha and inhibiting expression of estrogen receptor alpha,

PT useful for treating a disease or condition e.g. a hyperproliferative

PT disease.

XX Example 15; Page 78; 232pp; English.

XX This invention relates to human oestrogen receptor alpha (ESR-alpha), and

CC the novel antisense oligonucleotides that modulate its expression. The

CC oestrogen receptor alpha protein is also known as oestrogen receptor 1,

CC ESR1, and NR3A1. Oestrogen, the steroid hormone ligand of ESR-alpha, is

CC important for bone maintenance and plays a protective role in the

CC cardiovascular system, as well as being required for normal sexual

CC maturation through promoting growth and differentiation. Splice variants

CC of ESR-alpha, however, have been associated with various cancers

CC including the breast and pituitary. Accordingly, antisense

CC oligonucleotides that inhibit the expression of ESR-alpha in cells or

CC tissues can be used in gene therapy to treat conditions such as

CC hyperproliferative disease, inflammation, tumour formation and to prevent

CC or delay infection. As such, the present invention describes these

CC antisense oligos as having cytostatic, antiinflammatory and antimicrobial

CC activities. This oligonucleotide sequence is an antisense oligo used to

CC inhibit expression of human oestrogen receptor alpha of the invention.

XX Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

SQ

Query Match 0.6%; Score 13.2; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 1.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1137 CCTGGAGAAGATCAACA 1154

Db 18 CCTGGACAGATCACAGA 1

|||||

RESULT 2139

ADB89951/c

ID ADB89951 standard; DNA; 20 BP.

XX ADB89951;

AC

XX 04-DEC-2003 (first entry)

DT

XX Complement C3 targeting antisense oligonucleotide #10.

DE

XX ss; antisense; complement component C3; inflammation; septic shock;

KW multiple organ failure; hyperacute organ failure; autoimmune disorder;

KW CNS inflammation; multiple sclerosis; atherosclerosis; tumour.

XX Unidentified.

OS

XX US2003096775-A1.

PN

XX 22-MAY-2003.

PD

XX 23-OCT-2001; 2001US-00001076.

PF

XX 23-OCT-2001; 2001US-00001076.

PR

XX (ISIS-) ISIS PHARM INC.

PA

XX Graham MJ, Watt AT;

PI

XX WPI; 2003-606441/57.

DR

XX New antisense oligonucleotides targeted to a nucleic acid molecule

PT encoding complement component C3, useful for treating a disease or

PT condition associated with complement component C3, e.g. autoimmune

PT disorder or infection.

XX Disclosure; Page 53; 72pp; English.

PS

XX The invention relates to a compound 8-50 nucleobases in length targeted

CC to a nucleic acid molecule encoding complement component C3. The compound

CC specifically hybridises with the nucleic acid molecule encoding

CC complement component C3 and inhibits the expression of complement
 CC component C3, or specifically hybridises with at least an 8-nucleobase
 CC portion of an active site on a nucleic acid molecule encoding complement
 CC component C3. Also included are a composition comprising the compound and
 CC a pharmaceutical carrier or diluent, inhibiting the expression of
 CC complement component C3 in cells or tissues (comprising contacting the
 CC cells or tissues with the compound cited above) and treating an animal
 CC having a disease or condition associated with complement component C3
 CC comprising administering to the animal the compound cited above so that
 CC expression of complement component C3 is inhibited. The antisense
 CC compounds are useful for inhibiting the expression of complement
 CC component C3 in cells or tissues, or for treating an animal having a
 CC disease or condition associated with complement component C3 such as an
 CC autoimmune disorder (e.g. multiple sclerosis), an infection, or
 CC atherosclerosis, inflammation, septic shock, multiple organ failure,
 CC hyperacute organ failure and CNS inflammation. The compounds are also
 CC useful as research reagents and diagnostics, in distinguishing functions
 CC of various members of a biological pathway, or for preventing or delaying
 CC infection, inflammation or tumour formation. The present sequence is an
 CC antisense oligonucleotide shown in the sequence listing but not mentioned
 CC anywhere else in the specification.

SQ Sequence 20 BP; 2 A; 8 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 319 GAGTACAGCAAGCAGATG 336

Db 20 GAGGAGAGCAAGCAGAAG 3

RESULT 2140

ADB47630/C

ID ADB47630 standard; DNA; 20 BP.

XX ADB47630;

DT 04-DEC-2003 (first entry)

DE PCR primer #2 for Arabidopsis thaliana FCA DNA.

XX FY; flowering time; plant; FCA; RNA binding protein;

KW juvenile phase length; PCR; primer; ss.

XX Arabidopsis thaliana.

OS US2003084483-A1.

PN 01-MAY-2003.

XX 11-JUL-2002; 2002US-00192985.

XX 12-JUL-2001; 2001GB-00017054.

PR (SIMP/) SIMPSON G G.

PA (DEAN/) DEAN C.

PA (DIJK/) DIJKWEL P P.

XX Simpson GG, Dean C, Dijkwel PP;

XX WPI; 2003-687673/65.

XX New isolated nucleic acid encoding an FY polypeptide for accelerating or
 PT delaying a plants flowering time or increasing or decreasing juvenile
 PT phase length.

XX Example 7; Page 16; 22pp; English.

CC The present invention relates to the isolation of a polynucleotide
 CC sequence encoding Arabidopsis thaliana FY protein, and the encoding FY
 CC protein. The FY gene is mutated to genetically control the flowering time

CC of plants. Also disclosed are methods for using the FY polynucleotide
 CC sequence to express or down-regulate FY in plants. The methods are used
 CC in conjunction with the expression of a FCA (RNA binding protein)
 CC polynucleotide, mutant, variant, allele or derivative of it. The methods
 CC may be used to alter a flowering time or juvenile phase length in plants.
 CC The present sequence represents a PCR primer used in the examples of the
 CC present invention.

SQ Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1042 GAGCTTCCATACATGAC 1059

Db 20 GAGCTGCCAACAAATGGC 3

RESULT 2141

ADC42580
 ID ADC42580 standard; DNA; 20 BP.

XX ADC42580;

DT 18-DEC-2003 (first entry)

XX Human FANCD2 PCR primer hFANCD2_exon1_R.

DE cancer; Fanconi Anaemia; FA; BRCA; cytostatic; microarray;

KW chemosensitising; ss; PCR; primer.

XX Synthetic.

XX WO2003039327-A2.

XX 15-MAY-2003.

XX 06-JUN-2002; 2002WO-US018153.

XX 02-NOV-2001; 2001US-00998027.

XX 02-NOV-2001; 2001WO-US045561.

XX (DAND) DANA FARBER CANCER INST.

XX (UYOR-) UNIV OREGON HEALTH SCI.

XX D'andrea AD, Taniguchi T, Timmers C, Grompe M, Fox EA;

XX WPI; 2003-441436/41.

XX Diagnosing or determining cancer or increased risk of cancer in a
 PT patient, by testing Fanconi Anemia/BRCA pathway gene or protein for a
 PT cancer-associated defect, that indicates cancer or increased risk of
 PT cancer.

XX Example 14; Page 100; 160pp; English.

XX The invention relates to a novel method of diagnosing or determining if a
 CC patient has cancer or is at increased risk of cancer, involving testing a
 CC Fanconi Anaemia (FA)/BRCA pathway gene or protein for the presence of a
 CC cancer-associated defect, where the presence of one or more cancer-
 CC associated defects is indicative of cancer or an increased risk of cancer
 CC in the patient. The method of the invention has cytostatic activity. The
 CC method is useful for determining if a patient has cancer, or is at
 CC increased risk of developing cancer, e.g. breast, ovarian or prostate
 CC cancer. A microarray of the invention is useful for determining if a
 CC patient has cancer, or is at increased risk of developing cancer, by
 CC hybridising a nucleic acid sample to the nucleic acid sequences from the
 CC array, and detecting the presence of mutations in FA/BRCA pathway genes
 CC in the nucleic acid sample from the patient, where detecting the presence
 CC of mutations is indicative of a patient who has cancer, or is at
 CC increased risk of developing cancer. A method of the invention is useful
 CC for screening a chemosensitising agent, and the agent obtained is useful

CC for treating a patient having a cancer. The present sequence is used in
 CC the exemplification of the invention.
 XX
 SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1654 CCGAGCTCAGGGCAGCTG 1671
 DB 2 CCCATCTCAGGGCAGATG 19
 RESULT 2142
 ADC63313/c
 ID ADC633132 standard; DNA; 20 BP.
 XX
 AC ADC633132;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE 9'-specific lipoxigenase gene related primer, SEQ ID NO 6.
 XX
 KW 9-specific lipoxigenase; 9'-specific lipoxigenase activity; microbe;
 KW animal; plant; ss; primer.
 XX
 OS Unidentified.
 XX
 PN JP2002325577-A.
 XX
 PD 12-NOV-2002.
 XX
 PF 27-APR-2001; 2001JP-00133611.
 XX
 PR 27-APR-2001; 2001JP-00133611.
 XX
 PA (SHIS) SHISEIDO CO LTD.
 XX
 DR WPI; 2003-460714/44.
 XX
 PT A new rice-derived 9-specific lipoxigenase gene useful for production of
 PT 9-specific lipoxigenase.
 XX
 PS Example 1; SEQ ID NO 6; 17pp; Japanese.
 XX
 CC The invention relates to a novel 9-specific lipoxigenase comprising a
 CC fully defined sequence of 863 amino acid residues, as given in the
 CC specification and a derivative having 9'-specific lipoxigenase activity.
 CC The 9-specific lipoxigenase gene is useful for production of the 9-
 CC specific lipoxigenase in microbes, animal or plant cells. This
 CC polynucleotide sequence represents a primer relating to the 9'-specific
 CC lipoxigenase gene of the invention.
 XX
 SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1656 GAGCTCAGGGCAGCTGTG 1673
 DB 18 GAGCTCAGGCAAGCTCTG 1
 RESULT 2143
 ADC63313/c
 ID ADC63313 standard; DNA; 20 BP.
 XX
 AC ADC63313;
 XX
 DT 18-DEC-2003 (first entry)
 XX

DE Human BRCA1 gene, PCR primer #21.
 XX
 KW Human; BRCA1; omi1; omi2; omi3; gene pool; gene therapy;
 KW BRCA1 gene mutation; breast cancer; ovarian cancer; cytostatic; PCR;
 KW primer; ss.
 OS Homo sapiens.
 PN US2002183268-A1.
 XX
 PD 05-DEC-2002.
 XX
 PF 13-DEC-2000; 2000US-00734672.
 XX
 PR 12-FEB-1996; 96US-00598591.
 PR 07-NOV-1997; 97US-00966436.
 XX
 PA (MURP/) MURPHY P D.
 PA (ALLE/) ALLEN A C.
 PA (ALVA/) ALVARES C P.
 PA (CRIT/) CRITZ B S.
 PA (OLSO/) OLSON S J.
 PA (SCHE/) SCHELTER D B.
 PA (ZENG/) ZENG B.
 XX
 XX Murphy PD, Allen AC, Alvares CP, Critz BS, Olson SJ, Schelter DB;
 PI Zeng B;
 PI
 DR WPI; 2003-765230/72.
 XX
 PT New isolated DNA sequence of the BRCA1 coding sequence, useful for the
 PT diagnosis and treatment of disorders with BRCA1 gene mutation, such as
 PT breast and ovarian cancer.
 XX
 PS Example 1; SEQ ID NO 27; 59pp; English.
 XX
 CC The present invention relates to the isolation of a consensus DNA
 CC sequence of the human BRCA1 coding sequence (omi1), and two polymorphic
 CC coding sequences for human BRCA1 (omi2 and omi3). The gene encoding human
 CC BRCA1 maps to chromosome 17q21. Also disclosed are the three proteins
 CC encoded by these polynucleotide sequences, and a method of determining
 CC the consensus sequence for BRCA1. Omi1 represents the most commonly
 CC occurring coding sequence in the human gene pool. The coding sequences
 CC are useful for gene therapy and can be administered by direct injection
 CC into the tissue. The methods and compositions of the present invention
 CC are useful for the diagnosis and treatment of disorders with BRCA1 gene
 CC mutations, such as breast and ovarian cancer. The present sequence
 CC represents a PCR primer used for amplifying the human BRCA1 gene.
 XX
 SQ Sequence 20 BP; 6 A; 2 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 846 TGGCTCAGACTCCCTATC 863
 DB 19 TGATTTCAGACTCCCATC 2
 RESULT 2144
 ADD25305
 ID ADD25305 standard; DNA; 20 BP.
 XX
 AC ADD25305;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Hedgehog associated DNA #12.
 XX
 KW hedgehog; patched receptor; spermatogenesis inhibition;
 KW ovary function inhibition; embryogenesis;
 KW differential tissue maintenance; ds.

XX OS Unidentified.
 XX PN US6576237-B1.
 XX XX 10-JUN-2003.
 XX PF 16-AUG-2000; 2000US-00639695.
 XX PR 30-DEC-1993; 93US-00176427.
 PR 14-DEC-1994; 94US-00356060.
 PR 04-MAY-1995; 95US-00435093.
 PR 05-JUN-1995; 95US-00460900.
 XX XX (HARD) HARVARD COLLEGE.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 XX Ingham PW, McMahon AP, Tabin CJ, Bumcrot DA, Marti-Gorostiza E;
 XX WPI; 2003-799823/75.
 XX Novel isolated antibody which is immunoreactive with a vertebrate
 PT hedgehog protein sequence that binds with patched receptor, useful for
 PT blocking action of naturally occurring hedgehog protein, and for
 PT inhibiting spermatogenesis.
 XX PS Disclosure; SEQ ID NO 58; 120pp; English.
 XX CC The invention relates to an isolated antibody (I) which is immunoreactive
 CC with a hedgehog polypeptide (II) that binds to a patched receptor, where
 CC (II) is encoded by nucleic acid which hybridise to a fully defined
 CC vertebrate hedgehog (hh) protein. (I) is useful as a hedgehog antagonist
 CC by blocking action of naturally occurring hedgehog protein, and therefore
 CC for inhibiting spermatogenesis. (I) is also useful for inhibiting normal
 CC ovarian function. (I) is useful for blocking the action of one or more
 CC hedgehog proteins and allows the study of the role of these proteins
 CC e.g., embryogenesis and/or maintenance of differential tissue. (I) is
 CC also useful in immunohistochemical staining of tissue samples in order to
 CC evaluate the abundance and pattern of expression of the hedgehog
 CC polypeptides. (I) is also useful diagnostically in immunoprecipitation
 CC and immunoblotting to detect and evaluate hedgehog protein levels as a
 CC part of clinical testing procedure. The present sequence represents
 CC hedgehog associated DNA.
 XX Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1436 AAGTCACCGAGGAGGAGA 1453
 Db 1 AAGTCACCGAGGAGGAGA 18
 RESULT 2145
 ADD25275
 ID ADD25275 standard; DNA; 20 BP.
 XX AC ADD25275;
 XX XX 15-JAN-2004 (first entry)
 XX DE pWEX2 expression vector analysis primer #4.
 XX patched receptor; spermatogenesis inhibition; ovary function inhibition;
 KW embryogenesis; differential tissue maintenance; ss; primer; PCR.
 XX Synthetic.
 XX US6576237-B1.
 XX 10-JUN-2003.

XX PF 16-AUG-2000; 2000US-00639695.
 XX PR 30-DEC-1993; 93US-00176427.
 PR 14-DEC-1994; 94US-00356060.
 PR 04-MAY-1995; 95US-00435093.
 PR 05-JUN-1995; 95US-00460900.
 XX XX (HARD) HARVARD COLLEGE.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 XX Ingham PW, McMahon AP, Tabin CJ, Bumcrot DA, Marti-Gorostiza E;
 XX WPI; 2003-799823/75.
 XX Novel isolated antibody which is immunoreactive with a vertebrate
 PT hedgehog protein sequence that binds with patched receptor, useful for
 PT blocking action of naturally occurring hedgehog protein, and for
 PT inhibiting spermatogenesis.
 XX PS Example 2; SEQ ID NO 28; 120pp; English.
 XX CC The invention relates to an isolated antibody (I) which is immunoreactive
 CC with a hedgehog polypeptide (II) that binds to a patched receptor, where
 CC (II) is encoded by nucleic acid which hybridise to a fully defined
 CC vertebrate hedgehog (hh) protein. (I) is useful as a hedgehog antagonist
 CC by blocking action of naturally occurring hedgehog protein, and therefore
 CC for inhibiting spermatogenesis. (I) is also useful for inhibiting normal
 CC ovarian function. (I) is useful for blocking the action of one or more
 CC hedgehog proteins and allows the study of the role of these proteins
 CC e.g., embryogenesis and/or maintenance of differential tissue. (I) is
 CC also useful in immunohistochemical staining of tissue samples in order to
 CC evaluate the abundance and pattern of expression of the hedgehog
 CC polypeptides. (I) is also useful diagnostically in immunoprecipitation
 CC and immunoblotting to detect and evaluate hedgehog protein levels as a
 CC part of clinical testing procedure. The present sequence represents an
 CC oligonucleotide used in the construction of the pWEX2 expression vector.
 XX Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1436 AAGTCACCGAGGAGGAGA 1453
 Db 1 AAGTCACCGAGGAGGAGA 18
 RESULT 2146
 ADD19989/c
 ID ADD19989 standard; DNA; 20 BP.
 XX AC ADD19989;
 XX DT 15-JAN-2004 (first entry)
 XX DE Oreochromis niloticus microsatellite primer SEQ ID NO:624.
 XX single nucleotide polymorphism; SNP; fish; Salmo salar;
 KW Oreochromis niloticus; Atlantic halibut; microsatellite; cod;
 KW polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;
 KW detection; primer; ss.
 XX OS Synthetic.
 OS Oreochromis niloticus.
 XX PN WO2003060160-A2.
 XX 24-JUL-2003.
 XX PF 17-JAN-2003; 2003WO-IB000112.
 XX

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PR 18-JAN-2002; 2002US-0349950P.
PR 16-AUG-2002; 2002US-0404200P.
XX
XX
XX (GENO-) GENOMAR ASA.
XX
XX Lie O, Slettan A, Hoyum M, Lingaas F;
XX WPI; 2003-627388/59.
XX
XX Novel isolated nucleic acid molecule comprising single nucleotide
XX polymorphism associated with fish, useful for forming PCR primers which
XX are used for detecting single nucleotide polymorphisms in fish nucleic
XX acids.
XX
XX Claim 18; SEQ ID NO 624; 233bp; English.
XX
XX The present invention describes an isolated nucleic acid (I) comprising a
XX single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of
XX Salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic halibut SNPs;
XX and (ii) a nucleic acid having nucleotide sequence that hybridises to
XX (i), or its complement under highly stringent hybridisation conditions.
XX Also described: (1) an isolated oligonucleotide (II) comprising at least
XX 17 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O.
XX niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
XX polymorphic sites and seabass polymorphic sites; or their complement; (2)
XX a primer pair (III) suitable for use in PCR, comprising two (II) capable
XX of amplifying a nucleotide sequence chosen from S. salar SNPs and, O.
XX niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
XX polymorphic sites and seabass polymorphic sites; and determining (M1) the
XX origin of fish sample comprising providing a parentage genotype database
XX candidate parent genotype represents a distinct origin, and comparing a
XX sample genotype to the parentage genotype database, where a match between
XX the sample genotype and one of the candidate parent genotype identifies
XX to the origin of the sample. (M1) is useful for determining the origin of
XX a fish sample such as family salmonidae, S. salar, Tilapia, O. niloticus,
XX rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for
XX detecting nucleic acid molecule comprising SNP in a sample, which
XX involves contacting the sample containing nucleic acids with one or more
XX (II) derived from nucleotide sequence of S. salar SNPs and O. niloticus
XX SNPs, and identifying nucleic acid that hybridises to (II). (II) is
XX useful for detecting nucleic acid molecule comprising a polymorphic
XX sequence in a sample, comprising contacting the sample containing nucleic
XX acids with one or more (II) which is derived from O. niloticus
XX microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic
XX sites or seabass polymorphic sites, and identifying a nucleic acid that
XX hybridises to (II). (III) is useful for detecting nucleic acid molecule
XX comprising a microsatellite sequence in sample. The present sequence is
XX used in the exemplification of the present invention.
XX
XX SQ Sequence 20 BP; 3 A; 1 C; 8 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX Qy 149 CAATGAGCCTCACCAGAA 166
XX ||||| ||||| ||||| |||||
XX Db 18 CAATAAGCCTCCGCCAA 1
XX
XX RESULT 2147
XX ID ADD20570 standard; DNA; 20 BP.
XX
XX AC ADD20570;
XX
XX DT 15-JAN-2004 (first entry)
XX
XX DE Oreochromis niloticus microsatellite primer SEQ ID NO:1205.
XX
XX KW single nucleotide polymorphism; SNP; fish; Salmo salar;
XX Oreochromis niloticus; Atlantic halibut; microsatellite; cod;

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KW polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;
KW detection; primer; ss.
XX
XX Synthetic.
XX Oreochromis niloticus.
XX WO2003060160-A2.
XX
XX 24-JUL-2003.
XX
XX 17-JAN-2003; 2003WO-IB000112.
XX
XX 18-JAN-2002; 2002US-0349950P.
XX 16-AUG-2002; 2002US-0404200P.
XX (GENO-) GENOMAR ASA.
XX
XX Lie O, Slettan A, Hoyum M, Lingaas F;
XX WPI; 2003-627388/59.
XX
XX Novel isolated nucleic acid molecule comprising single nucleotide
XX polymorphism associated with fish, useful for forming PCR primers which
XX are used for detecting single nucleotide polymorphisms in fish nucleic
XX acids.
XX
XX Claim 18; SEQ ID NO 1205; 233bp; English.
XX
XX The present invention describes an isolated nucleic acid (I) comprising a
XX single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of
XX Salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic halibut SNPs;
XX and (ii) a nucleic acid having nucleotide sequence that hybridises to
XX (i), or its complement under highly stringent hybridisation conditions.
XX Also described: (1) an isolated oligonucleotide (II) comprising at least
XX 17 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O.
XX niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
XX polymorphic sites and seabass polymorphic sites; or their complement; (2)
XX a primer pair (III) suitable for use in PCR, comprising two (II) capable
XX of amplifying a nucleotide sequence chosen from S. salar SNPs and, O.
XX niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
XX polymorphic sites and seabass polymorphic sites; and determining (M1) the
XX origin of fish sample comprising providing a parentage genotype database
XX candidate parent genotype represents a distinct origin, and comparing a
XX sample genotype to the parentage genotype database, where a match between
XX the sample genotype and one of the candidate parent genotype identifies
XX to the origin of the sample. (M1) is useful for determining the origin of
XX a fish sample such as family salmonidae, S. salar, Tilapia, O. niloticus,
XX rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for
XX detecting nucleic acid molecule comprising SNP in a sample, which
XX involves contacting the sample containing nucleic acids with one or more
XX (II) derived from nucleotide sequence of S. salar SNPs and O. niloticus
XX SNPs, and identifying nucleic acid that hybridises to (II). (II) is
XX useful for detecting nucleic acid molecule comprising a polymorphic
XX sequence in a sample, comprising contacting the sample containing nucleic
XX acids with one or more (II) which is derived from O. niloticus
XX microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic
XX sites or seabass polymorphic sites, and identifying a nucleic acid that
XX hybridises to (II). (III) is useful for detecting nucleic acid molecule
XX comprising a microsatellite sequence in sample. The present sequence is
XX used in the exemplification of the present invention.
XX
XX SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX Qy 1159 CTGTTTGAGACCTTAGA 1176
XX ||||| ||||| ||||| |||||
XX Db 2 CTGTGGAGCACCTTTGA 19

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RESULT 2148
ADD21672/c
ID ADD21672 standard; DNA; 20 BP.
XX
XX
AC ADD21672;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human mdm2 antisense oligonucleotide #235.
XX
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX atherosclerosis; restenosis; apoptosis modulation; p21; ss;
XX 2'-methoxyethoxy-residue; phosphorothioate backbone.
XX
XX Homo sapiens.
XX
XX WO2003048315-A2.
XX
XX 12-JUN-2003.
XX
XX 02-DEC-2002; 2002WO-US038281.
XX
XX 04-DEC-2001; 2001US-00005344.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY;
XX Manoharan M;
XX
XX WPI; 2003-577263/54.
XX
XX Novel antisense compound targeted to 5' untranslated region, coding
XX region, or intron:exon junction of nucleic acid molecule encoding mdm2,
XX useful for treating e.g. cancer, psoriasis or restenosis by inhibiting
XX mdm2 expression.
XX
XX Claim 4; SEQ ID NO 246; 289pp; English.
XX
XX The invention comprises antisense oligonucleotides which are targeted to
XX the human mdm2 gene. The antisense oligonucleotides of the invention are
XX useful for reducing hyperproliferation of human cells. The antisense
XX oligonucleotides are also useful for treating: hyperproliferative
XX disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or
XX restenosis. The antisense oligonucleotides are also useful for modulating
XX apoptosis, and for increasing expression of p21. The present DNA sequence
XX represents a human mdm2 gene antisense oligonucleotide of the invention.
XX The present sequence contains 2'-methoxyethoxy-residues and has a
XX phosphorothioate backbone.
XX
XX Sequence 20 BP; 11 A; 2 C; 1 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1613 TTATTAAATATATATAT 1630
XX 19 TTCTTAATATATATATAT 2
XX
XX RESULT 2149
ADD21681
ID ADD21681 standard; DNA; 20 BP.
XX
XX AC ADD21681;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human mdm2 antisense oligonucleotide #244.
XX
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1613 TTATTAAATATATATAT 1630
XX 19 TTCTTAATATATATATAT 2
XX
XX RESULT 2150
ADD18145
ID ADD18145 standard; DNA; 20 BP.
XX
XX AC ADD18145;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human G-protein coupled receptor (GPCR) related PCR primer Seq ID44.
XX
XX G protein coupled receptor; GPCR; signal transduction pathway; G protein;
XX Alzheimer's disease; Parkinson's disease; diabetes; dwarfism;
XX colour blindness; retinal pigmentosa; asthma; depression; schizophrenia;
XX sleeplessness; hypertension; anxiety; stress; renal failure;
XX cardiovascular disorder; neural disorder; oncology disorder;
XX immune disorder; neuroprotective; gene therapy; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX WO2003016478-A2.
XX
XX 27-FEB-2003.
XX
XX 15-AUG-2002; 2002WO-US026017.
XX

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KW atherosclerosis; restenosis; apoptosis modulation; p21; ss;
KW 2'-methoxyethoxy-residue; phosphorothioate backbone.
XX
XX Homo sapiens.
XX
XX WO2003048315-A2.
XX
XX 12-JUN-2003.
XX
XX 02-DEC-2002; 2002WO-US038281.
XX
XX 04-DEC-2001; 2001US-00005344.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY;
XX Manoharan M;
XX
XX WPI; 2003-577263/54.
XX
XX Novel antisense compound targeted to 5' untranslated region, coding
XX region, or intron:exon junction of nucleic acid molecule encoding mdm2,
XX useful for treating e.g. cancer, psoriasis or restenosis by inhibiting
XX mdm2 expression.
XX
XX Claim 4; SEQ ID NO 246; 289pp; English.
XX
XX The invention comprises antisense oligonucleotides which are targeted to
XX the human mdm2 gene. The antisense oligonucleotides of the invention are
XX useful for reducing hyperproliferation of human cells. The antisense
XX oligonucleotides are also useful for treating: hyperproliferative
XX disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or
XX restenosis. The antisense oligonucleotides are also useful for modulating
XX apoptosis, and for increasing expression of p21. The present DNA sequence
XX represents a human mdm2 gene antisense oligonucleotide of the invention.
XX The present sequence contains 2'-methoxyethoxy-residues and has a
XX phosphorothioate backbone.
XX
XX Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 13.2; DB 1; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1951 GCTCTAAGTGAGCCCAAGA 1968
XX ||| ||||| |||||
XX 3 GCTTGCAGTGAGCCCAAGA 20
XX
XX RESULT 2150
ADD18145
ID ADD18145 standard; DNA; 20 BP.
XX
XX AC ADD18145;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human G-protein coupled receptor (GPCR) related PCR primer Seq ID44.
XX
XX G protein coupled receptor; GPCR; signal transduction pathway; G protein;
XX Alzheimer's disease; Parkinson's disease; diabetes; dwarfism;
XX colour blindness; retinal pigmentosa; asthma; depression; schizophrenia;
XX sleeplessness; hypertension; anxiety; stress; renal failure;
XX cardiovascular disorder; neural disorder; oncology disorder;
XX immune disorder; neuroprotective; gene therapy; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX WO2003016478-A2.
XX
XX 27-FEB-2003.
XX
XX 15-AUG-2002; 2002WO-US026017.
XX

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XX 20-AUG-2001; 2001US-0313658P.
PR 12-SEP-2001; 2001US-0318675P.
PR 30-OCT-2001; 2001US-0340703P.
PR 26-NOV-2001; 2001US-0333417P.
PR 06-DEC-2001; 2001US-0338367P.
PR 06-FEB-2002; 2002US-035596P.
XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX PI Feder JN, Ramanathan CS, Gopal S, Mintier GA;
XX WPI; 2003-278558/27.
XX New nucleic acid, useful for manufacturing a medicament for preventing,
PT treating or ameliorating a medical condition e.g., neural disorder.
XX Example 1; SEQ ID NO 44; 251pp; English.
XX This invention relates to novel G protein coupled receptors (GPCRs) and
CC their encoding nucleotide sequences. Many medically significant
CC biological processes are mediated by proteins participating in signal
CC transduction pathways involving G proteins. GPCRs are one of the largest
CC receptor superfamilies known. These receptors are biologically important
CC and malfunction of these receptors results in diseases such as
CC Alzheimer's, Parkinson's, diabetes, dwarfism, colour blindness, retinal
CC pigmentosa and asthma. They are also involved in depression,
CC schizophrenia, sleeplessness, hypertension, anxiety, stress, renal
CC failure and other cardiovascular, neural, oncology and immune disorders.
CC A modulator of the GPCRs of the invention may have neuroprotective
CC activity whilst the sequences of the invention may be useful for gene
CC therapy. The invention may also be useful for manufacturing a medicament
CC for preventing, treating or ameliorating a medical condition. The present
CC sequence is that of a PCR primer which was used for amplification of a
CC region of a gene encoding a human GPCR during the exemplification of the
CC invention.
XX SQ Sequence 20 BP; 9 A; 3 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1460 AGGAGGAGAGCCGAGG 1477
DB 3 AGGAGGAGAGCCGAGTG 20
RESULT 2151
AAD61223
ID AAD61223 standard; DNA; 20 BP.
XX AC AAD61223;
XX DT 15-JAN-2004 (first entry)
XX DE Human Ship-1 antisense oligonucleotide ISIS #168304.
XX KW Human; Ship-1; SH2-containing phosphatidylinositol phosphatase-1; INPP5D;
KW insensitivity to apoptotic signal; developmental disorder; inflammation;
KW immunosuppressive; autoimmune disorder; antisense therapy; antisense;
KW phosphorothioate backbone; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methyl cytidines"
FT modified_base 1..5
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FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
XX PN US2003114401-A1.
XX PD 19-JUN-2003.
XX PF 06-DEC-2001; 2001US-00003919.
XX PR 06-DEC-2001; 2001US-00003919.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Freier SM;
XX WPI; 2003-801302/75.
XX Antisense compounds targeted to nucleic acid molecule encoding Ship-1,
PT useful for treating diseases associated with expression of Ship-1, such
PT as autoimmune and developmental disorders.
XX Claim 3; Page 25; Opp; English.
XX The present invention provides antisense compounds targetted to nucleic
CC acid molecule encoding Ship-1 (also known as SH2-containing
CC phosphatidylinositol phosphatase-1 and INPP5D) to modulate/inhibit the
CC expression of Ship-1. The invention is useful in treatment of diseases
CC such as insensitivity to apoptotic signals, autoimmune disorders,
CC developmental disorders and inflammatory disorders. The present sequence
CC is human Ship-1 antisense oligonucleotide
XX SQ Sequence 20 BP; 6 A; 6 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1631 CCCGAGGAGACAGAAACCA 1648
DB 2 CCCCTTGGAGAGAAACCA 19
RESULT 2152
AAD62109
ID AAD62109 standard; DNA; 20 BP.
XX AC AAD62109;
XX DT 15-JAN-2004 (first entry)
XX DE Chicken sonic hedgehog specific DNA amplifying PCR primer, 924.
XX KW Chicken; cell differentiation; Desert hedgehog; Dhh; Sonic hedgehog; shh;
KW Indian hedgehog; Ihh; skeletogenesis; degenerative disorder; ischaemia;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW Huntington's disease; multiple sclerosis; Pick's disease; aging process;
KW trauma; anoxia; antisense gene therapy; neuroprotective; anticonvulsant;
KW neurotropic; PCR; primer; ss.
XX OS Gallus sp.
XX PN US2003186357-A1.
XX PD 02-OCT-2003.
XX PF 05-JUN-1995; 95US-00462386.
XX PR 30-DEC-1993; 93US-00176427.
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PR 14-DEC-1994; 94US-00356060.
PR 04-MAY-1995; 95US-00435093.
XX
XX
PA (INGH/) INGHAM P W.
PA (MCMA/) MCMAHON A P.
PA (TABIN/) TABIN C J.
XX
XX
PI Ingham PW, McMahon AP, Tabin CJ;
XX
XX WPI; 2003-803151/75.
DR
XX
XX Modulating cell growth, differentiation or survival, for treating
PT neurodegenerative diseases, such as Alzheimer's or Parkinson's disease,
PT comprises contacting the cell with a hedgehog polypeptide.
XX
XX
PS Example 2; Page 39; Opp; English.
XX
XX The present invention relates to a novel method for modulating growth,
CC differentiation or survival of a cell. The method involves contacting the
CC cell with a hedgehog polypeptide such as Desert hedgehog (Dhh), Sonic
CC hedgehog (shh) and Indian hedgehog (Ihh). The method is used to induce a
CC cell to differentiate to a neuronal cell phenotype. It is used to
CC modulate skeletogenesis. The method is used to treat a degenerative
CC disorders of the nervous system such as neuromuscular, autonomic or
CC central nervous system disorders (e.g., Alzheimer's disease, Parkinson's
CC disease, amyotrophic lateral sclerosis, Huntington's disease, multiple
CC sclerosis, Pick's disease, neuronal degeneration associated with a
CC natural aging process and neuronal damage resulting from trauma and
CC neuronal damage resulting from anoxia-ischaemia. The invention is also
CC used for antisense gene therapy. The present sequence is chicken Shh
CC specific DNA amplifying PCR primer. This sequence is used in the
CC exemplification of the invention
XX
XX Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1436 AAGTCACCGAAGAGGAGA 1453
Db 1 AAGTCAGCCCGAGGAGA 18
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
RESULT 2153
ADD71398
ID ADD71398 standard; DNA; 20 BP.
XX
XX AC ADD71398;
XX
XX 15-JAN-2004 (first entry)
DE Mouse wnt-1 related oligonucleotide seqid 28.
XX
XX hedgehog polypeptide; tissue array generation; tissue array maintainance;
KW mouse; wnt-1; ss.
XX
XX Synthetic.
OS
XX
XX US2003190696-A1.
PN
XX
XX 09-OCT-2003.
PD
XX
XX 13-DEC-2000; 2000US-00736476.
PF
XX
XX 30-DEC-1993; 93US-00176427.
PR
XX 14-DEC-1994; 94US-00356060.
PR
XX 04-MAY-1995; 95US-00435093.
PR
XX 05-JUN-1995; 95US-00460900.
XX
XX (HARD ) HARVARD COLLEGE.
PA
XX
XX Ingham PW, McMahon AP, Tabin CJ, Bumcrot DA, Marti-Gorostiza E;
PI
```

```
XX
DR
XX WPI; 2003-831623/77.
XX
XX New nucleic acid encoding a hedgehog polypeptide having an amino acid
PT sequence identical or homologous to a vertebrate hedgehog protein, useful
PT for generating or maintaining an array of different vertebrate tissue in
PT vitro and in vivo.
XX
XX
XX Example 2; SEQ ID NO 28; 118pp; English.
PS
XX
XX The invention describes an isolated nucleic acid encoding a hedgehog
CC polypeptide having an amino acid sequence identical or homologous to a
CC vertebrate hedgehog protein or its portion and not identical to a fully
CC defined 471-bp sequence. The nucleic acid is useful for generating and/or
CC maintaining an array of different vertebrate tissue both in vitro and in
CC vivo. This sequence represents an oligonucleotide associated with the
CC creation of a plasmid for expression of mouse wnt-1.
XX
XX Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1436 AAGTCACCGAAGAGGAGA 1453
Db 1 AAGTCAGCCCGAGGAGA 18
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
RESULT 2154
ADD69015
ID ADD69015 standard; DNA; 20 BP.
XX
XX AC ADD69015;
XX
XX 15-JAN-2004 (first entry)
DT
XX
XX Human B-cell associated protein-targeted antisense oligo - SED ID 82.
DE
XX
XX B-cell associated protein; BAP; cytostatic; antiinflammatory;
KW antimicrobial; antisense therapy; hyperproliferative; breast;
KW prostate cancer; apoptosis; infection; inflammation; human; ss;
KW phosphorothioate backbone; 2'-MOE wing; 2'-methoxyethyl.
XX
XX
XX Homo sapiens.
OS
XX
XX WO2003052065-A2.
PN
XX
XX 26-JUN-2003.
PD
XX
XX 10-DEC-2002; 2002WO-US039580.
PF
XX
XX 13-DEC-2001; 2001US-00020478.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Bennett CF, Dobie KW;
PI
XX
XX WPI; 2003-569148/53.
DR
XX
XX New antisense compound that hybridizes and inhibits a nucleic acid
PT encoding a B-cell associated protein, useful for treating animal having
PT disease or condition associated with B-cell associated protein, e.g.
PT cancer.
XX
XX
XX Example 15; SEQ ID NO 82; 107pp; English.
PS
XX
XX The invention relates to a novel compound targeted to a nucleic acid
CC molecule encoding a B-cell associated protein (BAP), where the compound
CC specifically hybridises with the nucleic acid and inhibits expression of
CC the protein. The compound of the invention demonstrates cytostatic,
CC antiinflammatory and antimicrobial activities and may be useful for
CC inhibiting the expression of BAP in cells or tissues thus, via antisense
```

CC therapy, preventing a hyperproliferative disorder such as cancer,
 CC particularly breast or prostate cancer, as well as a disorder
 CC characterised by altered levels of apoptosis, infection or inflammation.
 CC The current sequence is that of the human B-cell associated protein-
 CC targeted antisense oligonucleotide of the invention which comprises 2'-
 CC MOE (2'-methoxyethyl) "wings" and a phosphorothioate backbone. In
 CC addition, all cytidine residues are 5' methylcytidines.
 XX
 SQ Sequence 20 BP; 9 A; 1 C; 2 G; 8 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1607 TAAAAATTATTAAATAT 1624
 |||||
 Db 1 TAAAAATTATTGAGAT 18
 |||||
 RESULT 2155
 ADD29134
 ID ADD29134 standard; DNA; 20 BP.
 XX
 AC ADD29134;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Nitrication bacteria 16s rRNA PCR primer EUB2.
 XX
 KW Nitrication bacteria; 16s rRNA; PCR; primer; ss; aquarium water;
 KW fermented solution; ginkgo tree; ganoderma; chestnut tree bark; acorn;
 KW evergreen oak tree; bamboo; persimmon tree; pine tree; chitosan powder;
 KW barley natural stone powder; bamboo salt; potato starch;
 KW aquarium fish breeding; eutrophication; fish-like smell;
 KW interior-air-pollution; heavy metal pollution; copper; phosphorus;
 KW gill decay; wound; loss of appetite; stress.
 XX
 OS Eubacteria .
 XX
 XX US5528062-B1.
 XX
 XX 04-MAR-2003.
 XX
 XX 19-JUN-2001; 2001US-00883405.
 XX
 XX 12-MAY-2001; 2001KR-00026000.
 XX
 XX (KOST-) KOSTARWORLD CO LTD.
 XX
 XX Kim J;
 XX
 XX WPI; 2003-810318/76.
 XX
 XX Aquarium water for breeding fish, contains mixture of extracts from
 XX leaves of ginkgo tree, ganoderma, bark of chestnut tree, acorns, leaves
 XX of evergreen oak tree, bamboo, leaves of persimmon tree and leaves of
 XX pine tree.
 XX
 XX Disclosure; SEQ ID NO 2; 11pp; English.
 XX
 CC The invention relates to aquarium water comprising a fermented solution
 CC of a mixture of an extract from leaves of ginkgo tree, extract from
 CC ganoderma, extract from bark of chestnut tree, extract from acorns,
 CC extract from leaves of evergreen oak tree, extract from bamboo, extract
 CC from leaves of persimmon tree, extract from leaves of pine tree, water-
 CC soluble chitosan powder, barley natural stone powder, bamboo salt, potato
 CC starch, and distilled water. Yeast is added and fermented. Organic
 CC germanium, mineral component extracted from yellow soil, and extract from
 CC combustion of oak trees are added, fermented again and refined to a
 CC liquid state. The aquarium water and water ratio is 1:4. Also included is
 CC the preparation of aquarium water by adding a mixture of extracts to a
 CC fermentation solution which is then fermented by mixing yeast. The
 CC aquarium water is for use in breeding fish, especially aquarium fish. The

CC incorporation of extract mixture accelerates multiplication and
 CC activation of the nitrification bacteria, increases the amount of oxygen
 CC dissolved by preventing eutrophication, enables easy breeding of aquarium
 CC fishes without the need for replacement of aquarium water by preventing
 CC fish-like smell and removing interior-air-pollution materials, and forms
 CC a pleasant in-aquarium and peripheral environment. The extract mixture
 CC suppresses generation of moss, green algae and yellow algae, decomposes
 CC harmful heavy metals such as copper and phosphorus, prevents decay of
 CC gills of aquarium fishes, helps cure wounds of aquarium fish, prevents
 CC generation of germs, prevents decay of aquarium water by maintaining the
 CC amount of oxygen dissolved in aquarium water at high level and increases
 CC nutritious components and immunity in case of loss of appetite of
 CC aquarium fishes due to stress. The present sequence is a Nitrification
 CC bacteria 16s rRNA PCR primer, used to check the level of nitrification
 CC bacteria.
 XX
 SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
 Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 807 AATGGAGATGTTCCAGCC 824
 |||||
 Db 3 AAAGGAGTGATCCAGCC 20
 |||||
 RESULT 2156
 ADD42149
 ID ADD42149 standard; DNA; 20 BP.
 XX
 AC ADD42149;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human infertility associated primer SEQ ID 10.
 XX
 KW primer; male infertility; infertility-associated mutation;
 KW azoospermia factor; Y-chromosome;
 KW cystic fibrosis transmembrane conductance regulator; CTFR;
 KW Kallmann syndrome; KALI; androgen resistance; steroid 21-hydroxylase;
 KW CYP21; microarray; quantitative trait locus; in vitro fertilization;
 KW oligospermia; SS..
 XX
 OS Homo sapiens.
 XX
 XX WO2003050299-A2.
 XX
 XX 19-JUN-2003.
 XX
 XX 10-DEC-2002; 2002WO-EP013995.
 XX
 XX 10-DEC-2001; 2001DE-01060563.
 XX
 XX (OGHA-) OGHAM GMBH.
 XX
 XX Cullen P, Seedorf U;
 XX
 XX WPI; 2003-505402/47.
 XX
 XX Investigating male genetic infertility, useful for diagnosis e.g. for
 XX assessing suitability for in vitro fertilization, based on multifactorial
 XX analysis of infertility-related mutations.
 XX
 XX Claim 13; SEQ ID NO 10; 110pp; German.
 XX
 CC This invention describes a novel method for investigating genetic
 CC infertility or predisposition in males. The method involves selecting at
 CC least two infertility-associated mutations which are recessive or
 CC intermediate that are associated with infertility in the heterozygous
 CC state and/or only in the homozygous state. Preferably at least one
 CC azoospermia factor is detected which may be lost by microdeletions in
 CC intervals 5 or 6 of the Y-chromosome. Also any of several hundred

CC mutations, listed, present in the cystic fibrosis transmembrane
 CC conductance regulator (CFTR), Kallmann syndrome (KAL1), androgen
 CC resistance (AR) or steroid 21-hydroxylase (CYP21) genes may be detected.
 CC Probes for the mutated genes and/or native nucleic acid, or their
 CC complementary strands, are fixed to a carrier, particularly as a
 CC microarray, then tested for hybridization with oligonucleotides from or
 CC synthesized from, a patient sample and hybridization detected.
 CC Multifactorial analysis is by standard statistical methods, particularly
 CC the quantitative trait locus method. The method is used to diagnose
 CC inherited male infertility or predisposition to its, especially in
 CC conjunction with in vitro fertilization programs, e.g. for assessing
 CC subjects with oligospermia for possible application of the
 CC intracytoplasmic sperm injection method. Analysis of many mutations
 CC improves diagnosis of the genetic basis of male infertility, including
 CC polygenic origins (complex interactions between different heterozygotic
 CC mutations). A chip for analyzing genetic infertility in males comprises
 CC oligonucleotides that represent known mutations (nonsense or missense,
 CC insertions, allelic variants deletions or rearrangements) in the cystic
 CC fibrosis transmembrane conductance regulator, Kallmann syndrome, androgen
 CC resistance and steroid 21-hydroxylase genes. ADD42140-ADD42633 represent
 CC oligonucleotides used in the microarray described in the method of the
 CC invention. NOTE: there are no SEQ ID's 133, 472 or 473 represented in the
 CC SEQ ID list of the specification.

XX Sequence 20 BP; 9 A; 1 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1397 CAGAGATGTAAGAGAGA 1414
 ||||| ||||| |||||
 Db 2 CAGAGATGGAATAGAGA 19

RESULT 2157

ADD56742
 ID ADD56742 standard; DNA; 20 BP.

AC ADD56742;

DT 15-JAN-2004 (first entry)

XX Human gene expression analysis multiplex Start-PCR primer #262.

XX Gene expression; multiplex standardised reverse transcriptase-PCR;
 KW Start-PCR; high density oligonucleotide array; cDNA array;
 KW small biological sample; fine needle aspirate biopsy;
 KW laser captured microdissected material; human; primer; ss.

XX Homo sapiens.

XX US2003186246-A1.

XX 02-OCT-2003.

XX 28-MAR-2002; 2002US-00109349.

XX 28-MAR-2002; 2002US-00109349.

XX (WILL/) WILLEY J C.

PA (CRAW/) CRAWFORD E L.

XX Willey JC, Crawford EL;

XX WPI; 2003-811730/76.

XX Direct comparison of numerical gene expression values between samples of
 PT genes comprises using multiplex standardized reverse transcription-
 PT polymerase chain reaction.

XX Example 1; SEQ ID NO 262; 59pp; English.

CC The present invention relates to a method for the direct comparison of
 CC numerical gene expression values between samples of genes. The method
 CC comprises amplifying cDNA in the presence of a competitive template
 CC mixture and primer pairs for several genes and then amplifying aliquots
 CC of the PCR products using a primer pair specific for each gene. The
 CC method of amplification is by multiplex standardised reverse
 CC transcriptase-polymerase chain reaction (Start-PCR). High density
 CC oligonucleotide or cDNA arrays are used to measure PCR products following
 CC quantitative Start-PCR. The method is useful for the assessment of gene
 CC expression in small biological samples such as fine needle aspirate
 CC biopsies, and laser captured microdissected materials. The method allows
 CC for the standardised measurement of hundreds of genes from the same
 CC sample, which in prior art, could only be assessed for one gene. The
 CC present sequence represents a multiplex Start-PCR primer which can be
 CC used in the method of the present invention.

XX Sequence 20 BP; 8 A; 1 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 708 GGCTGGCAAGGCAAGTA 725
 || ||||| |||||
 Db 2 GGCTGGCAAGGCAAGTA 19

RESULT 2158

ADE77579
 ID ADE77579 standard; DNA; 20 BP.

AC ADE77579;

DT 29-JAN-2004 (first entry)

XX DRB3*0201 probe designed to analyse the HLA-DRB polymorphic region.

XX HLA-DRB; probe; ss; human; multiplexed elongation assay;

XX enzymatic recognition;

XX cystic fibrosis conductance transmembrane regulator; CFTR;

XX human leukocyte antigen; HLA; genetic testing; carrier screening;

XX genotyping; profiling; polymorphic.

XX Homo sapiens.

XX WO2003034029-A2.

XX 24-APR-2003.

XX 15-OCT-2002; 2002WO-US033012.

XX 15-OCT-2001; 2001US-0329427P.

XX 15-OCT-2001; 2001US-0329428P.

XX 15-OCT-2001; 2001US-0329619P.

XX 15-OCT-2001; 2001US-0329620P.

XX 14-MAR-2002; 2002US-0364416P.

XX (BIOA-) BIOARRAY SOLUTIONS LTD.

XX Li AX, Hashmi G, Seul M;

XX WPI; 2003-393553/37.

XX Concurrent interrogation of a number of polymorphic sites, useful for
 PT genetic testing, carrier screening, genetic profiling, and identity
 PT testing, comprises conducting a multiplexed elongation assay using
 PT probes.

XX Example 2; Page 38; 143pp; English.

XX This invention relates to a novel method for the concurrent interrogation
 CC of a number of polymorphic sites in the presence of, and without
 CC interference from, non-designated polymorphic sites. Specifically, it


```
Db      3 CCAGCAGGAGAGACAGA 20
      ||| ||||| |||||
RESULT 2161
ACA98739
ID ACA98739 standard; DNA; 19 BP.
XX
AC ACA98739;
XX
XX 28-JUL-2003 (first entry)
XX
XX Human CYP2C8 SNP detection PCR primer #179.
XX
XX Cytochrome P450 polypeptide 2C8; CYP2C8; arachidonic acid metabolism;
XX cancer; cardiovascular disease; cytostatic; cardiovascular; gene therapy;
XX single nucleotide polymorphism detection; SNP detection; PCR; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200299099-A2.
XX
XX 12-DEC-2002.
XX
XX 31-MAY-2002; 2002WO-EP006000.
XX
XX 01-JUN-2001; 2001EP-00112899.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Penger A, Sprenger R, Brinkmann U;
XX
XX WPI; 2003-167344/16.
XX
XX New polymorphic variants of the gene encoding Cytochrome P450 polypeptide
XX 2C8 (CYP2C8), useful for diagnosing or treating a disease, e.g.
XX arachidonic acid metabolism, cancer or cardiovascular diseases.
XX
XX Example 2; Page 52; 178pp; English.
XX
XX The invention describes a new polynucleotide comprises a polynucleotide:
XX (a) having any of 101 nucleic acid sequences with 18-19 bp fully defined
XX in the specification; (b) encoding any of seven polypeptides having 7
XX amino acids, or a polypeptide with 3 amino acids; (c) capable of
XX hybridizing to a Cytochrome P450 polypeptide 2C8 (CYP2C8) gene; (d)
XX encoding a molecular CYP2C8 variant polypeptide or its fragment. The
XX polynucleotide, gene, vector, polypeptide or antibody is useful for
XX diagnosing or treating a disease, for preparing a diagnostic composition
XX for diagnosing a disease, or for preparing a pharmaceutical composition
XX for treating a disease. This disease includes arachidonic acid
XX metabolism, cancer or cardiovascular diseases. This sequence represents a
XX primer used to isolate regions of the human cytochrome P450 polypeptide
XX 2C8 gene (CYP2C8) in order to identify the single nucleotide polymorphism
XX (SNP) in that region of different individuals useful in disease diagnosis
XX
XX Sequence 19 BP; 10 A; 0 C; 0 G; 8 T; 0 U; 1 Other;
XX
XX Query Match 0.6%; Score 13; DB 1; Length 19;
XX Best Local Similarity 86.7%; Pred. No. 1.3e+03;
XX Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1600 ATTTATATAAAATT 1614
XX ||||| |||||
XX Db 3 ATTTTAWAAAAATT 17
XX
RESULT 2162
ACA98736/c
ID ACA98736 standard; DNA; 19 BP.
XX
AC ACA98736;
XX
XX 28-JUL-2003 (first entry)
XX
XX Human CYP2C8 SNP detection PCR primer #176.
XX
XX Cytochrome P450 polypeptide 2C8; CYP2C8; arachidonic acid metabolism;
XX cancer; cardiovascular disease; cytostatic; cardiovascular; gene therapy;
XX single nucleotide polymorphism detection; SNP detection; PCR; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200299099-A2.
XX
XX 12-DEC-2002.
XX
XX 31-MAY-2002; 2002WO-EP006000.
XX
XX 01-JUN-2001; 2001EP-00112899.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Penger A, Sprenger R, Brinkmann U;
XX
XX WPI; 2003-167344/16.
XX
XX New polymorphic variants of the gene encoding Cytochrome P450 polypeptide
XX 2C8 (CYP2C8), useful for diagnosing or treating a disease, e.g.
XX arachidonic acid metabolism, cancer or cardiovascular diseases.
XX
XX Example 2; Page 52; 178pp; English.
XX
XX The invention describes a new polynucleotide comprises a polynucleotide:
XX (a) having any of 101 nucleic acid sequences with 18-19 bp fully defined
XX in the specification; (b) encoding any of seven polypeptides having 7
XX amino acids, or a polypeptide with 3 amino acids; (c) capable of
XX hybridizing to a Cytochrome P450 polypeptide 2C8 (CYP2C8) gene; (d)
XX encoding a molecular CYP2C8 variant polypeptide or its fragment. The
XX polynucleotide, gene, vector, polypeptide or antibody is useful for
XX diagnosing or treating a disease, for preparing a diagnostic composition
XX for diagnosing a disease, or for preparing a pharmaceutical composition
XX for treating a disease. This disease includes arachidonic acid
XX metabolism, cancer or cardiovascular diseases. This sequence represents a
XX primer used to isolate regions of the human cytochrome P450 polypeptide
XX 2C8 gene (CYP2C8) in order to identify the single nucleotide polymorphism
XX (SNP) in that region of different individuals useful in disease diagnosis
XX
XX Sequence 19 BP; 10 A; 0 C; 0 G; 8 T; 0 U; 1 Other;
XX
XX Query Match 0.6%; Score 13; DB 1; Length 19;
XX Best Local Similarity 86.7%; Pred. No. 1.3e+03;
XX Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1600 ATTTATATAAAATT 1614
XX ||||| |||||
XX Db 3 ATTTTAWAAAAATT 17
XX
RESULT 2162
ACA98736/c
ID ACA98736 standard; DNA; 19 BP.
XX
AC ACA98736;
XX
XX 28-JUL-2003 (first entry)
XX
XX Human CYP2C8 SNP detection PCR primer #176.
XX
XX Cytochrome P450 polypeptide 2C8; CYP2C8; arachidonic acid metabolism;
XX cancer; cardiovascular disease; cytostatic; cardiovascular; gene therapy;
XX single nucleotide polymorphism detection; SNP detection; PCR; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200299099-A2.
XX
XX 12-DEC-2002.
XX
XX 31-MAY-2002; 2002WO-EP006000.
XX
XX 01-JUN-2001; 2001EP-00112899.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Penger A, Sprenger R, Brinkmann U;
XX
XX WPI; 2003-167344/16.
XX
XX New polymorphic variants of the gene encoding Cytochrome P450 polypeptide
XX 2C8 (CYP2C8), useful for diagnosing or treating a disease, e.g.
XX arachidonic acid metabolism, cancer or cardiovascular diseases.
XX
XX Example 2; Page 52; 178pp; English.
XX
XX The invention describes a new polynucleotide comprises a polynucleotide:
XX (a) having any of 101 nucleic acid sequences with 18-19 bp fully defined
XX in the specification; (b) encoding any of seven polypeptides having 7
XX amino acids, or a polypeptide with 3 amino acids; (c) capable of
XX hybridizing to a Cytochrome P450 polypeptide 2C8 (CYP2C8) gene; (d)
XX encoding a molecular CYP2C8 variant polypeptide or its fragment. The
XX polynucleotide, gene, vector, polypeptide or antibody is useful for
XX diagnosing or treating a disease, for preparing a diagnostic composition
XX for diagnosing a disease, or for preparing a pharmaceutical composition
XX for treating a disease. This disease includes arachidonic acid
XX metabolism, cancer or cardiovascular diseases. This sequence represents a
XX primer used to isolate regions of the human cytochrome P450 polypeptide
XX 2C8 gene (CYP2C8) in order to identify the single nucleotide polymorphism
XX (SNP) in that region of different individuals useful in disease diagnosis
XX
XX Sequence 19 BP; 10 A; 0 C; 0 G; 8 T; 0 U; 1 Other;
XX
XX Query Match 0.6%; Score 13; DB 1; Length 19;
XX Best Local Similarity 86.7%; Pred. No. 1.3e+03;
XX Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1600 ATTTATATAAAATT 1614
XX ||||| |||||
XX Db 17 ATTTTAWAAAAATT 3
XX
Search completed: September 10, 2004, 11:37:20
Job time : 62 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2004, 11:43:43 ; Search time 39 Seconds
 (without alignments)
 3.627 Million cell updates/sec

Title: us-09-745-167a-3
 Perfect score: 2091
 Sequence: 1 gagcgagcgccggcgga.....taataaatgtacattct 2091

Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 0.5

Searched: 1806 seqs, 33828 residues

Total number of hits satisfying chosen parameters: 3612

Minimum DB seq length: 8
 Maximum DB seq length: 50

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1833 summaries

Database : rni3.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	19.4	0.9	29	1	US-09-328-925-18
C 2	18.2	0.9	24	1	US-08-245-758-13
C 3	18.2	0.9	24	1	PCT-US95-05134-13
C 4	18.2	0.9	25	1	US-09-866-108A-13560
C 5	18.2	0.9	25	1	US-09-866-108A-13561
C 6	18.2	0.9	25	1	US-09-866-108A-13562
C 7	18.2	0.9	26	1	US-08-856-331-16
C 8	18.2	0.9	27	1	US-08-584-040-756
C 9	18	0.9	24	1	US-08-066-325-49
C 10	17.6	0.8	25	1	US-09-866-108A-13968
C 11	17.6	0.8	25	1	US-09-866-108A-13969
C 12	17.2	0.8	22	1	US-07-814-964-1
C 13	17.2	0.8	22	1	US-08-258-442-1
C 14	17.2	0.8	22	1	PCT-US92-11107-1
C 15	17.2	0.8	25	1	US-09-866-108A-13559
C 16	17.2	0.8	25	1	US-09-866-108A-13563
C 17	17	0.8	25	1	US-09-866-108A-13970
C 18	16.6	0.8	24	1	US-08-467-264-8
C 19	16.6	0.8	25	1	US-08-450-905B-52
C 20	16.6	0.8	25	1	US-07-982-759F-52
C 21	16.6	0.8	25	1	US-09-808-658-1
C 22	16.6	0.8	25	1	US-09-866-108A-13967
C 23	16.6	0.8	25	1	US-09-866-108A-13971
C 24	16.6	0.8	25	1	US-09-866-108A-13972
C 25	16.4	0.8	20	1	US-08-250-856A-27
C 26	16.4	0.8	20	1	US-08-468-037A-13
C 27	16.4	0.8	20	1	US-08-471-973A-13
C 28	16.4	0.8	20	1	US-08-756-806A-27
C 29	16.4	0.8	20	1	US-08-465-880-13
C 30	16.4	0.8	20	1	US-09-035-357-13
C 31	16.4	0.8	20	1	US-09-143-214-27
C 32	16.4	0.8	20	1	US-09-000-136-13
C 33	16.4	0.8	20	1	US-09-135-202-13

C 34	16.4	0.8	20	1	US-09-506-073-28	Sequence 28, Appl
C 35	16.4	0.8	20	1	US-08-802-331-13	Sequence 13, Appl
C 36	16.4	0.8	20	1	US-09-389-283-13	Sequence 13, Appl
C 37	16.4	0.8	20	1	PCT-US95-07111A-27	Sequence 27, Appl
C 38	16.2	0.8	22	1	US-09-918-696-23	Sequence 23, Appl
C 39	16.2	0.8	22	1	US-09-918-696-24	Sequence 24, Appl
C 40	16	0.8	21	1	US-08-218-592A-10	Sequence 10, Appl
C 41	16	0.8	24	1	US-08-450-905B-64	Sequence 64, Appl
C 42	16	0.8	24	1	US-08-824-701A-2	Sequence 2, Appl
C 43	16	0.8	24	1	US-07-982-759F-64	Sequence 64, Appl
C 44	16	0.8	24	1	PCT-US91-02942-12	Sequence 12, Appl
C 45	15.8	0.8	20	1	US-08-261-822A-55	Sequence 55, Appl
C 46	15.8	0.8	20	1	US-09-780-045-26	Sequence 26, Appl
C 47	15.8	0.8	20	1	PCT-US95-07744A-55	Sequence 55, Appl
C 48	15.8	0.8	21	1	US-09-257-799-54	Sequence 54, Appl
C 49	15.8	0.8	21	1	US-08-920-919A-54	Sequence 54, Appl
C 50	15.8	0.8	22	1	US-09-033-936-30	Sequence 30, Appl
C 51	15.8	0.8	24	1	US-08-478-470-7	Sequence 7, Appl
C 52	15.8	0.8	24	1	US-08-478-470-9	Sequence 9, Appl
C 53	15.8	0.8	24	1	US-08-214-599-7	Sequence 7, Appl
C 54	15.8	0.8	24	1	US-08-214-599-9	Sequence 9, Appl
C 55	15.8	0.8	24	1	US-08-473-015-7	Sequence 7, Appl
C 56	15.8	0.8	24	1	US-08-473-015-9	Sequence 9, Appl
C 57	15.8	0.8	24	1	US-08-465-368-7	Sequence 7, Appl
C 58	15.8	0.8	24	1	US-08-465-368-9	Sequence 9, Appl
C 59	15.8	0.8	24	1	US-08-477-306-7	Sequence 7, Appl
C 60	15.8	0.8	24	1	US-08-477-306-9	Sequence 9, Appl
C 61	15.8	0.8	24	1	US-08-700-448-7	Sequence 7, Appl
C 62	15.8	0.8	24	1	US-08-700-448-9	Sequence 9, Appl
C 63	15.8	0.8	24	1	US-08-923-386A-7	Sequence 7, Appl
C 64	15.8	0.8	24	1	US-08-923-386A-9	Sequence 9, Appl
C 65	15.8	0.8	24	1	US-09-033-936-69	Sequence 69, Appl
C 66	15.6	0.7	22	1	US-07-814-964-2	Sequence 2, Appl
C 67	15.6	0.7	22	1	US-07-814-964-5	Sequence 5, Appl
C 68	15.6	0.7	22	1	US-08-238-963A-10	Sequence 10, Appl
C 69	15.6	0.7	22	1	US-08-258-442-2	Sequence 2, Appl
C 70	15.6	0.7	22	1	US-08-258-442-5	Sequence 5, Appl
C 71	15.6	0.7	22	1	US-09-387-341-197	Sequence 197, App
C 72	15.6	0.7	22	1	US-10-134-890-3	Sequence 3, Appl
C 73	15.6	0.7	22	1	PCT-US92-11107-2	Sequence 2, Appl
C 74	15.6	0.7	22	1	US-08-390-850-574	Sequence 5, Appl
C 75	15.4	0.7	17	1	US-08-390-850-575	Sequence 574, App
C 76	15.4	0.7	17	1	US-08-390-850-575	Sequence 574, App
C 77	15.4	0.7	17	1	US-08-435-634-574	Sequence 574, App
C 78	15.4	0.7	17	1	US-08-435-634-575	Sequence 575, App
C 79	15.4	0.7	18	1	US-08-390-850-1130	Sequence 1130, Ap
C 80	15.4	0.7	18	1	US-08-435-634-1130	Sequence 1130, Ap
C 81	15.4	0.7	18	1	US-09-255-912-44	Sequence 44, Appl
C 82	15.4	0.7	19	1	US-09-422-978-6129	Sequence 6129, Ap
C 83	15.4	0.7	22	1	US-08-203-905B-17	Sequence 17, Appl
C 84	15.4	0.7	23	1	US-09-686-179A-20	Sequence 20, Appl
C 85	15.4	0.7	23	1	US-09-422-978-5835	Sequence 5835, Ap
C 86	15.4	0.7	23	1	US-09-981-621-20	Sequence 20, Appl
C 87	15.2	0.7	20	1	US-09-429-323-36	Sequence 36, Appl
C 88	15.2	0.7	20	1	US-08-857-076-4	Sequence 4, Appl
C 89	15.2	0.7	20	1	US-09-428-583-74	Sequence 74, Appl
C 90	15.2	0.7	20	1	US-09-198-452A-1484	Sequence 1484, Ap
C 91	15.2	0.7	20	1	US-09-780-045-31	Sequence 31, Appl
C 92	15.2	0.7	21	1	US-08-219-842-53	Sequence 53, Appl
C 93	15.2	0.7	21	1	US-08-219-842-86	Sequence 86, Appl
C 94	15.2	0.7	21	1	US-08-451-096-53	Sequence 53, Appl
C 95	15.2	0.7	21	1	US-08-451-096-86	Sequence 86, Appl
C 96	15.2	0.7	21	1	US-08-413-740A-14	Sequence 14, Appl
C 97	15.2	0.7	21	1	US-09-367-007C-9	Sequence 9, Appl
C 98	15.2	0.7	21	1	PCT-US95-04063-14	Sequence 14, Appl
C 99	15.2	0.7	22	1	US-08-338-579A-79	Sequence 79, Appl
C 100	15.2	0.7	22	1	PCT-US94-05388-28	Sequence 28, Appl
C 101	15.2	0.7	22	1	PCT-US94-09851-79	Sequence 79, Appl
C 102	15.2	0.7	23	1	US-08-192-942-1	Sequence 1, Appl
C 103	15.2	0.7	23	1	US-09-052-469-9	Sequence 9, Appl
C 104	15.2	0.7	23	1	US-08-422-582-9	Sequence 9, Appl
C 105	15.2	0.7	23	1	US-09-052-262-9	Sequence 22, Appl
C 106	15	0.7	20	1	US-08-250-856A-22	

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c 107	15	0.7	20	1	US-08-468-037A-12	Sequence 12, Appl	180	14.6	0.7	22	1	US-09-618-166-1	Sequence 1, Appl
c 108	15	0.7	20	1	US-08-471-973A-12	Sequence 12, Appl	181	14.6	0.7	22	1	US-09-618-166-167	Sequence 167, App
c 109	15	0.7	20	1	US-08-756-806A-22	Sequence 22, Appl	c 182	14.6	0.7	22	1	US-09-375-673B-62	Sequence 62, Appl
c 110	15	0.7	20	1	US-08-465-880-12	Sequence 12, Appl	c 183	14.6	0.7	22	1	US-09-650-324A-28	Sequence 28, Appl
c 111	15	0.7	20	1	US-09-035-357-12	Sequence 12, Appl	c 184	14.4	0.7	16	1	US-09-313-942-3	Sequence 3, Appl
c 112	15	0.7	20	1	US-09-143-214-22	Sequence 22, Appl	c 185	14.4	0.7	16	1	US-09-371-772B-5827	Sequence 5827, Ap
c 113	15	0.7	20	1	US-09-000-136-8	Sequence 8, Appl	c 186	14.4	0.7	17	1	US-08-390-850-576	Sequence 576, App
c 114	15	0.7	20	1	US-09-702-251-47	Sequence 47, Appl	c 187	14.4	0.7	17	1	US-08-435-634-576	Sequence 4754, Ap
c 115	15	0.7	20	1	US-09-135-202-12	Sequence 12, Appl	c 188	14.4	0.7	17	1	US-09-371-772B-4754	Sequence 971, App
c 116	15	0.7	20	1	US-09-506-073-22	Sequence 22, Appl	c 189	14.4	0.7	17	1	US-09-866-108A-971	Sequence 972, App
c 117	15	0.7	20	1	US-08-802-331-12	Sequence 12, Appl	c 190	14.4	0.7	17	1	US-09-866-108A-972	Sequence 972, App
c 118	15	0.7	20	1	US-09-389-283-12	Sequence 12, Appl	c 191	14.4	0.7	17	1	US-09-866-108A-8945	Sequence 8945, Ap
c 119	15	0.7	20	1	PCT-US95-07111A-22	Sequence 22, Appl	c 192	14.4	0.7	17	1	US-09-866-108A-8946	Sequence 8946, Ap
c 120	15	0.7	23	1	US-09-431-480-21	Sequence 21, Appl	c 193	14.4	0.7	18	1	US-08-943-087-4	Sequence 4, Appl
c 121	15	0.7	23	1	US-09-617-302-21	Sequence 21, Appl	c 194	14.4	0.7	18	1	US-09-422-978-9179	Sequence 46, Appl
c 122	15	0.7	23	1	US-09-462-671-2	Sequence 2, Appl	c 195	14.4	0.7	18	1	US-09-422-978-9179	Sequence 9179, Ap
c 123	15	0.7	24	1	US-09-033-936-69	Sequence 69, Appl	c 196	14.4	0.7	18	1	US-09-422-978-9179	Sequence 4, Appl
c 124	14.8	0.7	18	1	US-08-530-452-60	Sequence 60, Appl	c 197	14.4	0.7	19	1	US-09-422-978-6157	Sequence 6157, Ap
c 125	14.8	0.7	18	1	US-08-282-197C-14	Sequence 14, Appl	c 198	14.4	0.7	20	1	US-09-422-978-6157	Sequence 12, Appl
c 126	14.8	0.7	18	1	US-08-906-517-60	Sequence 60, Appl	c 199	14.4	0.7	20	1	US-07-959-119A-12	Sequence 12, Appl
c 127	14.8	0.7	18	1	US-09-522-217-23	Sequence 23, Appl	c 200	14.4	0.7	20	1	US-09-444-053-60	Sequence 60, Appl
c 128	14.8	0.7	18	1	US-09-404-641-22	Sequence 22, Appl	c 201	14.4	0.7	20	1	US-08-154-364-18	Sequence 18, Appl
c 129	14.8	0.7	18	1	US-09-404-641-39	Sequence 39, Appl	c 202	14.4	0.7	20	1	US-09-629-645A-33	Sequence 33, Appl
c 130	14.8	0.7	18	1	US-09-923-246-23	Sequence 23, Appl	c 203	14.4	0.7	20	1	US-09-422-978-10071	Sequence 10071, A
c 131	14.8	0.7	19	1	US-10-295-723-23	Sequence 23, Appl	c 204	14.4	0.7	20	1	US-09-705-267A-61	Sequence 61, Appl
c 132	14.8	0.7	19	1	US-08-687-820-3	Sequence 3, Appl	c 205	14.4	0.7	20	1	US-09-198-452A-6177	Sequence 6177, Ap
c 133	14.8	0.7	19	1	US-09-305-856B-79	Sequence 79, Appl	c 206	14.4	0.7	20	1	US-09-112-580-57	Sequence 57, Appl
c 134	14.8	0.7	20	1	US-08-157-235-12	Sequence 12, Appl	c 207	14.4	0.7	21	1	US-09-445-283C-43	Sequence 43, Appl
c 135	14.8	0.7	20	1	US-09-132-028-3	Sequence 3, Appl	c 208	14.4	0.7	21	1	US-08-639-501-56	Sequence 56, Appl
c 136	14.8	0.7	20	1	US-09-210-748A-12	Sequence 12, Appl	c 209	14.4	0.7	21	1	US-09-044-946-56	Sequence 56, Appl
c 137	14.8	0.7	20	1	US-09-844-525A-23	Sequence 23, Appl	c 210	14.4	0.7	21	1	US-08-755-587-182	Sequence 182, App
c 138	14.8	0.7	20	1	US-09-198-452A-1656	Sequence 1656, Ap	c 211	14.4	0.7	21	1	US-09-044-908-56	Sequence 56, Appl
c 139	14.8	0.7	20	1	US-09-198-452A-6144	Sequence 6144, Ap	c 212	14.4	0.7	21	1	US-08-899-367-16	Sequence 16, Appl
c 140	14.8	0.7	21	1	US-09-009-913-112	Sequence 112, Appl	c 213	14.4	0.7	21	1	US-09-111-667C-3	Sequence 3, Appl
c 141	14.8	0.7	21	1	US-09-428-583-6	Sequence 6, Appl	c 214	14.4	0.7	21	1	US-09-422-978-10830	Sequence 10830, A
c 142	14.8	0.7	21	1	US-09-434-066-15	Sequence 15, Appl	c 215	14.2	0.7	19	1	US-08-242-664-37	Sequence 37, Appl
c 143	14.8	0.7	21	1	US-09-422-978-10680	Sequence 10680, A	c 216	14.2	0.7	19	1	US-08-484-138-37	Sequence 37, Appl
c 144	14.8	0.7	22	1	US-09-102-830-15	Sequence 15, Appl	c 217	14.2	0.7	19	1	US-09-305-856B-77	Sequence 77, Appl
c 145	14.8	0.7	22	1	US-09-102-830-30	Sequence 30, Appl	c 218	14.2	0.7	19	1	US-09-305-856B-77	Sequence 77, Appl
c 146	14.8	0.7	22	1	US-08-938-641C-1	Sequence 1, Appl	c 219	14.2	0.7	19	1	US-09-422-978-11276	Sequence 11276, A
c 147	14.8	0.7	22	1	US-09-050-516-32	Sequence 32, Appl	c 220	14.2	0.7	20	1	PCT-US95-06379-37	Sequence 37, Appl
c 148	14.8	0.7	22	1	US-10-278-547-32	Sequence 32, Appl	c 221	14.2	0.7	20	1	US-07-838-264-7	Sequence 7, Appl
c 149	14.6	0.7	21	1	US-08-852-807-31	Sequence 31, Appl	c 222	14.2	0.7	20	1	US-08-029-327-3	Sequence 3, Appl
c 150	14.6	0.7	21	1	US-08-882-083-11	Sequence 11, Appl	c 223	14.2	0.7	20	1	US-08-222-177A-261	Sequence 261, App
c 151	14.6	0.7	21	1	US-08-558-107-11	Sequence 11, Appl	c 224	14.2	0.7	20	1	US-08-750-532-13	Sequence 13, Appl
c 152	14.6	0.7	21	1	US-08-863-639A-63	Sequence 63, Appl	c 225	14.2	0.7	20	1	US-08-750-532-16	Sequence 16, Appl
c 153	14.6	0.7	21	1	US-08-863-639A-75	Sequence 75, Appl	c 226	14.2	0.7	20	1	US-08-147-843-1	Sequence 1, Appl
c 154	14.6	0.7	21	1	US-08-863-639A-75	Sequence 75, Appl	c 227	14.2	0.7	20	1	US-08-602-203-7	Sequence 7, Appl
c 155	14.6	0.7	21	1	US-08-722-240-5	Sequence 5, Appl	c 228	14.2	0.7	20	1	US-08-465-485A-26	Sequence 26, Appl
c 156	14.6	0.7	21	1	US-08-722-240-5	Sequence 5, Appl	c 229	14.2	0.7	20	1	US-08-837-201C-78	Sequence 78, Appl
c 157	14.6	0.7	21	1	US-09-258-408-63	Sequence 63, Appl	c 230	14.2	0.7	20	1	US-08-975-211-6	Sequence 95, Appl
c 158	14.6	0.7	21	1	US-09-243-539-11	Sequence 11, Appl	c 231	14.2	0.7	20	1	US-08-837-201C-95	Sequence 1, Appl
c 159	14.6	0.7	21	1	US-08-591-840A-12	Sequence 12, Appl	c 232	14.2	0.7	20	1	US-09-065-858-1	Sequence 1, Appl
c 160	14.6	0.7	21	1	US-09-525-392-15	Sequence 15, Appl	c 233	14.2	0.7	20	1	US-09-065-858-1	Sequence 26, Appl
c 161	14.6	0.7	21	1	US-08-338-509B-5	Sequence 5, Appl	c 234	14.2	0.7	20	1	US-09-095-769-1	Sequence 1, Appl
c 162	14.6	0.7	22	1	US-08-457-273B-18	Sequence 18, Appl	c 235	14.2	0.7	20	1	US-09-289-267-69	Sequence 69, Appl
c 163	14.6	0.7	22	1	US-08-117-952-370	Sequence 370, App	c 236	14.2	0.7	20	1	US-09-344-001-12	Sequence 12, Appl
c 164	14.6	0.7	22	1	US-08-450-905B-82	Sequence 82, Appl	c 237	14.2	0.7	20	1	US-09-344-001-14	Sequence 14, Appl
c 165	14.6	0.7	22	1	US-08-450-905B-82	Sequence 167, App	c 238	14.2	0.7	20	1	US-09-009-913-312	Sequence 312, App
c 166	14.6	0.7	22	1	US-08-770-544-28	Sequence 28, Appl	c 239	14.2	0.7	20	1	US-08-666-221B-32	Sequence 32, Appl
c 167	14.6	0.7	22	1	US-07-982-759F-82	Sequence 82, Appl	c 240	14.2	0.7	20	1	US-09-490-692-151	Sequence 151, App
c 168	14.6	0.7	22	1	US-07-982-759F-167	Sequence 167, App	c 241	14.2	0.7	20	1	US-08-927-219-65	Sequence 65, Appl
c 169	14.6	0.7	22	1	US-08-781-891-1	Sequence 1, Appl	c 242	14.2	0.7	20	1	US-09-311-260-179	Sequence 179, App
c 170	14.6	0.7	22	1	US-08-781-891-167	Sequence 167, App	c 243	14.2	0.7	20	1	US-09-282-736-6	Sequence 6, Appl
c 171	14.6	0.7	22	1	US-09-010-641-19	Sequence 19, Appl	c 244	14.2	0.7	20	1	US-09-377-309-76	Sequence 76, Appl
c 172	14.6	0.7	22	1	US-09-356-281-19	Sequence 19, Appl	c 245	14.2	0.7	20	1	US-08-884-427-1	Sequence 1, Appl
c 173	14.6	0.7	22	1	US-09-240-918-10	Sequence 10, Appl	c 246	14.2	0.7	20	1	US-09-488-744A-14	Sequence 14, Appl
c 174	14.6	0.7	22	1	US-09-367-206-25	Sequence 25, Appl	c 247	14.2	0.7	20	1	US-09-364-416-95	Sequence 95, Appl
c 175	14.6	0.7	22	1	US-09-043-149-9	Sequence 9, Appl	c 248	14.2	0.7	20	1	US-09-326-186B-178	Sequence 178, App
c 176	14.6	0.7	22	1	US-09-638-509C-12	Sequence 12, Appl	c 249	14.2	0.7	20	1	US-09-079-812B-3	Sequence 3, Appl
c 177	14.6	0.7	22	1	US-09-638-509C-13	Sequence 13, Appl	c 250	14.2	0.7	20	1	US-09-559-791A-22	Sequence 22, Appl
c 178	14.6	0.7	22	1	US-09-579-259-28	Sequence 28, Appl	c 251	14.2	0.7	20	1	US-09-798-096-75	Sequence 75, Appl
c 179	14.6	0.7	22	1			c 252	14.2	0.7	20	1	US-09-724-426-26	Sequence 26, Appl

c 253	14.2	0.7	20	1	US-09-640-101-100	Sequence 100, App	c 326	13.8	0.7	18	1	US-09-422-978-3943	Sequence 3943, Ap
c 254	14.2	0.7	20	1	US-09-658-688A-45	Sequence 15, Appl	327	13.8	0.7	18	1	US-09-925-388-15	Sequence 15, Appl
c 255	14.2	0.7	20	1	US-09-470-661A-18	Sequence 48, Appl	328	13.8	0.7	18	1	US-09-913-514-20	Sequence 20, Appl
c 256	14.2	0.7	20	1	US-09-920-759-65	Sequence 65, Appl	329	13.8	0.7	18	1	PCT-US96-09915-7	Sequence 7, Appl
c 257	14.2	0.7	20	1	US-09-198-452A-2212	Sequence 2212, Ap	c 330	13.8	0.7	19	1	US-08-050-073-98	Sequence 98, Appl
c 258	14.2	0.7	20	1	US-09-198-452A-4965	Sequence 4965, Ap	331	13.8	0.7	19	1	US-08-642-684-8	Sequence 8, Appl
c 259	14.2	0.7	20	1	US-09-198-452A-5034	Sequence 5034, Ap	332	13.8	0.7	19	1	US-09-345-882-106	Sequence 106, App
c 260	14.2	0.7	20	1	US-09-198-452A-6815	Sequence 6815, Ap	333	13.8	0.7	19	1	US-09-018-125-9	Sequence 9, Appl
c 261	14.2	0.7	20	1	US-09-915-229-1	Sequence 8, Appl	c 334	13.8	0.7	19	1	US-09-422-978-6984	Sequence 9, Appl
c 262	14.2	0.7	20	1	US-09-825-497A-6	Sequence 1, Appl	c 335	13.8	0.7	19	1	US-09-422-978-7755	Sequence 9, Appl
c 263	14.2	0.7	20	1	PCT-US94-00185-1	Sequence 6, Appl	c 336	13.8	0.7	19	1	US-09-422-978-7755	Sequence 9, Appl
c 264	14.2	0.7	20	1	US-08-208-886C-35	Sequence 1, Appl	c 337	13.8	0.7	19	1	US-09-422-978-7755	Sequence 9, Appl
c 265	14.2	0.7	21	1	US-08-587-209-15	Sequence 35, Appl	c 338	13.8	0.7	20	1	US-07-958-140-11	Sequence 11, Appl
c 266	14.2	0.7	21	1	US-08-704-744-35	Sequence 15, Appl	c 339	13.8	0.7	20	1	US-08-478-470-8	Sequence 8, Appl
c 267	14.2	0.7	21	1	US-08-613-805-5	Sequence 35, Appl	c 340	13.8	0.7	20	1	US-08-214-599-8	Sequence 8, Appl
c 268	14.2	0.7	21	1	US-08-613-805-6	Sequence 5, Appl	c 341	13.8	0.7	20	1	US-08-473-015-8	Sequence 8, Appl
c 269	14.2	0.7	21	1	US-08-689-236-15	Sequence 6, Appl	342	13.8	0.7	20	1	US-08-480-552-21	Sequence 21, Appl
c 270	14.2	0.7	21	1	US-08-689-236-15	Sequence 15, Appl	343	13.8	0.7	20	1	US-08-339-912-2	Sequence 2, Appl
c 271	14.2	0.7	21	1	US-08-689-235-15	Sequence 15, Appl	344	13.8	0.7	20	1	US-08-089-996-50	Sequence 50, Appl
c 272	14.2	0.7	21	1	US-08-692-725-15	Sequence 15, Appl	345	13.8	0.7	20	1	US-08-089-996-62	Sequence 62, Appl
c 273	14.2	0.7	21	1	US-08-469-557-35	Sequence 35, Appl	c 346	13.8	0.7	20	1	US-08-465-368-8	Sequence 8, Appl
c 274	14.2	0.7	21	1	US-08-692-726-15	Sequence 15, Appl	347	13.8	0.7	20	1	US-08-477-306-8	Sequence 8, Appl
c 275	14.2	0.7	21	1	US-08-925-444A-5	Sequence 5, Appl	c 348	13.8	0.7	20	1	US-08-531-927B-14	Sequence 14, Appl
c 276	14.2	0.7	21	1	US-08-925-444A-5	Sequence 15, Appl	c 349	13.8	0.7	20	1	US-08-173-489C-17	Sequence 17, Appl
c 277	14.2	0.7	21	1	US-08-925-444A-6	Sequence 6, Appl	350	13.8	0.7	20	1	US-08-650-598-10	Sequence 10, Appl
c 278	14.2	0.7	21	1	US-08-290-793B-35	Sequence 35, Appl	351	13.8	0.7	20	1	US-08-478-178A-50	Sequence 50, Appl
c 279	14.2	0.7	21	1	US-08-873-479-48	Sequence 48, Appl	352	13.8	0.7	20	1	US-08-488-177-50	Sequence 50, Appl
c 280	14.2	0.7	21	1	US-08-972-661A-34	Sequence 34, Appl	353	13.8	0.7	20	1	US-08-488-177-62	Sequence 62, Appl
c 281	14.2	0.7	21	1	US-08-863-639A-37	Sequence 37, Appl	354	13.8	0.7	20	1	US-08-481-072A-50	Sequence 50, Appl
c 282	14.2	0.7	21	1	US-08-863-639A-54	Sequence 54, Appl	355	13.8	0.7	20	1	US-08-481-072A-62	Sequence 62, Appl
c 283	14.2	0.7	21	1	US-08-863-639A-57	Sequence 57, Appl	356	13.8	0.7	20	1	US-08-664-336-50	Sequence 50, Appl
c 284	14.2	0.7	21	1	US-08-863-639A-84	Sequence 84, Appl	357	13.8	0.7	20	1	US-08-664-336-62	Sequence 62, Appl
c 285	14.2	0.7	21	1	US-09-121-920-6	Sequence 6, Appl	358	13.8	0.7	20	1	US-08-664-336-62	Sequence 62, Appl
c 286	14.2	0.7	21	1	US-09-384-305-25	Sequence 25, Appl	359	13.8	0.7	20	1	US-08-481-066A-50	Sequence 50, Appl
c 287	14.2	0.7	21	1	US-09-927-219-113	Sequence 113, App	c 360	13.8	0.7	20	1	US-08-481-066A-62	Sequence 62, Appl
c 288	14.2	0.7	21	1	US-09-177-650-13	Sequence 13, App	361	13.8	0.7	20	1	US-08-700-448-8	Sequence 8, Appl
c 289	14.2	0.7	21	1	US-09-360-545-52	Sequence 52, App	362	13.8	0.7	20	1	US-08-193-039B-2	Sequence 2, Appl
c 290	14.2	0.7	21	1	US-09-422-978-5690	Sequence 62, Appl	363	13.8	0.7	20	1	US-08-578-615A-50	Sequence 50, Appl
c 291	14.2	0.7	21	1	US-09-422-978-6821	Sequence 6821, Ap	364	13.8	0.7	20	1	US-08-578-615A-62	Sequence 62, Appl
c 292	14	0.7	15	1	US-10-139-842B-40	Sequence 40, Appl	c 365	13.8	0.7	20	1	US-09-344-001-11	Sequence 11, Appl
c 293	14	0.7	15	1	US-08-291-932A-258	Sequence 258, App	366	13.8	0.7	20	1	US-09-120-853-14	Sequence 14, Appl
c 294	14	0.7	18	1	US-09-920-760-19	Sequence 19, App	367	13.8	0.7	20	1	US-08-929-208-21	Sequence 21, Appl
c 295	14	0.7	20	1	US-09-489-869-27	Sequence 27, Appl	368	13.8	0.7	20	1	US-09-253-691-1	Sequence 1, Appl
c 296	14	0.7	20	1	US-09-659-791A-44	Sequence 44, Appl	c 369	13.8	0.7	20	1	US-09-287-796-112	Sequence 112, App
c 297	13.8	0.7	17	1	US-09-198-452A-1984	Sequence 1984, Ap	370	13.8	0.7	20	1	US-08-923-386A-8	Sequence 8, Appl
c 298	13.8	0.7	17	1	US-08-373-124A-1058	Sequence 1058, Ap	c 371	13.8	0.7	20	1	US-09-490-692-154	Sequence 154, App
c 299	13.8	0.7	17	1	US-08-435-628-1058	Sequence 1058, Ap	372	13.8	0.7	20	1	US-09-358-683-37	Sequence 37, Appl
c 300	13.8	0.7	17	1	US-08-584-040-2402	Sequence 2402, Ap	c 373	13.8	0.7	20	1	US-09-130-616-112	Sequence 112, App
c 301	13.8	0.7	17	1	US-08-584-040-5499	Sequence 5499, Ap	374	13.8	0.7	20	1	US-09-128-508-10	Sequence 10, Appl
c 302	13.8	0.7	17	1	US-08-679-645-678	Sequence 678, App	c 375	13.8	0.7	20	1	US-09-038-637-85	Sequence 85, Appl
c 303	13.8	0.7	17	1	US-08-679-645-886	Sequence 886, App	376	13.8	0.7	20	1	US-09-487-445-145	Sequence 145, App
c 304	13.8	0.7	17	1	US-09-371-772B-947	Sequence 947, App	c 377	13.8	0.7	20	1	US-08-943-731-542	Sequence 542, App
c 305	13.8	0.7	17	1	US-09-371-772B-2390	Sequence 2390, Ap	c 378	13.8	0.7	20	1	US-09-484-617-19	Sequence 19, Appl
c 306	13.8	0.7	17	1	US-09-371-772B-4755	Sequence 4755, Ap	c 379	13.8	0.7	20	1	US-09-568-315-21	Sequence 21, Appl
c 307	13.8	0.7	17	1	US-09-371-772B-4757	Sequence 4757, Ap	c 380	13.8	0.7	20	1	US-08-829-637A-50	Sequence 50, Appl
c 308	13.8	0.7	17	1	US-09-371-772B-4758	Sequence 4758, Ap	c 381	13.8	0.7	20	1	US-08-829-637A-62	Sequence 62, Appl
c 309	13.8	0.7	17	1	US-09-371-772B-5394	Sequence 5394, Ap	c 382	13.8	0.7	20	1	US-09-742-703-16	Sequence 16, Appl
c 310	13.8	0.7	17	1	US-09-866-108A-6562	Sequence 6562, Ap	c 383	13.8	0.7	20	1	US-09-702-327-63	Sequence 63, Appl
c 311	13.8	0.7	17	1	US-09-866-108A-7084	Sequence 7084, Ap	c 384	13.8	0.7	20	1	US-09-676-610B-120	Sequence 120, App
c 312	13.8	0.7	17	1	US-09-866-108A-8667	Sequence 8667, Ap	c 385	13.8	0.7	20	1	US-09-780-173A-85	Sequence 85, Appl
c 313	13.8	0.7	17	1	US-09-866-108A-8668	Sequence 8668, Ap	c 386	13.8	0.7	20	1	US-09-422-978-7724	Sequence 7724, Ap
c 314	13.8	0.7	17	1	US-09-866-108A-8944	Sequence 8944, Ap	c 387	13.8	0.7	20	1	US-10-025-139-50	Sequence 50, Appl
c 315	13.8	0.7	17	1	US-09-866-108A-8947	Sequence 8947, Ap	c 388	13.8	0.7	20	1	US-10-025-139-62	Sequence 62, Appl
c 316	13.8	0.7	17	1	5240847-22	Patent No. 5240847	389	13.8	0.7	20	1	US-09-198-452A-1948	Sequence 1948, Ap
c 317	13.8	0.7	18	1	US-08-105-483-101	Sequence 101, App	390	13.8	0.7	20	1	US-09-198-452A-3817	Sequence 3817, Ap
c 318	13.8	0.7	18	1	US-08-709-209-101	Sequence 101, App	c 391	13.8	0.7	20	1	US-09-198-452A-3917	Sequence 3917, Ap
c 319	13.8	0.7	18	1	US-08-458-101-101	Sequence 101, App	c 392	13.8	0.7	20	1	US-09-198-452A-4382	Sequence 4382, Ap
c 320	13.8	0.7	18	1	US-09-205-922-23	Sequence 23, Appl	c 393	13.8	0.7	20	1	US-09-198-452A-5538	Sequence 5538, Ap
c 321	13.8	0.7	18	1	US-08-994-824-7	Sequence 7, Appl	c 394	13.8	0.7	20	1	US-09-198-452A-6831	Sequence 6831, Ap
c 322	13.8	0.7	18	1	US-09-205-143-57	Sequence 57, Appl	c 395	13.8	0.7	20	1	US-09-944-036-61	Sequence 61, Appl
c 323	13.8	0.7	18	1	US-09-306-595C-15	Sequence 15, Appl	c 396	13.8	0.7	20	1	US-09-081-385-100	Sequence 100, Appl
c 324	13.8	0.7	18	1	US-08-884-866A-15	Sequence 15, Appl	c 397	13.8	0.7	20	1	US-09-972-115A-51	Sequence 51, Appl
c 325	13.8	0.7	18	1	US-09-167-109-135	Sequence 135, App	398	13.8	0.7	20	1	US-09-860-761-2	Sequence 2, Appl

C 545	13.4	0.6	17	1	US-08-584-040-2508	Sequence 2508, Ap	C 618	13.4	0.6	20	1	US-08-851-896-45	Sequence 45, Appl
C 546	13.4	0.6	17	1	US-09-371-772B-1032	Sequence 1032, Ap	C 619	13.4	0.6	20	1	US-09-629-645A-106	Sequence 106, Appl
C 547	13.4	0.6	17	1	US-09-371-772B-4644	Sequence 4644, Ap	C 620	13.4	0.6	20	1	US-09-702-246-50	Sequence 50, Appl
C 548	13.4	0.6	17	1	US-09-866-108A-970	Sequence 970, Appl	C 621	13.4	0.6	20	1	US-09-633-659-3	Sequence 3, Appl
C 549	13.4	0.6	17	1	US-09-866-108A-970	Sequence 970, Appl	C 622	13.4	0.6	20	1	US-09-689-964-8	Sequence 8, Appl
C 550	13.4	0.6	17	1	US-09-866-108A-2209	Sequence 2209, Appl	C 623	13.4	0.6	20	1	US-09-689-964-8	Sequence 8, Appl
C 551	13.4	0.6	17	1	US-09-866-108A-2210	Sequence 2210, Appl	C 624	13.4	0.6	20	1	US-09-689-964-9	Sequence 9, Appl
C 552	13.4	0.6	17	1	US-09-866-108A-2211	Sequence 2211, Appl	C 625	13.4	0.6	20	1	US-09-689-964-9	Sequence 9, Appl
C 553	13.4	0.6	17	1	US-09-866-108A-2736	Sequence 2736, Ap	C 626	13.4	0.6	20	1	US-09-657-452A-96	Sequence 96, Appl
C 554	13.4	0.6	17	1	US-09-866-108A-2737	Sequence 2737, Ap	C 627	13.4	0.6	20	1	US-09-422-978-4896	Sequence 4896, Ap
C 555	13.4	0.6	17	1	US-09-866-108A-2738	Sequence 2738, Ap	C 628	13.4	0.6	20	1	US-09-422-978-10868	Sequence 10868, A
C 556	13.4	0.6	17	1	US-09-866-108A-5563	Sequence 5563, Ap	C 629	13.4	0.6	20	1	US-09-060-299-358	Sequence 268, App
C 557	13.4	0.6	17	1	US-09-866-108A-5564	Sequence 5564, Ap	C 630	13.4	0.6	20	1	US-09-402-923A-268	Sequence 268, App
C 558	13.4	0.6	17	1	US-09-866-108A-7085	Sequence 7085, Ap	C 631	13.4	0.6	20	1	US-09-198-452A-1900	Sequence 1900, Ap
C 559	13.4	0.6	17	1	US-09-866-108A-7086	Sequence 7086, Ap	C 632	13.4	0.6	20	1	US-09-198-452A-4696	Sequence 4696, Ap
C 560	13.4	0.6	17	1	US-09-866-108A-8669	Sequence 8669, Ap	C 633	13.4	0.6	20	1	US-09-198-452A-5555	Sequence 5555, Ap
C 561	13.4	0.6	17	1	US-09-866-108A-8670	Sequence 8670, Ap	C 634	13.4	0.6	20	1	US-09-249-247-28	Sequence 28, Appl
C 562	13.4	0.6	18	1	US-08-317-431A-1	Sequence 1, Appl	C 635	13.4	0.6	20	1	US-10-027-983-22	Sequence 22, Appl
C 563	13.4	0.6	18	1	US-08-117-952-183	Sequence 183, Ap	C 636	13.4	0.6	20	1	PCT-US93-02059-6	Sequence 6, Appl
C 564	13.4	0.6	18	1	US-08-585-684B-2739	Sequence 2739, Ap	C 637	13.4	0.6	20	1	PCT-US93-08367A-8	Sequence 8, Appl
C 565	13.4	0.6	18	1	US-08-931-072A-11	Sequence 11, Appl	C 638	13.4	0.6	20	1	PCT-US93-08367A-9	Sequence 9, Appl
C 566	13.4	0.6	18	1	US-08-931-072A-27	Sequence 27, Appl	C 639	13.4	0.6	20	1	PCT-US94-02891-56	Sequence 56, Appl
C 567	13.4	0.6	18	1	US-09-205-922-39	Sequence 39, Appl	C 640	13.4	0.6	20	1	PCT-US96-09388-8	Sequence 8, Appl
C 568	13.4	0.6	18	1	US-09-156-253-15	Sequence 15, Appl	C 641	13.2	0.6	18	1	US-07-874-334-14	Sequence 14, Appl
C 569	13.4	0.6	18	1	US-09-106-038A-57	Sequence 57, Appl	C 642	13.2	0.6	18	1	US-08-010-997-2	Sequence 2, Appl
C 570	13.4	0.6	18	1	US-09-177-359-15	Sequence 15, Appl	C 643	13.2	0.6	18	1	US-08-152-019A-15	Sequence 15, Appl
C 571	13.4	0.6	18	1	US-09-038-073-2739	Sequence 39, Appl	C 644	13.2	0.6	18	1	US-08-117-952-740	Sequence 2, Appl
C 572	13.4	0.6	18	1	US-09-474-922A-39	Sequence 39, Appl	C 645	13.2	0.6	18	1	US-09-006-232-2	Sequence 2, Appl
C 573	13.4	0.6	18	1	US-08-584-040-3066	Sequence 3066, Ap	C 646	13.2	0.6	18	1	US-08-863-639A-20	Sequence 2, Appl
C 574	13.4	0.6	18	1	US-08-920-760-23	Sequence 23, Appl	C 647	13.2	0.6	18	1	US-08-738-381-43	Sequence 20, Appl
C 575	13.4	0.6	18	1	US-09-422-978B-6640	Sequence 6640, Ap	C 648	13.2	0.6	18	1	US-09-211-408-2	Sequence 2, Appl
C 576	13.4	0.6	18	1	US-09-371-772B-1493	Sequence 1493, Ap	C 649	13.2	0.6	18	1	US-09-289-466-64	Sequence 24, Appl
C 577	13.4	0.6	18	1	PCT-US93-12600-26	Sequence 26, Appl	C 650	13.2	0.6	18	1	US-09-034-205-64	Sequence 64, Appl
C 578	13.4	0.6	19	1	US-08-683-839B-17	Sequence 17, Appl	C 651	13.2	0.6	18	1	US-08-584-040-3053	Sequence 64, Appl
C 579	13.4	0.6	19	1	US-08-332-766A-67	Sequence 67, Appl	C 652	13.2	0.6	18	1	US-09-677-218B-64	Sequence 3053, Ap
C 580	13.4	0.6	19	1	US-08-181-664-68	Sequence 68, Appl	C 653	13.2	0.6	18	1	US-09-677-192-64	Sequence 64, Appl
C 581	13.4	0.6	19	1	US-09-545-435-2	Sequence 2, Appl	C 654	13.2	0.6	18	1	US-09-000-286A-23	Sequence 23, Appl
C 582	13.4	0.6	19	1	US-09-422-978B-5823	Sequence 5823, Ap	C 655	13.2	0.6	18	1	US-09-000-286A-24	Sequence 24, Appl
C 583	13.4	0.6	20	1	US-09-710-693-16	Sequence 16, Appl	C 656	13.2	0.6	18	1	US-09-422-978-4124	Sequence 4124, Ap
C 584	13.4	0.6	20	1	US-08-031-143B-56	Sequence 56, Appl	C 657	13.2	0.6	18	1	US-09-422-978-5112	Sequence 5112, Ap
C 585	13.4	0.6	20	1	US-08-390-256-4	Sequence 4, Appl	C 658	13.2	0.6	18	1	US-09-371-772B-1481	Sequence 1481, Ap
C 586	13.4	0.6	20	1	US-08-205-507-6	Sequence 6, Appl	C 659	13.2	0.6	18	1	US-08-050-743-38	Sequence 38, Appl
C 587	13.4	0.6	20	1	US-08-487-141B-8	Sequence 8, Appl	C 660	13.2	0.6	19	1	US-08-474-542A-190	Sequence 190, App
C 588	13.4	0.6	20	1	US-08-255-892-90	Sequence 90, Appl	C 661	13.2	0.6	19	1	US-08-457-648-190	Sequence 190, App
C 589	13.4	0.6	20	1	US-08-295-743-6	Sequence 6, Appl	C 662	13.2	0.6	19	1	US-08-452-055-38	Sequence 38, Appl
C 590	13.4	0.6	20	1	US-08-361-858-8	Sequence 8, Appl	C 663	13.2	0.6	19	1	US-08-817-926-36	Sequence 36, Appl
C 591	13.4	0.6	20	1	US-08-361-858-9	Sequence 9, Appl	C 664	13.2	0.6	19	1	US-09-358-972-114	Sequence 114, App
C 592	13.4	0.6	20	1	US-08-361-858-9	Sequence 9, Appl	C 665	13.2	0.6	19	1	US-09-102-491-8	Sequence 8, Appl
C 593	13.4	0.6	20	1	US-08-609-443B-45	Sequence 45, Appl	C 666	13.2	0.6	19	1	US-09-268-140-38	Sequence 38, Appl
C 594	13.4	0.6	20	1	US-08-927-561-8	Sequence 8, Appl	C 667	13.2	0.6	19	1	US-09-406-064-95	Sequence 95, Appl
C 595	13.4	0.6	20	1	US-08-680-326-136	Sequence 136, App	C 668	13.2	0.6	19	1	US-09-286-959B-9	Sequence 9, Appl
C 596	13.4	0.6	20	1	US-08-904-901-28	Sequence 20, Appl	C 669	13.2	0.6	19	1	US-09-228-342A-46	Sequence 46, Appl
C 597	13.4	0.6	20	1	US-08-750-064-20	Sequence 20, Appl	C 670	13.2	0.6	19	1	US-08-857-046A-1	Sequence 1, Appl
C 598	13.4	0.6	20	1	US-09-289-267-91	Sequence 91, Appl	C 671	13.2	0.6	19	1	US-09-383-316-13	Sequence 13, Appl
C 599	13.4	0.6	20	1	US-08-810-641-4	Sequence 4, Appl	C 672	13.2	0.6	19	1	US-09-360-416-106	Sequence 106, App
C 600	13.4	0.6	20	1	US-08-850-347-9	Sequence 9, Appl	C 673	13.2	0.6	19	1	US-09-573-252-1	Sequence 1, Appl
C 601	13.4	0.6	20	1	US-08-713-742-6	Sequence 6, Appl	C 674	13.2	0.6	19	1	US-09-422-978-4050	Sequence 4050, Ap
C 602	13.4	0.6	20	1	US-08-862-431-34	Sequence 34, Appl	C 675	13.2	0.6	19	1	US-09-422-978-4973	Sequence 4973, Ap
C 603	13.4	0.6	20	1	US-09-249-730-28	Sequence 28, Appl	C 676	13.2	0.6	19	1	US-09-422-978-6092	Sequence 6092, Ap
C 604	13.4	0.6	20	1	US-08-990-065-9	Sequence 9, Appl	C 677	13.2	0.6	19	1	US-09-422-978-7300	Sequence 7300, Ap
C 605	13.4	0.6	20	1	US-08-211-882-3	Sequence 3, Appl	C 678	13.2	0.6	19	1	US-09-422-978-7654	Sequence 7654, Ap
C 606	13.4	0.6	20	1	US-09-428-696-69	Sequence 69, Appl	C 679	13.2	0.6	19	1	US-09-096-724B-88	Sequence 8884, Ap
C 607	13.4	0.6	20	1	US-09-433-694-36	Sequence 36, Appl	C 680	13.2	0.6	19	1	US-09-788-847-95	Sequence 95, Appl
C 608	13.4	0.6	20	1	US-09-433-694-47	Sequence 47, Appl	C 681	13.2	0.6	20	1	US-07-874-334-13	Sequence 13, Appl
C 609	13.4	0.6	20	1	US-09-372-856-6	Sequence 6, Appl	C 682	13.2	0.6	20	1	US-08-031-143B-11	Sequence 11, Appl
C 610	13.4	0.6	20	1	US-09-103-875-122	Sequence 122, App	C 683	13.2	0.6	20	1	US-08-587-209-9	Sequence 9, Appl
C 611	13.4	0.6	20	1	US-09-128-508-4	Sequence 4, Appl	C 684	13.2	0.6	20	1	US-08-598-591-23	Sequence 23, Appl
C 612	13.4	0.6	20	1	US-09-389-896-4	Sequence 4, Appl	C 685	13.2	0.6	20	1	US-08-664-487A-10	Sequence 10, Appl
C 613	13.4	0.6	20	1	US-08-397-277A-8	Sequence 8, Appl	C 686	13.2	0.6	20	1		
C 614	13.4	0.6	20	1	US-08-397-277A-9	Sequence 9, Appl	C 687	13.2	0.6	20	1		
C 615	13.4	0.6	20	1	US-09-330-330-4	Sequence 4, Appl	C 688	13.2	0.6	20	1		
C 616	13.4	0.6	20	1	US-09-467-642-42	Sequence 42, Appl	C 689	13.2	0.6	20	1		
C 617	13.4	0.6	20	1	US-09-688-394-6	Sequence 6, Appl	C 690	13.2	0.6	20	1		

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691	13.2	0.6	20	1	US-08-664-487A-14	Sequence 14, Appl	764	13.2	0.6	20	1	US-09-135-080-19	Sequence 19, Appl
c 692	13.2	0.6	20	1	US-08-689-236-9	Sequence 9, Appl	c 765	13.2	0.6	20	1	US-09-702-327-60	Sequence 60, Appl
c 693	13.2	0.6	20	1	US-08-698-691-27	Sequence 27, Appl	c 766	13.2	0.6	20	1	US-09-907-843-18	Sequence 18, Appl
c 694	13.2	0.6	20	1	US-08-699-235-9	Sequence 9, Appl	767	13.2	0.6	20	1	US-09-613-444-8	Sequence 8, Appl
c 695	13.2	0.6	20	1	US-08-692-725-9	Sequence 9, Appl	c 768	13.2	0.6	20	1	US-09-517-467B-237	Sequence 237, Appl
c 696	13.2	0.6	20	1	US-08-640-517A-12	Sequence 12, Appl	769	13.2	0.6	20	1	US-09-690-364-56	Sequence 56, Appl
c 697	13.2	0.6	20	1	US-08-640-517A-16	Sequence 16, Appl	770	13.2	0.6	20	1	US-09-706-197-72	Sequence 72, Appl
c 698	13.2	0.6	20	1	US-08-592-658-4	Sequence 4, Appl	c 771	13.2	0.6	20	1	US-09-277-196-13	Sequence 13, Appl
c 699	13.2	0.6	20	1	US-08-176-427B-28	Sequence 28, Appl	c 772	13.2	0.6	20	1	US-09-305-856B-34	Sequence 34, Appl
700	13.2	0.6	20	1	US-08-982-867-10	Sequence 10, Appl	773	13.2	0.6	20	1	US-09-920-668-33	Sequence 33, Appl
701	13.2	0.6	20	1	US-08-982-867-14	Sequence 14, Appl	774	13.2	0.6	20	1	US-09-659-845A-28	Sequence 28, Appl
702	13.2	0.6	20	1	US-08-568-271-1	Sequence 1, Appl	775	13.2	0.6	20	1	US-09-542-552-11	Sequence 11, Appl
703	13.2	0.6	20	1	US-08-592-126-52	Sequence 52, Appl	c 776	13.2	0.6	20	1	US-09-668-313A-43	Sequence 43, Appl
c 704	13.2	0.6	20	1	US-08-571-983-12	Sequence 12, Appl	c 777	13.2	0.6	20	1	US-09-668-313A-80	Sequence 80, Appl
c 705	13.2	0.6	20	1	US-08-452-967-2	Sequence 2, Appl	778	13.2	0.6	20	1	US-09-668-313A-179	Sequence 179, Appl
706	13.2	0.6	20	1	US-08-332-766A-59	Sequence 59, Appl	c 779	13.2	0.6	20	1	US-09-647-133-9	Sequence 9, Appl
707	13.2	0.6	20	1	US-08-356-060A-28	Sequence 28, Appl	780	13.2	0.6	20	1	US-09-216-393B-285	Sequence 285, Appl
c 708	13.2	0.6	20	1	US-08-692-726-9	Sequence 9, Appl	c 781	13.2	0.6	20	1	US-08-921-497-6	Sequence 6, Appl
c 709	13.2	0.6	20	1	US-08-117-952-476	Sequence 476, Appl	c 782	13.2	0.6	20	1	US-09-883-405-2	Sequence 2, Appl
710	13.2	0.6	20	1	US-08-414-657D-29	Sequence 29, Appl	783	13.2	0.6	20	1	US-09-422-978-4567	Sequence 4567, Appl
711	13.2	0.6	20	1	US-08-414-657D-31	Sequence 31, Appl	c 784	13.2	0.6	20	1	US-09-422-978-7064	Sequence 7064, Appl
c 712	13.2	0.6	20	1	US-09-205-922-2	Sequence 2, Appl	c 785	13.2	0.6	20	1	US-09-422-978-7084	Sequence 7084, Appl
713	13.2	0.6	20	1	US-08-687-080-42	Sequence 42, Appl	c 786	13.2	0.6	20	1	Sequence 10993, A	
c 714	13.2	0.6	20	1	US-08-538-711A-11	Sequence 11, Appl	c 787	13.2	0.6	20	1	Sequence 81, Appl	
715	13.2	0.6	20	1	US-08-904-901-121	Sequence 121, Appl	c 788	13.2	0.6	20	1	Sequence 52, Appl	
c 716	13.2	0.6	20	1	US-08-825-487A-27	Sequence 27, Appl	789	13.2	0.6	20	1	Sequence 1559, Appl	
717	13.2	0.6	20	1	US-09-120-853-15	Sequence 15, Appl	790	13.2	0.6	20	1	Sequence 1586, Appl	
718	13.2	0.6	20	1	US-09-166-186-73	Sequence 73, Appl	791	13.2	0.6	20	1	Sequence 1586, Appl	
719	13.2	0.6	20	1	US-09-166-186-83	Sequence 83, Appl	792	13.2	0.6	20	1	Sequence 1695, Appl	
720	13.2	0.6	20	1	US-08-660-645A-13	Sequence 13, Appl	c 793	13.2	0.6	20	1	Sequence 1972, Appl	
721	13.2	0.6	20	1	US-09-249-730-121	Sequence 121, Appl	794	13.2	0.6	20	1	Sequence 2937, Appl	
c 722	13.2	0.6	20	1	US-09-298-718-13	Sequence 13, Appl	c 795	13.2	0.6	20	1	Sequence 2965, Appl	
c 723	13.2	0.6	20	1	US-09-418-641-39	Sequence 39, Appl	c 796	13.2	0.6	20	1	Sequence 3522, Appl	
c 724	13.2	0.6	20	1	US-09-074-475-27	Sequence 27, Appl	c 797	13.2	0.6	20	1	Sequence 3617, Appl	
c 725	13.2	0.6	20	1	US-08-973-273-24	Sequence 24, Appl	c 798	13.2	0.6	20	1	Sequence 3864, Appl	
c 726	13.2	0.6	20	1	US-09-429-323-30	Sequence 30, Appl	799	13.2	0.6	20	1	Sequence 3972, Appl	
727	13.2	0.6	20	1	US-09-288-461-44	Sequence 44, Appl	800	13.2	0.6	20	1	Sequence 4808, Appl	
728	13.2	0.6	20	1	US-08-460-900C-28	Sequence 28, Appl	801	13.2	0.6	20	1	Sequence 4937, Appl	
729	13.2	0.6	20	1	US-08-460-900C-58	Sequence 58, Appl	802	13.2	0.6	20	1	Sequence 5002, Appl	
c 730	13.2	0.6	20	1	US-09-433-699-35	Sequence 35, Appl	803	13.2	0.6	20	1	Sequence 5682, Appl	
c 731	13.2	0.6	20	1	US-09-433-699-41	Sequence 41, Appl	804	13.2	0.6	20	1	Sequence 5852, Appl	
c 732	13.2	0.6	20	1	US-09-433-699-59	Sequence 59, Appl	805	13.2	0.6	20	1	Sequence 6074, Appl	
c 733	13.2	0.6	20	1	US-09-428-696-62	Sequence 62, Appl	806	13.2	0.6	20	1	Sequence 6132, Appl	
c 734	13.2	0.6	20	1	US-09-428-692-161	Sequence 70, Appl	807	13.2	0.6	20	1	Sequence 6589, Appl	
c 735	13.2	0.6	20	1	US-09-280-805-237	Sequence 237, Appl	c 808	13.2	0.6	20	1	Sequence 6592, Appl	
c 736	13.2	0.6	20	1	US-09-280-805-246	Sequence 246, Appl	809	13.2	0.6	20	1	Sequence 1, Appl	
c 737	13.2	0.6	20	1	US-08-822-516-10	Sequence 10, Appl	810	13.2	0.6	20	1	Sequence 13, Appl	
c 738	13.2	0.6	20	1	US-09-546-969-13	Sequence 13, Appl	811	13.2	0.6	20	1	Sequence 28, Appl	
739	13.2	0.6	20	1	US-09-446-504-24	Sequence 24, Appl	812	13.2	0.6	20	1	Sequence 58, Appl	
c 740	13.2	0.6	20	1	US-09-103-875-119	Sequence 119, Appl	c 813	13.2	0.6	20	1	Sequence 149, Appl	
c 741	13.2	0.6	20	1	US-09-313-932-72	Sequence 72, Appl	814	13.2	0.6	20	1	Sequence 121, Appl	
c 742	13.2	0.6	20	1	US-09-313-932-83	Sequence 83, Appl	815	13.2	0.6	20	1	Sequence 140, Appl	
743	13.2	0.6	20	1	US-09-313-932-319	Sequence 319, Appl	816	13.2	0.6	20	1	Sequence 32, Appl	
c 744	13.2	0.6	20	1	US-08-706-344C-6	Sequence 6, Appl	817	13.2	0.6	20	1	Sequence 28, Appl	
745	13.2	0.6	20	1	US-08-725-027-11	Sequence 11, Appl	818	13.2	0.6	20	1	Sequence 28, Appl	
c 746	13.2	0.6	20	1	US-09-042-353-162	Sequence 162, Appl	819	13.2	0.6	20	1	Sequence 13, Appl	
c 747	13.2	0.6	20	1	US-08-674-509B-28	Sequence 28, Appl	820	13.2	0.6	20	1	Sequence 141, Appl	
748	13.2	0.6	20	1	US-08-954-698-28	Sequence 6, Appl	c 821	13.2	0.6	20	1	Sequence 67, Appl	
c 749	13.2	0.6	20	1	US-09-516-357-6	Sequence 34, Appl	822	13.2	0.6	20	1	Sequence 28, Appl	
c 750	13.2	0.6	20	1	US-09-254-733-34	Sequence 34, Appl	823	13.2	0.6	20	1	Sequence 3, Appl	
c 751	13.2	0.6	20	1	US-08-980-832-39	Sequence 39, Appl	c 824	13.2	0.6	20	1	Sequence 3, Appl	
752	13.2	0.6	20	1	US-09-167-375-18	Sequence 18, Appl	c 825	13.2	0.6	20	1	Sequence 75, Appl	
c 753	13.2	0.6	20	1	US-08-758-417A-10	Sequence 10, Appl	826	13.2	0.6	20	1	Sequence 28, Appl	
c 754	13.2	0.6	20	1	US-09-721-822A-91	Sequence 91, Appl	c 827	13.2	0.6	20	1	Sequence 55, Appl	
755	13.2	0.6	20	1	US-09-270-542-93	Sequence 93, Appl	828	13.2	0.6	20	1	Sequence 19, Appl	
c 756	13.2	0.6	20	1	US-09-131-684-10	Sequence 10, Appl	c 829	13.2	0.6	20	1	Sequence 91, Appl	
c 757	13.2	0.6	20	1	US-08-712-266-24	Sequence 24, Appl	830	13.2	0.6	20	1	Sequence 39, Appl	
c 758	13.2	0.6	20	1	US-08-722-015A-31	Sequence 31, Appl	c 831	13.2	0.6	20	1	Sequence 23, Appl	
759	13.2	0.6	20	1	US-08-957-874-28	Sequence 28, Appl	c 832	13.2	0.6	20	1	Sequence 11, Appl	
c 760	13.2	0.6	20	1	US-09-798-096-60	Sequence 60, Appl	c 833	13.2	0.6	20	1	Sequence 12, Appl	
c 761	13.2	0.6	20	1	US-09-798-096-69	Sequence 69, Appl	834	13	0.6	14	1	Sequence 7, Appl	
c 762	13.2	0.6	20	1	US-09-135-080-17	Sequence 17, Appl	835	13	0.6	14	1	Sequence 161, Appl	
763	13.2	0.6	20	1			c 836	13	0.6	14	1		

837	13	0.6	14	1	PCT-US95-04477-160	Sequence 160, App	c 910	12.8	0.6	17	1	US-08-435-628-828	Sequence 828, App
c 838	13	0.6	14	1	PCT-US95-04477-161	Sequence 161, App	c 911	12.8	0.6	17	1	US-08-435-628-830	Sequence 830, App
839	13	0.6	15	1	US-08-363-240A-225	Sequence 225, App	c 912	12.8	0.6	17	1	US-08-435-628-1935	Sequence 1935, App
840	13	0.6	15	1	US-08-363-240A-226	Sequence 226, App	c 913	12.8	0.6	17	1	US-08-435-628-2475	Sequence 2475, App
841	13	0.6	15	1	US-08-585-684B-662	Sequence 662, App	c 914	12.8	0.6	17	1	US-08-162-081B-19	Sequence 19, App
842	13	0.6	15	1	US-08-585-684B-663	Sequence 663, App	c 915	12.8	0.6	17	1	US-08-780-872-19	Sequence 19, App
843	13	0.6	15	1	US-08-952-597-2	Sequence 2, App	c 916	12.8	0.6	17	1	US-08-173-489C-38	Sequence 38, App
844	13	0.6	15	1	US-08-952-597-5	Sequence 5, App	c 917	12.8	0.6	17	1	US-08-725-976-20	Sequence 20, App
845	13	0.6	15	1	US-09-038-073-662	Sequence 662, App	c 918	12.8	0.6	17	1	US-08-671-978A-32	Sequence 32, App
846	13	0.6	15	1	US-09-038-073-663	Sequence 663, App	c 919	12.8	0.6	17	1	US-08-271-882B-20	Sequence 20, App
847	13	0.6	15	1	US-09-081-646-373	Sequence 373, App	c 920	12.8	0.6	17	1	US-08-985-162-14	Sequence 14, App
848	13	0.6	16	1	US-09-081-646-373	Sequence 27, App	c 921	12.8	0.6	17	1	US-08-985-162-15	Sequence 15, App
849	13	0.6	16	1	US-08-486-421-27	Sequence 27, App	c 922	12.8	0.6	17	1	US-08-985-162-42	Sequence 42, App
850	13	0.6	16	1	US-08-486-809-27	Sequence 27, App	c 923	12.8	0.6	17	1	US-08-726-278-20	Sequence 20, App
c 851	13	0.6	17	1	US-08-173-489C-2	Sequence 2, App	c 924	12.8	0.6	17	1	US-09-085-957-19	Sequence 19, App
852	13	0.6	17	1	US-08-733-816-2	Sequence 2, App	c 925	12.8	0.6	17	1	US-08-584-040-1936	Sequence 1936, App
853	13	0.6	17	1	US-08-892-540-2	Sequence 40, App	c 926	12.8	0.6	17	1	US-08-584-040-1937	Sequence 1937, App
854	13	0.6	17	1	US-08-953-171-40	Sequence 40, App	c 927	12.8	0.6	17	1	US-08-584-040-2351	Sequence 2351, App
855	13	0.6	17	1	US-08-584-040-5944	Sequence 5944, App	c 928	12.8	0.6	17	1	US-08-584-040-2403	Sequence 2403, App
856	13	0.6	17	1	US-08-584-040-5945	Sequence 5945, App	c 929	12.8	0.6	17	1	US-08-584-040-4181	Sequence 4181, App
857	13	0.6	17	1	US-08-584-040-5946	Sequence 5946, App	c 930	12.8	0.6	17	1	US-08-584-040-5498	Sequence 5498, App
858	13	0.6	17	1	US-09-371-772B-2781	Sequence 2781, App	c 931	12.8	0.6	17	1	US-08-584-040-5813	Sequence 5813, App
859	13	0.6	17	1	US-09-371-772B-2782	Sequence 2782, App	c 932	12.8	0.6	17	1	US-08-584-040-5815	Sequence 5815, App
860	13	0.6	17	1	US-09-371-772B-2783	Sequence 2783, App	c 933	12.8	0.6	17	1	US-08-584-040-5816	Sequence 5816, App
c 861	13	0.6	18	1	US-08-152-313-70	Sequence 70, App	c 934	12.8	0.6	17	1	US-08-679-645-883	Sequence 883, App
862	13	0.6	18	1	US-08-579-223-70	Sequence 70, App	c 935	12.8	0.6	17	1	US-08-679-645-884	Sequence 884, App
c 863	13	0.6	18	1	US-09-422-978-4796	Sequence 4796, App	c 936	12.8	0.6	17	1	US-09-474-432B-815	Sequence 815, App
864	13	0.6	18	1	US-08-780-562-36	Sequence 36, App	c 937	12.8	0.6	17	1	US-09-371-772B-481	Sequence 481, App
865	13	0.6	18	1	US-08-780-562-37	Sequence 37, App	c 938	12.8	0.6	17	1	US-09-371-772B-482	Sequence 482, App
c 866	13	0.6	18	1	PCT-US94-12947A-70	Sequence 70, App	c 939	12.8	0.6	17	1	US-09-371-772B-896	Sequence 896, App
867	13	0.6	19	1	US-08-242-435-29	Sequence 29, App	c 940	12.8	0.6	17	1	US-09-371-772B-948	Sequence 948, App
c 868	13	0.6	19	1	US-09-422-978-5976	Sequence 5976, App	c 941	12.8	0.6	17	1	US-09-371-772B-1948	Sequence 1948, App
869	13	0.6	19	1	US-09-422-978-7292	Sequence 7292, App	c 942	12.8	0.6	17	1	US-09-371-772B-2389	Sequence 2389, App
870	13	0.6	19	1	US-09-422-978-7382	Sequence 7382, App	c 943	12.8	0.6	17	1	US-09-371-772B-2678	Sequence 2678, App
871	13	0.6	20	1	US-08-179-738-22	Sequence 22, App	c 944	12.8	0.6	17	1	US-09-371-772B-2681	Sequence 2681, App
872	13	0.6	20	1	US-08-648-298-5	Sequence 5, App	c 945	12.8	0.6	17	1	US-09-371-772B-5395	Sequence 5395, App
873	13	0.6	20	1	US-08-628-145-22	Sequence 22, App	c 946	12.8	0.6	17	1	US-09-371-772B-5572	Sequence 5572, App
874	13	0.6	20	1	US-08-837-201C-129	Sequence 129, App	c 947	12.8	0.6	17	1	US-09-371-772B-5573	Sequence 5573, App
875	13	0.6	20	1	US-08-837-201C-137	Sequence 137, App	c 948	12.8	0.6	17	1	US-09-371-772B-6217	Sequence 6217, App
876	13	0.6	20	1	US-07-861-458C-84	Sequence 84, App	c 949	12.8	0.6	17	1	US-09-371-772B-6259	Sequence 6259, App
877	13	0.6	20	1	US-09-364-416-129	Sequence 129, App	c 950	12.8	0.6	17	1	US-09-371-772B-6593	Sequence 6593, App
c 878	13	0.6	20	1	US-09-364-416-137	Sequence 137, App	c 951	12.8	0.6	17	1	US-09-371-772B-6699	Sequence 6699, App
879	13	0.6	20	1	US-09-659-791A-45	Sequence 45, App	c 952	12.8	0.6	17	1	US-09-371-772B-6805	Sequence 6805, App
c 880	13	0.6	20	1	US-09-851-896-21	Sequence 21, App	c 953	12.8	0.6	17	1	US-09-401-063-14	Sequence 14, App
881	13	0.6	20	1	US-09-659-845A-57	Sequence 57, App	c 954	12.8	0.6	17	1	US-09-401-063-15	Sequence 15, App
882	13	0.6	20	1	US-09-403-343B-34	Sequence 34, App	c 955	12.8	0.6	17	1	US-09-827-998-317	Sequence 317, App
883	13	0.6	20	1	US-09-533-494A-19	Sequence 19, App	c 956	12.8	0.6	17	1	US-09-827-998-318	Sequence 318, App
c 884	13	0.6	20	1	US-09-081-385-33	Sequence 33, App	c 957	12.8	0.6	17	1	US-09-866-108A-2438	Sequence 2438, App
885	12.8	0.6	16	1	US-08-856-141-22	Sequence 22, App	c 958	12.8	0.6	17	1	US-09-866-108A-2439	Sequence 2439, App
886	12.8	0.6	16	1	US-09-094-714A-52	Sequence 52, App	c 959	12.8	0.6	17	1	US-09-866-108A-6561	Sequence 6561, App
887	12.8	0.6	16	1	US-09-495-140-22	Sequence 22, App	c 960	12.8	0.6	17	1	US-09-866-108A-7083	Sequence 7083, App
888	12.8	0.6	16	1	US-09-507-345A-11	Sequence 11, App	c 961	12.8	0.6	17	1	US-09-866-108A-8399	Sequence 8399, App
889	12.8	0.6	16	1	US-09-506-286B-35	Sequence 35, App	c 962	12.8	0.6	17	1	US-09-866-108A-8400	Sequence 8400, App
890	12.8	0.6	16	1	US-09-739-928-11	Sequence 11, App	c 963	12.8	0.6	17	1	US-09-866-108A-8666	Sequence 8666, App
c 891	12.8	0.6	16	1	US-09-762-861B-35	Sequence 35, App	c 964	12.8	0.6	17	1	US-09-866-108A-8943	Sequence 8943, App
892	12.8	0.6	16	1	US-09-762-861B-35	Sequence 35, App	c 965	12.8	0.6	17	1	US-09-866-108A-8948	Sequence 8948, App
c 893	12.8	0.6	16	1	US-09-479-005A-130	Sequence 130, App	c 966	12.8	0.6	17	1	US-09-866-108A-9076	Sequence 9076, App
894	12.8	0.6	16	1	US-10-065-133A-35	Sequence 35, App	c 967	12.8	0.6	17	1	US-09-866-108A-9226	Sequence 9226, App
c 895	12.8	0.6	17	1	US-08-152-313-57	Sequence 57, App	c 968	12.8	0.6	17	1	US-09-866-108A-9227	Sequence 9227, App
896	12.8	0.6	17	1	US-08-146-504-20	Sequence 20, App	c 969	12.8	0.6	17	1	US-09-866-108A-10559	Sequence 10559, App
c 897	12.8	0.6	17	1	US-08-390-850-529	Sequence 529, App	c 970	12.8	0.6	17	1	US-09-866-108A-10560	Sequence 10560, App
898	12.8	0.6	17	1	US-08-390-850-547	Sequence 547, App	c 971	12.8	0.6	17	1	PCT-US94-12947A-57	Sequence 57, App
c 899	12.8	0.6	17	1	US-08-390-850-568	Sequence 568, App	c 972	12.8	0.6	17	1	US-08-105-483-136	Sequence 136, App
900	12.8	0.6	17	1	US-08-373-124A-330	Sequence 330, App	c 973	12.8	0.6	17	1	US-08-105-483-287	Sequence 287, App
c 901	12.8	0.6	17	1	US-08-373-124A-828	Sequence 828, App	c 974	12.8	0.6	17	1	US-08-220-151-77	Sequence 77, App
c 902	12.8	0.6	17	1	US-08-373-124A-830	Sequence 830, App	c 975	12.8	0.6	17	1	US-07-977-284A-67	Sequence 67, App
c 903	12.8	0.6	17	1	US-08-373-124A-1935	Sequence 1935, App	c 976	12.8	0.6	17	1	US-08-050-073-70	Sequence 70, App
904	12.8	0.6	17	1	US-08-579-223-57	Sequence 57, App	c 977	12.8	0.6	17	1	US-08-379-081B-230	Sequence 230, App
c 905	12.8	0.6	17	1	US-08-435-634-529	Sequence 529, App	c 978	12.8	0.6	18	1		
906	12.8	0.6	17	1	US-08-435-634-547	Sequence 547, App	c 979	12.8	0.6	18	1		
907	12.8	0.6	17	1	US-08-435-634-568	Sequence 568, App	c 980	12.8	0.6	18	1		
c 908	12.8	0.6	17	1	US-08-435-634-568	Sequence 568, App	c 981	12.8	0.6	18	1		
909	12.8	0.6	17	1	US-08-435-628-330	Sequence 330, App	c 982	12.8	0.6	18	1		

c 983	12.8	0.6	18	1	US-08-146-504-6	Sequence 6, Appli	c1056	12.8	0.6	19	1	US-07-879-640A-3	Sequence 3, Appli
c 984	12.8	0.6	18	1	US-08-183-211-9	Sequence 9, Appli	c1057	12.8	0.6	19	1	US-07-879-594A-3	Sequence 3, Appli
c 985	12.8	0.6	18	1	US-08-379-078-230	Sequence 230, App	c1058	12.8	0.6	19	1	US-07-879-469A-3	Sequence 3, Appli
c 986	12.8	0.6	18	1	US-07-976-103A-11	Sequence 11, Appl	1059	12.8	0.6	19	1	US-08-505-509-26	Sequence 26, Appl
c 987	12.8	0.6	18	1	US-08-363-585-54	Sequence 54, Appl	1060	12.8	0.6	19	1	US-08-832-883-30	Sequence 30, Appl
c 988	12.8	0.6	18	1	US-08-363-585-94	Sequence 94, Appl	1061	12.8	0.6	19	1	US-08-832-877-30	Sequence 30, Appl
c 989	12.8	0.6	18	1	US-08-413-118-77	Sequence 77, Appl	1062	12.8	0.6	19	1	US-08-431-690A-26	Sequence 26, Appl
c 990	12.8	0.6	18	1	US-08-363-240A-1082	Sequence 1082, Ap	1063	12.8	0.6	19	1	US-08-491-690A-34	Sequence 34, Appl
c 991	12.8	0.6	18	1	US-08-224-657-53	Sequence 53, Appl	1064	12.8	0.6	19	1	US-08-496-944-5	Sequence 5, Appli
c 992	12.8	0.6	18	1	US-08-709-209-196	Sequence 196, App	c1065	12.8	0.6	19	1	US-08-950-720A-3	Sequence 3, Appli
c 993	12.8	0.6	18	1	US-08-709-209-287	Sequence 287, App	1066	12.8	0.6	19	1	US-09-280-409-5	Sequence 5, Appli
c 994	12.8	0.6	18	1	US-08-458-101-196	Sequence 196, App	1067	12.8	0.6	19	1	US-09-089-111-1	Sequence 11, Appl
c 995	12.8	0.6	18	1	US-08-458-101-287	Sequence 287, App	c1068	12.8	0.6	19	1	US-09-617-010C-11	Sequence 9, Appli
c 996	12.8	0.6	18	1	US-08-405-702A-15	Sequence 15, Appl	c1069	12.8	0.6	19	1	US-09-522-800-9	Sequence 11, Appl
c 997	12.8	0.6	18	1	US-08-473-481-11	Sequence 11, Appl	c1070	12.8	0.6	19	1	US-09-566-591-11	Sequence 478, App
c 998	12.8	0.6	18	1	US-08-184-009-31	Sequence 31, Appl	1071	12.8	0.6	19	1	US-09-338-907-78	Sequence 15, Appl
c 999	12.8	0.6	18	1	US-08-117-952-375	Sequence 375, App	c1072	12.8	0.6	19	1	US-08-718-388-15	Sequence 478, App
c1000	12.8	0.6	18	1	US-08-417-210A-51	Sequence 51, Appl	1073	12.8	0.6	19	1	US-09-218-207-478	Sequence 89, Appl
c1001	12.8	0.6	18	1	US-08-418-085-45	Sequence 45, Appl	1074	12.8	0.6	19	1	US-09-345-882-89	Sequence 199, App
c1002	12.8	0.6	18	1	US-08-725-976-6	Sequence 6, Appli	c1075	12.8	0.6	19	1	US-09-387-341-199	Sequence 21, Appl
c1003	12.8	0.6	18	1	US-08-458-356-51	Sequence 51, Appl	c1076	12.8	0.6	19	1	US-08-744-481A-21	Sequence 16, Appl
c1004	12.8	0.6	18	1	US-08-256-426B-67	Sequence 67, Appl	1077	12.8	0.6	19	1	US-09-434-408-16	Sequence 27, Appl
c1005	12.8	0.6	18	1	US-08-473-446-77	Sequence 77, Appl	1078	12.8	0.6	19	1	US-08-388-852B-2	Sequence 5302, Ap
c1006	12.8	0.6	18	1	US-08-271-882B-6	Sequence 6, Appli	1079	12.8	0.6	19	1	US-09-422-978-5302	Sequence 5401, Ap
c1007	12.8	0.6	18	1	US-08-617-256-33	Sequence 33, Appl	c1080	12.8	0.6	19	1	US-09-422-978-5401	Sequence 6462, Ap
c1008	12.8	0.6	18	1	US-08-912-272-83	Sequence 83, Appl	1081	12.8	0.6	19	1	US-09-422-978-5401	Sequence 24, Appl
c1009	12.8	0.6	18	1	US-09-205-143-21	Sequence 21, Appl	c1082	12.8	0.6	19	1	US-09-831-642-52	Sequence 52, Appl
c1010	12.8	0.6	18	1	US-09-094-714A-55	Sequence 45, Appl	c1083	12.8	0.6	19	1	PCT-US91-03680-2	Sequence 2, Appli
c1011	12.8	0.6	18	1	US-09-099-011A-45	Sequence 45, Appl	c1084	12.8	0.6	19	1	US-09-288-461-44	Sequence 44, Appl
c1012	12.8	0.6	18	1	US-09-287-141C-6	Sequence 6, Appli	c1085	12.8	0.6	19	1	US-08-478-470-7	Sequence 9, Appli
c1013	12.8	0.6	18	1	US-09-287-141-33	Sequence 33, Appl	1086	12.8	0.6	19	1	US-08-478-470-9	Sequence 7, Appli
c1014	12.8	0.6	18	1	US-09-431-613-33	Sequence 33, Appl	1087	12.8	0.6	19	1	US-08-214-599-7	Sequence 7, Appli
c1015	12.8	0.6	18	1	US-09-504-245-33	Sequence 33, Appl	1088	12.8	0.6	19	1	US-08-473-015-7	Sequence 9, Appli
c1016	12.8	0.6	18	1	US-09-287-682-33	Sequence 33, Appl	1089	12.8	0.6	19	1	US-08-473-015-9	Sequence 7, Appli
c1017	12.8	0.6	18	1	US-08-338-352-12	Sequence 12, Appl	1090	12.8	0.6	19	1	US-08-465-368-9	Sequence 9, Appli
c1018	12.8	0.6	18	1	US-08-726-278-6	Sequence 6, Appli	1091	12.8	0.6	19	1	US-08-477-306-9	Sequence 9, Appli
c1019	12.8	0.6	18	1	US-09-566-591-6	Sequence 6, Appli	1092	12.8	0.6	19	1	US-08-441-430-48	Sequence 4, Appli
c1020	12.8	0.6	18	1	US-09-287-679-33	Sequence 33, Appl	1093	12.8	0.6	19	1	US-08-663-023-4	Sequence 7, Appli
c1021	12.8	0.6	18	1	US-08-460-736-51	Sequence 51, Appl	1094	12.8	0.6	19	1	US-08-663-023-6	Sequence 6, Appli
c1022	12.8	0.6	18	1	US-09-397-768-33	Sequence 33, Appl	1095	12.8	0.6	19	1	US-08-540-104-6	Sequence 6, Appli
c1023	12.8	0.6	18	1	US-09-287-681-33	Sequence 33, Appl	1096	12.8	0.6	19	1	US-08-620-717A-6	Sequence 48, Appl
c1024	12.8	0.6	18	1	US-09-630-706-63	Sequence 63, Appl	1097	12.8	0.6	19	1	US-08-441-430-48	Sequence 4, Appli
c1025	12.8	0.6	18	1	US-09-495-444-33	Sequence 33, Appl	1098	12.8	0.6	19	1	US-08-132-168A-19	Sequence 19, Appl
c1026	12.8	0.6	18	1	US-09-354-138-53	Sequence 53, Appl	1099	12.8	0.6	19	1	US-08-832-883-44	Sequence 8, Appli
c1027	12.8	0.6	18	1	US-09-026-039-83	Sequence 83, Appl	1100	12.6	0.6	19	1	US-08-229-528-36	Sequence 36, Appl
c1028	12.8	0.6	18	1	US-08-584-040-3060	Sequence 3060, Ap	1101	12.6	0.6	19	1	US-08-832-877-44	Sequence 44, Appl
c1029	12.8	0.6	18	1	US-09-561-324-7	Sequence 7, Appli	c1102	12.6	0.6	19	1	US-08-650-125-8	Sequence 8, Appli
c1030	12.8	0.6	18	1	US-08-599-738A-11	Sequence 11, Appl	1103	12.6	0.6	19	1	US-08-132-168A-19	Sequence 19, Appl
c1031	12.8	0.6	18	1	US-08-744-481A-16	Sequence 16, Appl	1104	12.6	0.6	19	1	US-08-832-883-44	Sequence 44, Appl
c1032	12.8	0.6	18	1	US-09-000-286A-21	Sequence 21, Appl	1105	12.6	0.6	19	1	US-08-650-125-8	Sequence 8, Appli
c1033	12.8	0.6	18	1	US-09-000-286A-22	Sequence 22, Appl	c1106	12.6	0.6	19	1	US-08-663-023-4	Sequence 4, Appli
c1034	12.8	0.6	18	1	US-09-920-760-16	Sequence 16, Appl	1107	12.6	0.6	19	1	US-08-663-023-6	Sequence 7, Appli
c1035	12.8	0.6	18	1	US-09-920-760-84	Sequence 84, Appl	1108	12.6	0.6	19	1	US-08-663-023-7	Sequence 6, Appli
c1036	12.8	0.6	18	1	US-09-796-416-33	Sequence 33, Appl	1109	12.6	0.6	19	1	US-08-832-877-44	Sequence 8, Appli
c1037	12.8	0.6	18	1	US-09-535-370-51	Sequence 51, Appl	1110	12.6	0.6	19	1	US-08-494-151-9	Sequence 9, Appli
c1038	12.8	0.6	18	1	US-09-422-978-4190	Sequence 4190, Ap	1111	12.6	0.6	19	1	US-08-832-883-44	Sequence 44, Appl
c1039	12.8	0.6	18	1	US-09-422-978-4910	Sequence 4910, Ap	1112	12.6	0.6	19	1	US-08-832-883-44	Sequence 44, Appl
c1040	12.8	0.6	18	1	US-09-422-978-5052	Sequence 5052, Ap	c1113	12.6	0.6	19	1	US-08-832-877-44	Sequence 44, Appl
c1041	12.8	0.6	18	1	US-09-422-978-7185	Sequence 7185, Ap	1114	12.6	0.6	19	1	US-08-832-877-44	Sequence 44, Appl
c1042	12.8	0.6	18	1	US-09-422-978-7185	Sequence 7185, Ap	1115	12.6	0.6	19	1	US-08-832-877-44	Sequence 44, Appl
c1043	12.8	0.6	18	1	US-09-422-978-7185	Sequence 7185, Ap	1116	12.6	0.6	19	1	US-08-832-877-44	Sequence 44, Appl
c1044	12.8	0.6	18	1	US-09-422-978-7185	Sequence 7185, Ap	1117	12.6	0.6	19	1	US-08-832-877-44	Sequence 44, Appl
c1045	12.8	0.6	18	1	US-09-422-978-7185	Sequence 7185, Ap	1118	12.6	0.6	19	1	US-08-832-877-44	Sequence 44, Appl
c1046	12.8	0.6	18	1	US-09-422-978-7185	Sequence 7185, Ap	c1119	12.6	0.6	19	1	US-08-832-877-44	Sequence 44, Appl
c1047	12.8	0.6	18	1	US-09-422-978-7185	Sequence 7185, Ap	1120	12.6	0.6	19	1	US-08-832-877-44	Sequence 44, Appl
c1048	12.8	0.6	18	1	US-09-422-978-7185	Sequence 7185, Ap	c1121	12.6	0.6	19	1	US-08-832-877-44	Sequence 44, Appl
c1049	12.8	0.6	18	1	US-09-422-978-7185	Sequence 7185, Ap	1122	12.6	0.6	19	1	US-08-832-877-44	Sequence 44, Appl
c1050	12.8	0.6	18	1	US-09-422-978-7185	Sequence 7185, Ap	c1123	12.6	0.6	19	1	US-08-832-877-44	Sequence 44, Appl
c1051	12.8	0.6	18	1	US-09-422-978-7185	Sequence 7185, Ap	1124	12.6	0.6	19	1	US-08-832-877-44	Sequence 44, Appl
c1052	12.8	0.6	18	1	US-09-422-978-7185	Sequence 7185, Ap	1125	12.6	0.6	19	1	US-08-832-877-44	Sequence 44, Appl
c1053	12.8	0.6	18	1	US-09-422-978-7185	Sequence 7185, Ap	1126	12.6	0.6	19	1	US-08-832-877-44	Sequence 44, Appl
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c1055	12.8	0.6	18	1	US-09-422-978-7185	Sequence 7185, Ap	1128	12.6	0.6	19	1	US-08-832-877-44	Sequence 44, Appl

c1129	12.6	0.6	19	1	US-09-187-946-12	Sequence 12, Appl	1202	17	1	US-08-435-634-401	Sequence 401, App
1130	12.6	0.6	19	1	US-09-316-083-7	Sequence 7, Appl	1203	17	1	US-08-484-152-116	Sequence 116, App
1131	12.6	0.6	19	1	US-09-485-549-10	Sequence 10, Appl	c1204	17	1	US-08-435-628-190	Sequence 190, App
1132	12.6	0.6	19	1	US-08-294-312B-32	Sequence 32, Appl	c1205	17	1	US-08-435-628-192	Sequence 192, App
1133	12.6	0.6	19	1	US-09-224-048A-8	Sequence 8, Appl	c1206	17	1	US-08-541-950B-17	Sequence 17, Appl
1134	12.6	0.6	19	1	US-08-468-044B-32	Sequence 32, Appl	c1207	17	1	US-08-541-950B-17	Sequence 20, Appl
1135	12.6	0.6	19	1	US-09-306-828-36	Sequence 36, Appl	1208	17	1	US-08-292-620A-1905	Sequence 1905, App
1136	12.6	0.6	19	1	US-08-187-757D-30	Sequence 30, Appl	1209	17	1	US-08-292-620A-1940	Sequence 1940, App
1137	12.6	0.6	19	1	US-09-933-700-7	Sequence 7, Appl	1210	17	1	US-08-237-973-57	Sequence 57, Appl
1138	12.6	0.6	19	1	US-09-422-978-4976	Sequence 4976, App	1211	17	1	US-08-628-145-23	Sequence 23, Appl
1139	12.6	0.6	19	1	US-09-422-978-5450	Sequence 5450, App	1212	17	1	US-08-856-141-13	Sequence 13, Appl
1140	12.6	0.6	19	1	US-09-422-978-6658	Sequence 6658, App	1213	17	1	US-08-985-162-36	Sequence 36, Appl
1141	12.6	0.6	19	1	US-09-422-978-8800	Sequence 8800, App	c1214	17	1	US-08-985-162-37	Sequence 37, Appl
1142	12.6	0.6	19	1	US-09-422-978-11036	Sequence 11036, A	1215	17	1	US-08-658-136-8	Sequence 8, Appl
1143	12.6	0.6	19	1	US-09-422-978-11248	Sequence 11248, A	c1216	17	1	US-08-658-136-8	Sequence 8, Appl
1144	12.6	0.6	19	1	US-09-422-978-11269	Sequence 11269, A	c1217	17	1	US-08-658-136-8	Sequence 8, Appl
1145	12.6	0.6	19	1	US-09-422-978-11455	Sequence 11455, A	c1218	17	1	US-09-083-756A-17	Sequence 17, Appl
1146	12.6	0.6	19	1	US-08-192-943-28	Sequence 28, Appl	c1219	17	1	US-09-083-756A-20	Sequence 20, Appl
1147	12.6	0.6	19	1	US-09-184-072-8	Sequence 8, Appl	1220	17	1	US-09-071-845-1905	Sequence 1905, App
1148	12.6	0.6	19	1	US-08-465-679-32	Sequence 32, Appl	c1221	17	1	US-09-071-845-1940	Sequence 1940, App
1149	12.6	0.6	19	1	US-08-210-143C-30	Sequence 30, Appl	c1222	17	1	US-08-584-040-1461	Sequence 1461, App
1150	12.6	0.6	19	1	US-09-831-642-29	Sequence 29, Appl	1223	17	1	US-08-584-040-3886	Sequence 3886, App
1151	12.6	0.6	19	1	US-09-672-717-191	Sequence 191, App	c1224	17	1	US-08-584-040-3923	Sequence 3923, App
1152	12.6	0.6	19	1	US-08-672-717-214	Sequence 214, App	c1225	17	1	US-08-584-040-4183	Sequence 4183, App
1153	12.6	0.6	19	1	US-09-548-757B-69	Sequence 69, Appl	1226	17	1	US-08-584-040-5366	Sequence 5366, App
1154	12.6	0.6	19	1	PCT-US94-06331A-3	Sequence 3, Appl	c1227	17	1	US-08-584-040-5367	Sequence 5367, App
1155	12.6	0.6	19	1	PCT-US95-08605-2	Sequence 2, Appl	c1228	17	1	US-08-584-040-7624	Sequence 7624, App
1156	12.6	0.6	19	1	5169941-25	Patent No. 5169941	c1229	17	1	US-08-679-645-65	Sequence 65, Appl
1157	12.6	0.6	19	1	5352575-10	Patent No. 5352575	c1230	17	1	US-08-679-645-67	Sequence 67, Appl
1158	12.6	0.6	20	1	US-09-659-791A-44	Sequence 44, Appl	c1231	17	1	US-09-504-358-38	Sequence 38, Appl
1159	12.6	0.6	20	1	US-09-657-452A-96	Sequence 96, Appl	c1232	17	1	US-09-495-140-13	Sequence 13, Appl
1160	12.6	0.6	20	1	US-09-907-843-18	Sequence 18, Appl	c1233	17	1	US-09-954-314-38	Sequence 38, Appl
1161	12.4	0.6	14	1	US-07-803-633A-11	Sequence 11, Appl	c1234	17	1	US-09-371-772B-6	Sequence 6, Appl
1162	12.4	0.6	14	1	US-07-803-633A-11	Sequence 11, Appl	1235	17	1	US-09-371-772B-1653	Sequence 1653, App
1163	12.4	0.6	14	1	US-08-242-664-16	Sequence 16, Appl	c1236	17	1	US-09-371-772B-1690	Sequence 1690, App
1164	12.4	0.6	14	1	US-08-484-138-16	Sequence 16, Appl	1237	17	1	US-09-371-772B-1950	Sequence 1950, App
1165	12.4	0.6	14	1	US-08-525-742-21	Sequence 21, Appl	c1238	17	1	US-09-371-772B-2268	Sequence 2268, App
1166	12.4	0.6	14	1	US-08-525-742-21	Sequence 21, Appl	1239	17	1	US-09-371-772B-2269	Sequence 2269, App
1167	12.4	0.6	14	1	US-09-548-880B-4	Sequence 4, Appl	c1240	17	1	US-09-371-772B-6260	Sequence 6260, App
1168	12.4	0.6	14	1	PCT-US95-06379-16	Sequence 16, Appl	c1241	17	1	US-09-371-772B-6260	Sequence 6260, App
1169	12.4	0.6	15	1	US-08-311-760A-33	Sequence 33, Appl	c1242	17	1	US-09-371-772B-6747	Sequence 6747, App
1170	12.4	0.6	15	1	US-08-311-760A-34	Sequence 34, Appl	c1243	17	1	US-09-371-772B-6747	Sequence 6747, App
1171	12.4	0.6	15	1	US-08-291-932A-69	Sequence 69, Appl	c1244	17	1	US-09-371-772B-6748	Sequence 6748, App
1172	12.4	0.6	15	1	US-08-291-932A-69	Sequence 69, Appl	1245	17	1	US-09-371-772B-6863	Sequence 6863, App
1173	12.4	0.6	15	1	US-08-363-240A-14	Sequence 14, Appl	c1246	17	1	US-09-068-506-68	Sequence 68, Appl
1174	12.4	0.6	15	1	US-08-363-240A-14	Sequence 14, Appl	c1247	17	1	US-09-401-063-37	Sequence 37, Appl
1175	12.4	0.6	15	1	US-08-774-310-33	Sequence 33, Appl	1248	17	1	US-09-827-998-319	Sequence 319, App
1176	12.4	0.6	15	1	US-08-774-310-33	Sequence 33, Appl	1249	17	1	US-09-827-998-320	Sequence 320, App
1177	12.4	0.6	15	1	US-08-718-904-70	Sequence 70, Appl	c1250	17	1	US-09-866-108A-969	Sequence 969, App
1178	12.4	0.6	15	1	US-09-081-646-130	Sequence 130, App	c1251	17	1	US-09-866-108A-1460	Sequence 1460, App
1179	12.4	0.6	15	1	US-09-081-646-863	Sequence 863, App	c1252	17	1	US-09-866-108A-1461	Sequence 1461, App
1180	12.4	0.6	15	1	US-09-449-249-70	Sequence 70, Appl	c1253	17	1	US-09-866-108A-1462	Sequence 1462, App
1181	12.4	0.6	15	1	US-07-868-539C-13	Sequence 13, Appl	c1254	17	1	US-09-866-108A-1463	Sequence 1463, App
1182	12.4	0.6	15	1	PCT-US95-10973A-46	Sequence 46, Appl	c1255	17	1	US-09-866-108A-2208	Sequence 2208, App
1183	12.4	0.6	16	1	US-08-442-141-7	Sequence 7, Appl	c1256	17	1	US-09-866-108A-2212	Sequence 2212, App
1184	12.4	0.6	16	1	US-08-256-568B-22	Sequence 22, Appl	1257	17	1	US-09-866-108A-2735	Sequence 2735, App
1185	12.4	0.6	16	1	US-09-235-246-12	Sequence 12, Appl	1258	17	1	US-09-866-108A-2739	Sequence 2739, App
1186	12.4	0.6	16	1	US-09-038-369B-22	Sequence 22, Appl	1259	17	1	US-09-866-108A-2739	Sequence 2739, App
1187	12.4	0.6	16	1	US-08-535-249-43	Sequence 43, Appl	1260	17	1	US-09-866-108A-6565	Sequence 6565, App
1188	12.4	0.6	16	1	US-09-378-900A-22	Sequence 22, Appl	1261	17	1	US-09-866-108A-7087	Sequence 7087, App
1189	12.4	0.6	16	1	US-09-899-044-22	Sequence 22, Appl	1262	17	1	US-09-866-108A-8401	Sequence 8401, App
1190	12.4	0.6	16	1	US-09-371-772B-5804	Sequence 5804, App	1263	17	1	US-09-866-108A-8402	Sequence 8402, App
1191	12.4	0.6	17	1	US-08-357-399-5	Sequence 5, Appl	c1264	17	1	US-09-866-108A-8415	Sequence 8415, App
1192	12.4	0.6	17	1	US-08-357-666-5	Sequence 5, Appl	c1265	17	1	US-09-866-108A-8416	Sequence 8416, App
1193	12.4	0.6	17	1	US-08-206-175-5	Sequence 5, Appl	c1266	17	1	US-09-866-108A-8417	Sequence 8417, App
1194	12.4	0.6	17	1	US-08-179-738-23	Sequence 23, Appl	1267	17	1	US-09-866-108A-8418	Sequence 8418, App
1195	12.4	0.6	17	1	US-08-234-613-44	Sequence 44, Appl	c1268	17	1	US-09-866-108A-8418	Sequence 8418, App
1196	12.4	0.6	17	1	US-08-390-850-400	Sequence 400, App	1269	17	1	US-09-866-108A-8949	Sequence 8949, App
1197	12.4	0.6	17	1	US-08-390-850-401	Sequence 401, App	c1270	17	1	US-09-866-108A-8950	Sequence 8950, App
1198	12.4	0.6	17	1	US-08-373-124A-190	Sequence 190, App	c1271	17	1	US-09-866-108A-9224	Sequence 9224, App
1199	12.4	0.6	17	1	US-08-373-124A-192	Sequence 192, App	1272	17	1	US-09-866-108A-9225	Sequence 9225, App
1200	12.4	0.6	17	1	US-08-323-443B-6	Sequence 6, Appl	c1273	17	1	PCT-US95-11477-7	Sequence 7, Appl
1201	12.4	0.6	17	1	US-08-435-634-400	Sequence 400, App	c1274	18	1	US-07-766-351-17	Sequence 17, Appl

c1275	12.4	0.6	18	1	US-08-059-032-17	Sequence 17, Appl	c1348	12.4	0.6	19	1	US-09-127-480-147	Sequence 147, App
c1276	12.4	0.6	18	1	US-08-170-095B-34	Sequence 34, Appl	c1349	12.4	0.6	19	1	US-09-127-480-148	Sequence 148, App
1277	12.4	0.6	18	1	US-08-248-474-114	Sequence 114, App	c1350	12.4	0.6	19	1	US-08-456-841C-147	Sequence 147, App
c1278	12.4	0.6	18	1	US-08-396-866-34	Sequence 34, Appl	c1351	12.4	0.6	19	1	US-08-456-841C-148	Sequence 148, App
c1279	12.4	0.6	18	1	US-07-915-966C-6	Sequence 6, Appl	c1352	12.4	0.6	19	1	US-09-522-800-7	Sequence 7, Appl
1280	12.4	0.6	18	1	US-08-424-663-6	Sequence 6, Appl	c1353	12.4	0.6	19	1	US-09-342-479-2	Sequence 2, Appl
c1281	12.4	0.6	18	1	US-08-541-950B-23	Sequence 23, Appl	c1354	12.4	0.6	19	1	US-08-854-050-91	Sequence 91, Appl
1282	12.4	0.6	18	1	US-08-415-788-35	Sequence 35, Appl	c1355	12.4	0.6	19	1	US-09-430-323-91	Sequence 91, Appl
1283	12.4	0.6	18	1	US-08-771-182-6	Sequence 6, Appl	c1356	12.4	0.6	19	1	US-09-124-523-147	Sequence 147, App
1284	12.4	0.6	18	1	US-08-928-692-38	Sequence 38, Appl	c1357	12.4	0.6	19	1	US-09-124-523-148	Sequence 148, App
c1285	12.4	0.6	18	1	US-09-205-144-36	Sequence 36, Appl	c1358	12.4	0.6	19	1	US-08-145-826A-1	Sequence 1, Appl
1286	12.4	0.6	18	1	US-09-197-378-28	Sequence 28, Appl	c1359	12.4	0.6	19	1	US-09-616-796A-148	Sequence 148, App
1287	12.4	0.6	18	1	US-09-197-378-39	Sequence 39, Appl	c1360	12.4	0.6	19	1	US-09-688-532-1	Sequence 1, Appl
1288	12.4	0.6	18	1	US-09-156-425-32	Sequence 32, Appl	c1361	12.4	0.6	19	1	US-09-580-043B-6	Sequence 6, Appl
1289	12.4	0.6	18	1	US-08-872-446-10	Sequence 10, Appl	c1362	12.4	0.6	19	1	US-09-422-978-4030	Sequence 4030, App
c1290	12.4	0.6	18	1	US-08-138-024-14	Sequence 14, Appl	c1363	12.4	0.6	19	1	US-09-422-978-4225	Sequence 4225, App
1291	12.4	0.6	18	1	US-08-443-463B-26	Sequence 26, Appl	c1364	12.4	0.6	19	1	US-09-422-978-4225	Sequence 4225, App
c1292	12.4	0.6	18	1	US-09-339-993-34	Sequence 34, Appl	c1365	12.4	0.6	19	1	US-09-422-978-4756	Sequence 4756, App
1293	12.4	0.6	18	1	US-09-289-377-10	Sequence 10, Appl	c1366	12.4	0.6	19	1	US-09-422-978-4756	Sequence 4756, App
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1295	12.4	0.6	18	1	US-08-853-194-6	Sequence 6, Appl	c1368	12.4	0.6	19	1	US-09-422-978-4756	Sequence 4756, App
c1296	12.4	0.6	18	1	US-09-166-186-173	Sequence 173, App	c1369	12.4	0.6	19	1	US-09-422-978-4756	Sequence 4756, App
1297	12.4	0.6	18	1	US-09-166-186-174	Sequence 174, App	c1370	12.4	0.6	19	1	US-09-422-978-4756	Sequence 4756, App
1298	12.4	0.6	18	1	US-09-166-186-175	Sequence 175, App	c1371	12.4	0.6	19	1	US-09-422-978-4756	Sequence 4756, App
1299	12.4	0.6	18	1	US-09-166-186-176	Sequence 176, App	c1372	12.4	0.6	19	1	US-09-422-978-4756	Sequence 4756, App
c1300	12.4	0.6	18	1	US-08-756-849-114	Sequence 114, App	c1373	12.4	0.6	19	1	US-09-422-978-4756	Sequence 4756, App
c1301	12.4	0.6	18	1	US-09-058-489-83	Sequence 83, Appl	c1374	12.4	0.6	19	1	US-09-583-447A-31	Sequence 31, Appl
1302	12.4	0.6	18	1	US-09-058-489-83	Sequence 83, Appl	c1375	12.4	0.6	19	1	US-09-747-351-16	Sequence 16, Appl
c1303	12.4	0.6	18	1	US-09-083-756A-23	Sequence 23, Appl	c1376	12.4	0.6	19	1	US-09-672-717-129	Sequence 129, App
c1304	12.4	0.6	18	1	US-09-193-792-17	Sequence 17, Appl	c1377	12.4	0.6	19	1	US-09-672-717-129	Sequence 129, App
c1305	12.4	0.6	18	1	US-09-474-922A-48	Sequence 48, Appl	c1378	12.4	0.6	19	1	US-09-672-717-129	Sequence 129, App
c1306	12.4	0.6	18	1	US-09-071-433-41	Sequence 41, Appl	c1379	12.4	0.6	19	1	US-09-672-717-129	Sequence 129, App
1307	12.4	0.6	18	1	US-09-313-932-173	Sequence 173, App	c1380	12.4	0.6	19	1	US-09-672-717-129	Sequence 129, App
1308	12.4	0.6	18	1	US-09-313-932-174	Sequence 174, App	c1381	12.4	0.6	19	1	US-09-672-717-129	Sequence 129, App
1309	12.4	0.6	18	1	US-09-313-932-174	Sequence 174, App	c1382	12.4	0.6	19	1	US-09-672-717-129	Sequence 129, App
c1310	12.4	0.6	18	1	US-09-313-932-175	Sequence 175, App	c1383	12.4	0.6	19	1	US-09-672-717-129	Sequence 129, App
1311	12.4	0.6	18	1	US-09-313-932-176	Sequence 176, App	c1384	12.4	0.6	19	1	US-09-672-717-129	Sequence 129, App
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c1316	12.4	0.6	18	1	US-09-339-972-38	Sequence 38, Appl	c1389	12.4	0.6	19	1	US-09-672-717-129	Sequence 129, App
1317	12.4	0.6	18	1	US-08-584-040-8369	Sequence 8369, App	c1390	12.4	0.6	19	1	US-09-672-717-129	Sequence 129, App
c1318	12.4	0.6	18	1	US-09-342-681C-49	Sequence 49, Appl	c1391	12.4	0.6	19	1	US-09-672-717-129	Sequence 129, App
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1323	12.4	0.6	18	1	US-09-422-978-11485	Sequence 11485, A	c1396	12.4	0.6	19	1	US-09-672-717-129	Sequence 129, App
c1324	12.4	0.6	18	1	US-09-371-772B-4025	Sequence 4025, App	c1397	12.4	0.6	19	1	US-09-672-717-129	Sequence 129, App
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1337	12.4	0.6	19	1	US-08-592-541-148	Sequence 148, App	c1410	12.4	0.6	19	1	US-09-672-717-129	Sequence 129, App
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				c1566	17	1		

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c1568	12.2	0.6	17	1	US-09-866-108A-8301	Sequence 8301, Ap	c1641	12.2	0.6	18	1	US-08-710-330A-8	Sequence 8, Appl
1569	12.2	0.6	17	1	US-09-866-108A-8357	Sequence 8357, Ap	1642	12.2	0.6	18	1	US-08-450-905B-92	Sequence 92, Appl
1570	12.2	0.6	17	1	US-09-866-108A-8557	Sequence 8557, Ap	1643	12.2	0.6	18	1	US-08-173-489C-21	Sequence 21, Appl
1571	12.2	0.6	17	1	US-09-866-108A-8558	Sequence 8558, Ap	c1644	12.2	0.6	18	1	US-08-505-617-12	Sequence 12, Appl
1572	12.2	0.6	17	1	US-09-866-108A-8559	Sequence 8559, Ap	c1645	12.2	0.6	18	1	US-08-358-556A-30	Sequence 30, Appl
1573	12.2	0.6	17	1	US-09-866-108A-8560	Sequence 8560, Ap	c1646	12.2	0.6	18	1	US-08-282-197C-40	Sequence 40, Appl
1574	12.2	0.6	17	1	US-09-866-108A-8662	Sequence 8662, Ap	1647	12.2	0.6	18	1	US-08-585-888-7	Sequence 7, Appl
1575	12.2	0.6	17	1	US-09-866-108A-8663	Sequence 8663, Ap	c1648	12.2	0.6	18	1	US-08-432-871C-33	Sequence 33, Appl
1576	12.2	0.6	17	1	US-09-866-108A-8664	Sequence 8664, Ap	1649	12.2	0.6	18	1	US-08-585-684B-2582	Sequence 2582, Ap
1577	12.2	0.6	17	1	US-09-866-108A-8665	Sequence 8665, Ap	1650	12.2	0.6	18	1	US-08-474-450A-11	Sequence 11, Appl
1578	12.2	0.6	17	1	US-09-866-108A-8903	Sequence 8903, Ap	c1651	12.2	0.6	18	1	US-08-751-189-10	Sequence 10, Appl
c1579	12.2	0.6	17	1	US-09-866-108A-9020	Sequence 9020, Ap	c1652	12.2	0.6	18	1	US-08-912-129A-77	Sequence 77, Appl
c1580	12.2	0.6	17	1	US-09-866-108A-9072	Sequence 9072, Ap	1653	12.2	0.6	18	1	US-08-389-423-28	Sequence 28, Appl
c1581	12.2	0.6	17	1	US-09-866-108A-9073	Sequence 9073, Ap	c1654	12.2	0.6	18	1	US-08-567-375-14	Sequence 14, Appl
c1582	12.2	0.6	17	1	US-09-866-108A-9074	Sequence 9074, Ap	c1655	12.2	0.6	18	1	US-08-161-015-9	Sequence 9, Appl
c1583	12.2	0.6	17	1	US-09-866-108A-9075	Sequence 9075, Ap	1656	12.2	0.6	18	1	US-08-363-276B-18	Sequence 18, Appl
c1584	12.2	0.6	17	1	US-09-866-108A-9078	Sequence 9078, Ap	1657	12.2	0.6	18	1	US-08-532-979-1	Sequence 1, Appl
c1585	12.2	0.6	17	1	US-09-866-108A-9228	Sequence 9228, Ap	1658	12.2	0.6	18	1	US-08-313-979-4	Sequence 4, Appl
c1586	12.2	0.6	17	1	US-09-866-108A-9244	Sequence 9244, Ap	1659	12.2	0.6	18	1	US-08-532-979-4	Sequence 6, Appl
1587	12.2	0.6	17	1	US-09-866-108A-9891	Sequence 9891, A	1660	12.2	0.6	18	1	US-08-532-979-6	Sequence 22, Appl
1588	12.2	0.6	17	1	US-09-866-108A-10189	Sequence 10189, A	c1661	12.2	0.6	18	1	US-08-587-680A-23	Sequence 23, Appl
c1589	12.2	0.6	17	1	US-09-866-108A-10644	Sequence 10644, A	c1662	12.2	0.6	18	1	US-09-060-836-10	Sequence 10, Appl
c1590	12.2	0.6	17	1	PCT-US92-06821A-124	Sequence 124, App	c1663	12.2	0.6	18	1	US-09-213-768-17	Sequence 17, Appl
1591	12.2	0.6	18	1	US-07-702-163B-2	Sequence 2, Appl	1664	12.2	0.6	18	1	US-08-815-448-10	Sequence 10, Appl
1592	12.2	0.6	18	1	US-07-854-596B-17	Sequence 17, Appl	1665	12.2	0.6	18	1	US-08-815-448-30	Sequence 30, Appl
c1593	12.2	0.6	18	1	US-08-050-743-39	Sequence 39, Appl	c1666	12.2	0.6	18	1	US-08-890-980-86	Sequence 86, Appl
1594	12.2	0.6	18	1	US-08-244-113-21	Sequence 21, Appl	1667	12.2	0.6	18	1	US-09-156-253-41	Sequence 41, Appl
c1595	12.2	0.6	18	1	US-08-156-020-11	Sequence 11, Appl	1668	12.2	0.6	18	1	US-08-994-824-8	Sequence 8, Appl
c1596	12.2	0.6	18	1	US-08-474-542A-191	Sequence 191, App	1669	12.2	0.6	18	1	US-08-388-353-616	Sequence 616, App
1597	12.2	0.6	18	1	US-08-271-942A-108	Sequence 108, App	c1670	12.2	0.6	18	1	US-09-255-911-32	Sequence 32, Appl
c1598	12.2	0.6	18	1	US-08-164-200-13	Sequence 13, Appl	1671	12.2	0.6	18	1	US-09-255-888-31	Sequence 31, Appl
1599	12.2	0.6	18	1	US-08-411-795B-208	Sequence 208, App	c1672	12.2	0.6	18	1	US-08-488-551B-616	Sequence 616, App
c1600	12.2	0.6	18	1	US-08-390-850-1078	Sequence 1078, App	1673	12.2	0.6	18	1	US-08-404-796-112	Sequence 112, App
1601	12.2	0.6	18	1	US-08-390-850-1127	Sequence 1127, App	c1674	12.2	0.6	18	1	US-08-931-869-112	Sequence 112, App
c1603	12.2	0.6	18	1	US-08-319-492B-737	Sequence 737, App	1675	12.2	0.6	18	1	US-08-974-022-11	Sequence 11, Appl
1604	12.2	0.6	18	1	US-08-060-984-2	Sequence 2, Appl	1676	12.2	0.6	18	1	US-09-339-964-13	Sequence 13, Appl
1605	12.2	0.6	18	1	US-08-457-648-191	Sequence 191, App	c1677	12.2	0.6	18	1	US-08-890-979-75	Sequence 75, Appl
1606	12.2	0.6	18	1	US-08-373-124A-2227	Sequence 2227, App	c1678	12.2	0.6	18	1	US-09-156-807-32	Sequence 32, Appl
c1607	12.2	0.6	18	1	US-08-471-601-3	Sequence 3, Appl	c1679	12.2	0.6	18	1	US-09-344-520-8	Sequence 8, Appl
c1608	12.2	0.6	18	1	US-08-383-742-2	Sequence 2, Appl	c1680	12.2	0.6	18	1	US-09-344-520-34	Sequence 34, Appl
1609	12.2	0.6	18	1	US-08-363-240A-1083	Sequence 1083, Ap	1681	12.2	0.6	18	1	US-07-982-759P-92	Sequence 92, Appl
c1610	12.2	0.6	18	1	US-08-363-240A-1221	Sequence 1221, Ap	1682	12.2	0.6	18	1	US-08-779-916A-108	Sequence 108, App
c1611	12.2	0.6	18	1	US-08-363-240A-1224	Sequence 1224, Ap	c1683	12.2	0.6	18	1	US-08-516-859A-17	Sequence 17, Appl
1612	12.2	0.6	18	1	US-08-452-055-39	Sequence 39, Appl	1684	12.2	0.6	18	1	US-08-945-654-14	Sequence 14, Appl
c1613	12.2	0.6	18	1	US-08-458-067-40	Sequence 40, Appl	c1685	12.2	0.6	18	1	US-09-143-212-13	Sequence 13, Appl
c1614	12.2	0.6	18	1	US-08-435-634-1127	Sequence 1127, Ap	1686	12.2	0.6	18	1	US-09-147-550-115	Sequence 115, App
1615	12.2	0.6	18	1	US-08-435-634-1127	Sequence 1127, Ap	1687	12.2	0.6	18	1	US-09-205-143-71	Sequence 71, Appl
c1616	12.2	0.6	18	1	US-08-351-899-3	Sequence 3, Appl	c1688	12.2	0.6	18	1	US-09-205-143-71	Sequence 47, Appl
c1617	12.2	0.6	18	1	US-08-479-382-3	Sequence 29, Appl	1689	12.2	0.6	18	1	US-09-280-409-80	Sequence 80, Appl
c1618	12.2	0.6	18	1	US-08-505-509-29	Sequence 112, App	c1690	12.2	0.6	18	1	US-09-289-466-46	Sequence 46, Appl
1619	12.2	0.6	18	1	US-08-741-881-112	Sequence 3, Appl	c1691	12.2	0.6	18	1	US-09-289-466-65	Sequence 65, Appl
c1620	12.2	0.6	18	1	US-08-479-383-3	Sequence 3, Appl	c1692	12.2	0.6	18	1	US-09-032-894-86	Sequence 86, Appl
c1621	12.2	0.6	18	1	US-08-399-986B-13	Sequence 13, Appl	c1693	12.2	0.6	18	1	US-09-487-444-32	Sequence 32, Appl
c1622	12.2	0.6	18	1	US-08-727-003A-55	Sequence 55, Appl	c1694	12.2	0.6	18	1	US-09-184-445-10	Sequence 10, Appl
1623	12.2	0.6	18	1	US-08-758-306-517	Sequence 517, App	1695	12.2	0.6	18	1	US-09-071-433-66	Sequence 2582, Ap
c1624	12.2	0.6	18	1	US-08-758-306-527	Sequence 527, App	1696	12.2	0.6	18	1	US-08-983-466-42	Sequence 42, Appl
c1625	12.2	0.6	18	1	US-08-758-306-527	Sequence 527, App	1697	12.2	0.6	18	1	US-09-193-377B-28	Sequence 28, Appl
c1626	12.2	0.6	18	1	US-08-459-568-17	Sequence 17, Appl	1698	12.2	0.6	18	1	US-09-193-377B-28	Sequence 86, Appl
c1627	12.2	0.6	18	1	US-08-739-158-112	Sequence 112, App	1699	12.2	0.6	18	1	US-09-031-626-86	Sequence 10, Appl
1628	12.2	0.6	18	1	US-08-469-319A-208	Sequence 208, App	1700	12.2	0.6	18	1	US-09-307-392-10	Sequence 10, Appl
c1629	12.2	0.6	18	1	US-08-435-628-2227	Sequence 2227, Ap	c1701	12.2	0.6	18	1	US-09-307-392-10	Sequence 203, App
1630	12.2	0.6	18	1	US-08-493-754B-13	Sequence 3, Appl	c1702	12.2	0.6	18	1	US-09-358-972-203	Sequence 224, App
c1631	12.2	0.6	18	1	US-08-528-523-3	Sequence 3, Appl	1703	12.2	0.6	18	1	US-09-358-972-224	Sequence 20, Appl
c1632	12.2	0.6	18	1	US-08-528-523-3	Sequence 3, Appl	1704	12.2	0.6	18	1	US-09-431-480-20	Sequence 90, Appl
c1633	12.2	0.6	18	1	US-08-639-363-16	Sequence 16, Appl	c1705	12.2	0.6	18	1	US-09-018-584A-90	Sequence 13, Appl
c1634	12.2	0.6	18	1	US-08-399-411-17	Sequence 17, Appl	1706	12.2	0.6	18	1	US-09-290-577-13	Sequence 20, Appl
c1635	12.2	0.6	18	1	US-08-267-803B-69	Sequence 69, Appl	c1707	12.2	0.6	18	1	US-09-617-302-20	Sequence 20, Appl
1636	12.2	0.6	18	1	US-08-479-041-3	Sequence 3, Appl	1708	12.2	0.6	18	1	US-09-042-353-20	Sequence 16, Appl
c1637	12.2	0.6	18	1	US-08-479-041-3	Sequence 112, App	1709	12.2	0.6	18	1	US-08-955-918C-16	
c1638	12.2	0.6	18	1	US-08-739-167-112		1710	12.2	0.6	18	1		
1639	12.2	0.6	18	1			1711	12.2	0.6	18	1		
	12.2	0.6	18	1			1712	12.2	0.6	18	1		

c1713	12.2	0.6	18	1	US-09-268-140-41	Sequence 41, Appl	c1786	12.2	0.6	18	1	US-09-422-978-3939	Sequence 3939, Ap
c1714	12.2	0.6	18	1	US-09-406-064-31	Sequence 31, Appl	1787	12.2	0.6	18	1	US-09-422-978-4694	Sequence 4694, Ap
c1715	12.2	0.6	18	1	US-09-406-064-69	Sequence 69, Appl	1788	12.2	0.6	18	1	US-09-422-978-4802	Sequence 4802, Ap
c1716	12.2	0.6	18	1	US-09-430-615-39	Sequence 39, Appl	c1789	12.2	0.6	18	1	US-09-422-978-4840	Sequence 4840, Ap
c1717	12.2	0.6	18	1	US-09-430-615-60	Sequence 60, Appl	1790	12.2	0.6	18	1	US-09-422-978-5094	Sequence 5094, Ap
c1718	12.2	0.6	18	1	US-09-630-706-62	Sequence 62, Appl	c1791	12.2	0.6	18	1	US-09-422-978-5220	Sequence 5220, Ap
c1719	12.2	0.6	18	1	US-09-461-697-466	Sequence 466, Appl	1792	12.2	0.6	18	1	US-09-422-978-5991	Sequence 5991, Ap
c1720	12.2	0.6	18	1	US-09-109-663-78	Sequence 78, Appl	1793	12.2	0.6	18	1	US-09-422-978-6085	Sequence 6085, Ap
c1721	12.2	0.6	18	1	US-09-380-786A-10	Sequence 10, Appl	c1794	12.2	0.6	18	1	US-09-422-978-7395	Sequence 7395, Ap
c1722	12.2	0.6	18	1	US-09-380-786A-28	Sequence 28, Appl	c1795	12.2	0.6	18	1	US-09-422-978-7630	Sequence 7630, Ap
c1723	12.2	0.6	18	1	US-08-819-646-3	Sequence 3, Appl	c1796	12.2	0.6	18	1	US-09-422-978-7630	Sequence 7630, Ap
c1724	12.2	0.6	18	1	US-08-557-917-115	Sequence 115, Appl	c1797	12.2	0.6	18	1	US-09-422-978-7630	Sequence 7630, Ap
c1725	12.2	0.6	18	1	US-08-795-445A-11	Sequence 11, Appl	1798	12.2	0.6	18	1	US-09-422-978-7650	Sequence 7650, Ap
c1726	12.2	0.6	18	1	US-08-795-447A-11	Sequence 11, Appl	1799	12.2	0.6	18	1	US-09-422-978-8626	Sequence 8626, Ap
c1727	12.2	0.6	18	1	US-08-974-186-11	Sequence 11, Appl	c1799	12.2	0.6	18	1	US-09-422-978-11532	Sequence 11532, A
c1728	12.2	0.6	18	1	US-08-795-446B-11	Sequence 11, Appl	c1800	12.2	0.6	18	1	US-09-536-059-24	Sequence 24, Appl
c1729	12.2	0.6	18	1	US-09-723-534-20	Sequence 20, Appl	c1801	12.2	0.6	18	1	US-09-655-804B-49	Sequence 49, Appl
c1730	12.2	0.6	18	1	US-09-304-452-3	Sequence 3, Appl	1802	12.2	0.6	18	1	US-09-679-409-134	Sequence 134, Appl
c1731	12.2	0.6	18	1	US-08-758-417A-287	Sequence 287, Appl	1803	12.2	0.6	18	1	US-09-371-772B-2965	Sequence 2966, Ap
c1732	12.2	0.6	18	1	US-09-290-452-13	Sequence 13, Appl	c1804	12.2	0.6	18	1	US-09-371-772B-4002	Sequence 4002, Ap
c1733	12.2	0.6	18	1	US-09-406-065-44	Sequence 44, Appl	c1805	12.2	0.6	18	1	US-09-371-772B-4038	Sequence 4038, Ap
c1734	12.2	0.6	18	1	US-09-406-065-55	Sequence 55, Appl	c1806	12.2	0.6	18	1	US-09-601-144-19	Sequence 19, Appl
c1735	12.2	0.6	18	1	US-09-301-456-4	Sequence 4, Appl	c1807	12.2	0.6	18	1	US-09-762-861B-28	Sequence 28, Appl
c1736	12.2	0.6	18	1	US-09-430-201-3	Sequence 3, Appl	c1808	12.2	0.6	18	1	US-09-021-410-1	Sequence 1, Appl
c1737	12.2	0.6	18	1	US-09-355-947-6	Sequence 6, Appl	c1809	12.2	0.6	18	1	US-09-569-852B-8	Sequence 8, Appl
c1738	12.2	0.6	18	1	US-09-586-472-17	Sequence 17, Appl	c1810	12.2	0.6	18	1	US-09-356-806-126	Sequence 126, App
c1739	12.2	0.6	18	1	US-09-290-338-13	Sequence 13, Appl	c1811	12.2	0.6	18	1	US-09-356-806-131	Sequence 131, App
c1740	12.2	0.6	18	1	US-09-350-399-112	Sequence 112, App	c1812	12.2	0.6	18	1	US-09-356-806-142	Sequence 142, App
c1741	12.2	0.6	18	1	US-08-584-040-6204	Sequence 6204, Ap	c1813	12.2	0.6	18	1	US-09-954-594A-13	Sequence 13, Appl
c1742	12.2	0.6	18	1	US-08-584-040-8346	Sequence 8346, Ap	c1814	12.2	0.6	18	1	US-09-587-934B-20	Sequence 20, Appl
c1743	12.2	0.6	18	1	US-08-584-040-8382	Sequence 8382, Ap	c1815	12.2	0.6	18	1	US-08-993-765-2	Sequence 2, Appl
c1744	12.2	0.6	18	1	US-09-303-069-21	Sequence 21, Appl	c1816	12.2	0.6	18	1	US-08-993-765-3	Sequence 3, Appl
c1745	12.2	0.6	18	1	US-09-205-995-17	Sequence 17, Appl	c1817	12.2	0.6	18	1	US-08-577-788C-11	Sequence 11, Appl
c1746	12.2	0.6	18	1	US-08-706-945D-5	Sequence 5, Appl	c1818	12.2	0.6	18	1	US-09-663-834A-31	Sequence 31, Appl
c1747	12.2	0.6	18	1	US-09-395-345-10	Sequence 10, Appl	c1819	12.2	0.6	18	1	US-09-204-865-6	Sequence 6, Appl
c1748	12.2	0.6	18	1	US-09-236-409A-112	Sequence 112, Appl	c1820	12.2	0.6	18	1	US-09-321-249-20	Sequence 20, Appl
c1749	12.2	0.6	18	1	US-09-540-699-1	Sequence 1, Appl	c1821	12.2	0.6	18	1	US-09-913-514-19	Sequence 19, Appl
c1750	12.2	0.6	18	1	US-09-383-316-81	Sequence 81, Appl	c1822	12.2	0.6	18	1	US-09-788-847-31	Sequence 31, Appl
c1751	12.2	0.6	18	1	US-09-167-109-42	Sequence 42, Appl	c1823	12.2	0.6	18	1	US-09-788-847-69	Sequence 69, Appl
c1752	12.2	0.6	18	1	US-09-345-882-140	Sequence 140, Appl	c1824	12.2	0.6	18	1	US-09-367-513-6	Sequence 6, Appl
c1753	12.2	0.6	18	1	US-08-697-766A-13	Sequence 13, Appl	c1825	12.2	0.6	18	1	US-09-828-303-25	Sequence 25, Appl
c1754	12.2	0.6	18	1	US-09-195-716-3	Sequence 3, Appl	c1826	12.2	0.6	18	1	US-10-065-133A-28	Sequence 28, Appl
c1755	12.2	0.6	18	1	US-09-387-341-134	Sequence 134, Appl	c1827	12.2	0.6	18	1	PCT-US94-07297-28	Sequence 28, Appl
c1756	12.2	0.6	18	1	US-09-387-341-152	Sequence 152, Appl	c1828	12.2	0.6	18	1	PCT-US94-07297-30	Sequence 30, Appl
c1757	12.2	0.6	18	1	US-09-189-028-28	Sequence 28, Appl	c1829	12.2	0.6	18	1	PCT-US95-08604-108	Sequence 108, App
c1758	12.2	0.6	18	1	US-09-402-631A-40	Sequence 40, Appl	c1830	12.2	0.6	18	1	PCT-US95-16718-18	Sequence 18, Appl
c1759	12.2	0.6	18	1	US-08-764-114-208	Sequence 208, Appl	c1831	12.2	0.6	18	1	PCT-US96-07795-40	Sequence 40, Appl
c1760	12.2	0.6	18	1	US-09-270-356-33	Sequence 33, Appl	c1832	12.2	0.6	18	1	PCT-US96-07796-40	Sequence 40, Appl
c1761	12.2	0.6	18	1	US-09-502-558-40	Sequence 40, Appl	c1833	12.2	0.6	18	1	PCT-US96-09915-8	Sequence 8, Appl
c1762	12.2	0.6	18	1	US-09-750-580-6	Sequence 6, Appl	1833	12.2	0.6	18	1	5457089-24	Patent No. 5457089
c1763	12.2	0.6	18	1	US-09-091-952A-146	Sequence 146, Appl							
c1764	12.2	0.6	18	1	US-09-261-115-9	Sequence 9, Appl							
c1765	12.2	0.6	18	1	US-08-469-419-208	Sequence 208, Appl							
c1766	12.2	0.6	18	1	US-09-328-706-17	Sequence 17, Appl							
c1767	12.2	0.6	18	1	US-09-807-166-5	Sequence 5, Appl							
c1768	12.2	0.6	18	1	US-09-539-333D-231	Sequence 231, Appl							
c1769	12.2	0.6	18	1	US-09-126-851C-1	Sequence 1, Appl							
c1770	12.2	0.6	18	1	US-09-126-851C-2	Sequence 2, Appl							
c1771	12.2	0.6	18	1	US-09-126-851C-9	Sequence 9, Appl							
c1772	12.2	0.6	18	1	US-09-126-851C-10	Sequence 10, Appl							
c1773	12.2	0.6	18	1	US-09-126-851C-13	Sequence 13, Appl							
c1774	12.2	0.6	18	1	US-09-499-522-20	Sequence 20, Appl							
c1775	12.2	0.6	18	1	US-09-506-286B-28	Sequence 28, Appl							
c1776	12.2	0.6	18	1	US-09-725-265-20	Sequence 20, Appl							
c1777	12.2	0.6	18	1	US-09-555-313B-16	Sequence 16, Appl							
c1778	12.2	0.6	18	1	US-09-216-393B-346	Sequence 346, Appl							
c1779	12.2	0.6	18	1	US-07-868-539C-1	Sequence 1, Appl							
c1780	12.2	0.6	18	1	US-07-868-539C-2	Sequence 2, Appl							
c1781	12.2	0.6	18	1	US-09-671-317-493	Sequence 493, Appl							
c1782	12.2	0.6	18	1	US-09-292-542A-15	Sequence 15, Appl							
c1783	12.2	0.6	18	1	US-09-290-000-13	Sequence 13, Appl							
c1784	12.2	0.6	18	1	US-09-394-455-16	Sequence 16, Appl							
c1785	12.2	0.6	18	1	US-09-394-455-17	Sequence 17, Appl							

ALIGNMENTS

RESULT 1

US-09-328-925-18/c
; Sequence 18, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
; APPLICANT: Kurachi, Kotoku
; APPLICANT: Kurachi, Sumiko
; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: UM-03603
; CURRENT APPLICATION NUMBER: US/09/328,925
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

Thu Sep 16 13:16:23 2004

schultz167-3.rni

US-09-328-925-18

Query Match 0.9%; Score 19.4; DB 1; Length 29;
Best Local Similarity 79.3%; Pred. No. 32;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2031 TCCTTTTTCAGATACATATTTTCATTTTG 2059
Db 29 TCCATTTTGAGTTAATATTTTCATGCTTG 1

RESULT 2

US-08-245-758-13
; Sequence 13, Application US/08245758
; Patent No. 5607846
; GENERAL INFORMATION:
; APPLICANT: Murphy, Timothy F.
; APPLICANT: Brushan, Reva
; TITLE OF INVENTION: Vaccine for Moraxella catarrhalis
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Kb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/245,758
; FILING DATE: 17/05/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 11520.0051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 13 :
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; IMMEDIATE SOURCE: synthesized
; ORIGINAL SOURCE:
; ORGANISM: Moraxella catarrhalis
; STRAIN: 25240
; CELL TYPE: bacterium
; PCT-US95-05134-13

Query Match 0.9%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 43;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1097 TCAGTCCTTCCAATATGACTAAC 1119
Db 2 TCAGTCCTTCCAATATGATAAAC 24

RESULT 3

PCT-US95-05134-13
; Sequence 13, Application PC/TUS9505134
; GENERAL INFORMATION:
; APPLICANT: Murphy, Timothy F.
; APPLICANT: Brushan, Reva
; TITLE OF INVENTION: Vaccine for Moraxella catarrhalis
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Kb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/245,758
; FILING DATE: 17/05/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 11520.0051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 13 :
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; IMMEDIATE SOURCE: synthesized
; ORIGINAL SOURCE:
; ORGANISM: Moraxella catarrhalis
; STRAIN: 25240
; CELL TYPE: bacterium
; PCT-US95-05134-13

Query Match 0.9%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 43;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1097 TCAGTCCTTCCAATATGACTAAC 1119
Db 2 TCAGTCCTTCCAATATGATAAAC 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Kb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05134
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: U.S. Serial No. 08/245,758
FILING DATE: 17/05/94
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 11520.0063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 13 :
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
IMMEDIATE SOURCE: synthesized
ORIGINAL SOURCE:
ORGANISM: Moraxella catarrhalis
STRAIN: 25240
CELL TYPE: bacterium
PCT-US95-05134-13

Query Match 0.9%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 43;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1097 TCAGTCCTTCCAATATGACTAAC 1119
Db 2 TCAGTCCTTCCAATATGATAAAC 24

RESULT 4

US-09-866-108A-13560
; Sequence 13560, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667

Query Match 0.9%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 43;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1097 TCAGTCCTTCCAATATGACTAAC 1119
Db 2 TCAGTCCTTCCAATATGATAAAC 24

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13560
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13560

Query Match          0.9%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1449 GGAGAAACCAAGGAGGAGAGC 1471
      ||||| ||||| ||||| ||||| |||||
Db 3 GGAGGAAGCCCAAGAGGAGAGC 25

RESULT 5
US-09-866-108A-13561
; Sequence 13561, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13561
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13561

Query Match          0.9%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1449 GGAGAAACCAAGGAGGAGAGC 1471
      ||||| ||||| ||||| ||||| |||||
Db 3 GGAGGAAGCCCAAGAGGAGAGC 25

RESULT 5
US-09-866-108A-13561
; Sequence 13561, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13561
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13561

Query Match          0.9%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1449 GGAGAAACCAAGGAGGAGAGC 1471
      ||||| ||||| ||||| ||||| |||||
Db 1 GGAGGAAGCCCAAGAGGAGAGC 23

RESULT 7
US-08-856-331-16
; Sequence 16, Application US/08856331
; Patent No. 607705
; GENERAL INFORMATION:
; APPLICANT: Duan, Lingxun
```

```
; ORGANISM: Homo sapiens
US-09-866-108A-13561

Query Match          0.9%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1449 GGAGAAACCAAGGAGGAGAGC 1471
      ||||| ||||| ||||| ||||| |||||
Db 2 GGAGGAAGCCCAAGAGGAGAGC 24

RESULT 6
US-09-866-108A-13562
; Sequence 13562, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13562
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13562

Query Match          0.9%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1449 GGAGAAACCAAGGAGGAGAGC 1471
      ||||| ||||| ||||| ||||| |||||
Db 1 GGAGGAAGCCCAAGAGGAGAGC 23

RESULT 7
US-08-856-331-16
; Sequence 16, Application US/08856331
; Patent No. 607705
; GENERAL INFORMATION:
; APPLICANT: Duan, Lingxun
```

APPLICANT: Pomerantz, Roger J.
APPLICANT: Zeirn, Mark A.
TITLE OF INVENTION: RIBOZYME MEDIATE GENE REPLACEMENT
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6077705ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,331
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,132
FILING DATE: 17-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-2207
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: mRNA
US-08-856-331-16

Query Match 0.9%; Score 18.2; DB 1; Length 26;
Best Local Similarity 56.5%; Pred. No. 52;
Matches 13; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 915 TGTGAATTGTCAAGAGCTTTA 937
DB 4 UGUGGAUUGGUAAGAGCUGA 26

RESULT 8
US-08-584-040-756
Sequence 756, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 756:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: The letter "N" represents the stem II region
OTHER INFORMATION: of an HH ribozyme.
US-08-584-040-756

Query Match 0.9%; Score 18.2; DB 1; Length 27;
Best Local Similarity 79.2%; Pred. No. 57;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1389 AGTCAAAACAGAGGATGAAAAGA 1412
DB 1 AGUCAAAACUGAUGANGAAAAAA 24

RESULT 9
US-08-066-325-49/c
Sequence 49, Application US/08066325
Patent No. 5667967
GENERAL INFORMATION:
APPLICANT: Steinman, Lawrence
APPLICANT: Oksenberg, Jorge
APPLICANT: Bernard, Claude
TITLE OF INVENTION: T-CELL RECEPTOR VARIABLE TRANSCRIPTS AS DISEASE RELATED MARK
NUMBER OF SEQUENCES: 157
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/066,325
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5667967tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 690068.408C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 49:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-066-325-49

Query Match 0.9%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 643 ATGACTGTGCTCTTCAT 660
Db 24 ATGACTGTGCTCTTCAT 7

RESULT 10

US-09-866-108A-13968/c
; Sequence 13968, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOmica-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: AeoMica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 13968

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-13968

Query Match 0.8%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1511 GAATGGACCTCTCCAGCTCTGGCT 1534
Db 25 GAATGGATGTCTCCAGCTCTGTCT 2

RESULT 11

US-09-866-108A-13969/c
; Sequence 13969, Application US/09866108A
; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharon G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOmica-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: AeoMica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 13969

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-13969

Query Match 0.8%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1511 GAATGGACCTCTCCAGCTCTGGCT 1534
Db 24 GAATGGATGTCTCCAGCTCTGTCT 1

RESULT 12

US-07-814-964-1/c

; Sequence 1, Application US/07814964

; Patent No. 5359047

; GENERAL INFORMATION:

; APPLICANT: Donahue, Brian A.

; APPLICANT: Toney, Jeffrey H.

; APPLICANT: Bruhn, Suzanne L.

; APPLICANT: Pil, Pieter M.

; APPLICANT: Brown, Steven

; APPLICANT: Kellett, Patti

; APPLICANT: Essigmann, John M.

; APPLICANT: Lippard, Stephen J.

; TITLE OF INVENTION: DNA Structure Specific Recognition

; TITLE OF INVENTION: Protein and Uses Therefor

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: 2 Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,964
FILING DATE: 19911226
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-9540
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Synthetic oligonucleotide
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(11..12)
OTHER INFORMATION: /label= Pt-DNA
OTHER INFORMATION: /note= "cis-(Pt(NH3)3) 1,2-d(GpG) intrastrand
OTHER INFORMATION: Platinated DNA Structural Motif"
US-07-814-964-1
Query Match 0.8%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 64;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1447 GAGGAGAAAACCAAGGAGGAGA 1468
Db 22 GAGAGAGAACCAAGGAGGAGA 1
RESULT 13
PCT-US92-11107-1/c
Sequence 1, Application US/08258442
GENERAL INFORMATION:
APPLICANT: Donahue, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Pil, Pieter M.
APPLICANT: Brown, Steven
APPLICANT: Kellett, Patti
APPLICANT: Essigmann, John M.
APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/539,906
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-9540
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Synthetic oligonucleotide
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(11..12)
OTHER INFORMATION: /label= Pt-DNA
OTHER INFORMATION:
OTHER INFORMATION: Platinated DNA Structural Motif"
US-07-814-964-1
Query Match 0.8%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 64;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1447 GAGGAGAAAACCAAGGAGGAGA 1468
Db 22 GAGAGAGAACCAAGGAGGAGA 1
RESULT 14
PCT-US92-11107-1/c
Sequence 1, Application PC/TUS9211107
GENERAL INFORMATION:
APPLICANT: Donahue, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Pil, Pieter M.
APPLICANT: Brown, Steven
APPLICANT: Kellett, Patti
APPLICANT: Essigmann, John M.
APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: PCT/US92/11107
; FILING DATE: 19921218
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/539,906
; FILING DATE: 18-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/POCKET NUMBER: MIT-4787AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Synthetic oligonucleotide
; FEATURE:
; NAME/KEY: misc difference
; LOCATION: replace(11..12, "")
; OTHER INFORMATION: /label= Pt-DNA
; OTHER INFORMATION: /note= "cis-{Pt(NH3)3} 1,2-d(GpG) intrastrand
; OTHER INFORMATION: Platinated DNA Structural Motif"
; PCT-US92-11107-1

Query Match          0.8%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 64;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1447 GAGGAGAAACCAAGGAGGAGA 1468
Db 22 GAGAAGAGAAACCAAGAGGAGA 1

RESULT 15
US-09-866-108A-13559
; Sequence 13559, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-10-04
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13563
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-13563

Query Match          0.8%; Score 17.2; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 88;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1450 GAGAAACCAAGGAGGAGAAGC 1471
Db 4 GGAGGAAGCCCAAGAGGAGAAG 25

RESULT 16
US-09-866-108A-13563
; Sequence 13563, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13563
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-13563

Query Match          0.8%; Score 17.2; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 88;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1450 GAGAAACCAAGGAGGAGAAGC 1471
Db 4 GGAGGAAGCCCAAGAGGAGAAG 25
```

Db 1 GAGGAAGCCAGAGAGAGAGC 22

RESULT 17

US-09-866-108A-13970/c

; Sequence 13970, Application US/09866108A

; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharon G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aemica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 13970

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-13970

Query Match 0.8%; Score 17; DB 1; Length 25;

Best Local Similarity 80.0%; Pred. No. 99;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1509 CTGAATGGACCTCTCAGCTCTGGC 1533

Db 25 CCGAATGGATGTCCTCAGGTCGTC 1

RESULT 18

US-08-467-264-8/c

; Sequence 8, Application US/08467264

; Patent No. 5705156

; GENERAL INFORMATION:

; APPLICANT: Pastan, Ira

; APPLICANT: FitzGerald, David

; APPLICANT: Chaudhary, Vijay K.

; TITLE OF INVENTION: Pseudomonas Exotoxins of Low Animal

; TITLE OF INVENTION: Cytotoxicity and High Cytocidal Activity

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Crew

; STREET: One Market Plaza, Steuart Street Tower

; CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105-1492

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,264

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/522,182

FILING DATE: 11-MAY-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/130,322

FILING DATE: 01-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498

REFERENCE/DOCKET NUMBER: 15280-125-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-467-264-8

Query Match 0.8%; Score 16.6; DB 1; Length 24;

Best Local Similarity 82.6%; Pred. No. 1.2e+02;

Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1202 AAATCAGGCGATCTCTGAGGAC 1224

Db 23 AAGTCAGGCGATGACTGATGAC 1

RESULT 19

US-08-450-905B-52

; Sequence 52, Application US/08450905B

; Patent No. 5856301

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Stem Cell Inhibiting Proteins

; NUMBER OF SEQUENCES: 178

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HALE and DORR

; STREET: 60 State Street

; CITY: Boston

; STATE: MA

; ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,905B

FILING DATE: 26-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/982,759

FILING DATE: 08-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9127319.3

FILING DATE: 23-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9221587.0

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; FILING DATE: 14-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, HOLLIE L.
; REGISTRATION NUMBER: 31,321
; REFERENCE/DOCKET NUMBER: 102.378.120DV-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-526-6110
; TELEFAX: 617-526-5000
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..25
; OTHER INFORMATION: /product= "BB6302 oligomer"
US-08-450-905B-52

Query Match 0.8%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 916 GTGGAATTGTCAAGAGCTTTAA 938
Db 1 GTGGAATTGTGAGAAGAGGTGTAA 23

RESULT 20
US-07-982-759F-52
; Sequence 52, Application US/07982759F
; Patent No. 6057123
; GENERAL INFORMATION:
; APPLICANT: CRAIG, Stewart
; APPLICANT: GEORGE, Michael
; APPLICANT: EDWARDS, Richard Mark
; APPLICANT: CZAPLEWSKI, Lloyd George
; APPLICANT: GILBERT, Richard
; TITLE OF INVENTION: Stem Cell Inhibiting Proteins
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE and DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 08-MAR-1993
; APPLICATION NUMBER: US/07/982,759F
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9127319.3
; FILING DATE: 23-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9221587.0
; FILING DATE: 14-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, HOLLIE L.
; REGISTRATION NUMBER: 31,321
; REFERENCE/DOCKET NUMBER: 102378.120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-526-6000
; TELEFAX: 617-526-5000
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..25
; OTHER INFORMATION: /product= "BB6302 oligomer"
US-07-982-759F-52

Query Match 0.8%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 916 GTGGAATTGTCAAGAGCTTTAA 938
Db 1 GTGGAATTGTGAGAAGAGGTGTAA 23

RESULT 21
US-09-808-658-1
; Sequence 1, Application US/09808658
; Patent No. 6673567
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Pamela L
; APPLICANT: Nagarajan, Vasantha
; TITLE OF INVENTION: Method for Determination of Gene Function
; FILE REFERENCE: BCL027 US NA
; CURRENT APPLICATION NUMBER: US/09/808,658
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/191,561
; PRIOR FILING DATE: March 23, 2000
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer sequence
US-09-808-658-1

Query Match 0.8%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1899 AAAGTAACATCAGCCATTTTAG 1921
Db 3 AATGTAACATCAGAGATTTTGAG 25
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RESULT 22
US-09-866-108A-13967/c
; Sequence 13967, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13967
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13967

Query Match
Best Local Similarity 0.8%; Score 16.6; DB 1; Length 25;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1512 AATGGACCTCTCCAGCTGGCT 1534
| | | | | | | | | | | | | | | | | | | | |
DB 25 AATGGATGTCCTCCAGGTCTGCT 3

RESULT 23
US-09-866-108A-13971/c
; Sequence 13971, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13972
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13972

Query Match
Best Local Similarity 0.8%; Score 16.6; DB 1; Length 25;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1509 CTGAATGGACCTCTCCAGCTCTG 1531
| | | | | | | | | | | | | | | | | | | | |
DB 23 CCGAATGGATGTCCTCCAGGTCTG 1

RESULT 25
US-08-250-856A-27/c
; Sequence 27, Application US/08250856A
; Patent No. 5563255
; SEQ ID NO 13971

```

```

; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P. and Boggs, Russell T.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation
; TITLE OF INVENTION: of raf Gene Expression
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250.856A
; FILING DATE: May 31, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0094
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-08-250-856A-27

Query Match 0.8%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1460 AGGAGGAGAGCCAGAG 1477
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 26
US-08-468-037A-13/c
; Sequence 13, Application US/08468037A
; Patent No. 5859221
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: A. Kawasaki
; TITLE OF INVENTION: 2'-Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859221ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,973A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 835,932
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; US-08-471-973A-13

```

```

; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 835,932
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; US-08-468-037A-13

Query Match 0.8%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1460 AGGAGGAGAGCCAGAG 1477
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 27
US-08-471-973A-13/c
; Sequence 13, Application US/08471973A
; Patent No. 5872232
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: Andrew Kawasaki
; TITLE OF INVENTION: Sugar Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5872232ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,973A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 835,932
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; US-08-471-973A-13

```

Query Match 0.8%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1460 AGGAGGAGGAGGAGGAG 1477
DB 19 AGGAGGAGGAGGAGGAG 2

RESULT 28
US-08-756-806A-27/c
; Sequence 27, Application US/08756806A
; Patent No. 5952229
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P. and Boggs, Russell T.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation
; TITLE OF INVENTION: of raf Gene Expression
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,806A
; FILING DATE: No. 5952229ember 26, 1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07111
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250,856
; FILING DATE: May 31, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1454
; TELEFAX: (609) 779-2400
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-756-806A-27

Query Match 0.8%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1460 AGGAGGAGGAGGAGGAG 1477
DB 19 AGGAGGAGGAGGAGGAG 2

RESULT 29
US-08-465-880-13/c
; Sequence 13, Application US/08465880
; Patent No. 5955589
; GENERAL INFORMATION:
; APPLICANT: Philip Dan Cook
; TITLE OF INVENTION: Gapped 2' Modified Oligonucleotides
; NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5955589Tris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,880
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 244,993
FILING DATE: 21-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucchi
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-2002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: Yes
US-08-465-880-13

Query Match 0.8%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1460 AGGAGGAGGAGGAGGAG 1477
DB 19 AGGAGGAGGAGGAGGAG 2

RESULT 30
US-09-035-357-13/c
; Sequence 13, Application US/09035357
; Patent No. 6005087
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: A. Kawasaki
; TITLE OF INVENTION: 2'-Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6005087Tris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,357
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/468,037
FILING DATE:
ATTORNEY/AGENT INFORMATION:


```
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
US-09-035-357-13

Query Match 0.8%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1460 AGGAGGAGAGCCAGAG 1477
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 31
US-09-143-214-27/c
; Sequence 27, Application US/09143214
; Patent No. 6090626
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P. and Boggs, Russell T.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/143,214
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/756,806
; FILING DATE: No. 6090626ember 26, 1996
; APPLICATION NUMBER: PCT/US95/07111
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250,856
; FILING DATE: May 31, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-09-143-214-27
```

```
Query Match 0.8%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1460 AGGAGGAGAGCCAGAG 1477
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 32
US-09-000-136-13/c
; Sequence 13, Application US/09000136
; Patent No. 6096720
; GENERAL INFORMATION:
; APPLICANT: Love, William G
; APPLICANT: Sharman, Thomas
; APPLICANT: Phillips, Judith A
; APPLICANT: Nicklin, Paul L
; APPLICANT: Hamilton, Karen O
; TITLE OF INVENTION: Liposomal Oligonucleotide Compositions
; FILE REFERENCE: 4-20535/A/MA 2112/000,136
; CURRENT APPLICATION NUMBER: US/09/000,136
; CURRENT FILING DATE: 1998-04-23
; EARLIER APPLICATION NUMBER: GB 9515743.4
; EARLIER FILING DATE: 1995-08-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
; OTHER INFORMATION: oligonucleotide has uniform phosphorothiate
; OTHER INFORMATION: backbone and nucleotides 10-20 are substituted by
; OTHER INFORMATION: methoxy at the 2' position of the sugar moiety
US-09-000-136-13

Query Match 0.8%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1460 AGGAGGAGAGCCAGAG 1477
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 33
US-09-135-202-13/c
; Sequence 13, Application US/09135202
; Patent No. 6399754
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: Andrew Kawasaki
; TITLE OF INVENTION: Sugar Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6399754ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,202
; FILING DATE:
; CLASSIFICATION:
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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1460 AGGAGGAGCAGCCAGAG 1477
Db 19 AGGAGGAGCAGCCAGCAG 2

RESULT 37
PCT-US95-07111A-27/c
; Sequence 27, Application PC/TUS9507111A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P. and Boggs, Russell T.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation
; TITLE OF INVENTION: of raf Gene Expression
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07111A
; FILING DATE: May 31, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250,856
; FILING DATE: May 31, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0135
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
PCT-US95-07111A-27

Query Match 0.8%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1460 AGGAGGAGCAGCCAGAG 1477
Db 19 AGGAGGAGCAGCCAGCAG 2

RESULT 38
US-09-918-696-23
; Sequence 23, Application US/09918696
; Patent No. 6635244
; GENERAL INFORMATION:
; APPLICANT: Shen, Yuchiao
; APPLICANT: Nye, Julie
; APPLICANT: Hermiston, Terry
; TITLE OF INVENTION: ADENOVIRUS E1B-55K SINGLE AMINO ACID MUTANT AND METHODS OF USE
; FILE REFERENCE: ONYX1047-US
; CURRENT APPLICATION NUMBER: US/09/918,696
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US 60/222,887
; PRIOR FILING DATE: 2000-08-03
```

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; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ONYX-063
US-09-918-696-23

Query Match 0.8%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 949 CTGATGCTGGGAGCGGTGGT 969
Db 1 CTGCTGCTGGCGGGGTGGT 21

RESULT 39
US-09-918-696-24/c
; Sequence 24, Application US/09918696
; Patent No. 6635244
; GENERAL INFORMATION:
; APPLICANT: Shen, Yuchiao
; APPLICANT: Nye, Julie
; APPLICANT: Hermiston, Terry
; TITLE OF INVENTION: ADENOVIRUS E1B-55K SINGLE AMINO ACID MUTANT AND METHODS OF USE
; FILE REFERENCE: ONYX1047-US
; CURRENT APPLICATION NUMBER: US/09/918,696
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US 60/222,887
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ONYX-063; K290A MUTATION
US-09-918-696-24

Query Match 0.8%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 949 CTGATGCTGGGAGCGGTGGT 969
Db 22 CTGCTGCTGGCGGGGTGGT 2

RESULT 40
US-08-216-592A-10/c
; Sequence 10, Application US/08216592A
; Patent No. 6635429
; GENERAL INFORMATION:
; APPLICANT: LEID, MARK
; APPLICANT: KASTNER, PHILIPPE
; APPLICANT: CHAMRON, PIERRE
; TITLE OF INVENTION: NOVEL HETERODIMERIC STEROID RECEPTOR
; TITLE OF INVENTION: PROTEINS, GENES ENCODING SAME, AND USAGE THEREOF
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue NW Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/216,592A
; FILING DATE: 23-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 07/825,667
; FILING DATE: 24-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDSTEIN, JORGE A
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1383.0060002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-216-592A-10

Query Match 0.8%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1846 TTCTAGAGGGGTGC 1861
DB 16 TTCTAGAGGGGTGC 1

RESULT 41
US-08-450-905B-64
; Sequence 64, Application US/08450905B
; Patent No. 5856301
; GENERAL INFORMATION:
; APPLICANT: Stem Cell Inhibiting Proteins
; TITLE OF INVENTION: Stem Cell Inhibiting Proteins
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE and DORR
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,905B
; FILING DATE: 26-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,759
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9127319.3
; FILING DATE: 23-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9221587.0
; FILING DATE: 14-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, HOLLIE L.
; REGISTRATION NUMBER: 31,321
; REFERENCE/DOCKET NUMBER: 102.378.120DV-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-526-6110
; TELEFAX: 617-526-5000
; INFORMATION FOR SEQ ID NO: 64:

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..24
; OTHER INFORMATION: /product= "BB9110 oligomer"
; US-08-450-905B-64

Query Match 0.8%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 911 AGTGTGTGGAATTGTCAAGAGCT 934
DB 1 ATTTGTGGAATTTCTCTAGAGGT 24

RESULT 42
US-08-824-701A-2/c
; Sequence 2, Application US/08824701A
; Patent No. 5882868
; GENERAL INFORMATION:
; APPLICANT: Funanage, Vicky L.
; APPLICANT: Scavina, Mena
; TITLE OF INVENTION: Method of Diagnosing Spinal Muscular Atrophy
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jeffrey C. Lew
; STREET: 501 Silverside Road Suite 124
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19809
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: Windows for Workgroups 3.11
; SOFTWARE: Ami PRO 3.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,701A
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lew, Jeffrey C.
; REGISTRATION NUMBER: 35935
; REFERENCE/DOCKET NUMBER: 47066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 798-0700
; TELEFAX: (302) 798-5970
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: no
; US-08-824-701A-2

Query Match 0.8%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1327 GATTTCTGAAGAGGAGGAGGGG 1350
DB 24 GAATCTGAAGAGCAGGCTGAGAGG 1

RESULT 43
US-07-982-759F-64
```

Sequence 64, Application US/07982759F
Patent No. 6057123
GENERAL INFORMATION:
APPLICANT: CRAIG, Stewart
APPLICANT: GEORGE, Michael
APPLICANT: EDWARDS, Richard Mark
APPLICANT: CZAPLEWSKI, Lloyd George
APPLICANT: GILBERT, Richard
TITLE OF INVENTION: Stem Cell Inhibiting Proteins
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE and DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/982,759F
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9127319.3
FILING DATE: 23-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9221587.0
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, HOLLIE L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 102378.120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-526-6000
TELEFAX: 617-526-5000
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..24
OTHER INFORMATION: /product= "BB9110 oligomer"
US-07-982-759F-64
Query Match 0.8%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 911 AGTGTGGAATTGTCAGAGCT 934
DB 1 ATTTGTGGAATTCTCTAGAGT 24
RESULT 44
PCT-US91-02942-12/c
Sequence 12, Application PC/TUS9102942
GENERAL INFORMATION:
APPLICANT: ROTHLEIN, ROBERT
APPLICANT: ADAIR, JOHN R
APPLICANT: ATHWAL, DILJEET S
TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Ave. NW Suite 300
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02942
FILING DATE: 19910429
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9009549.8
FILING DATE: 27-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: FOX, SAM L
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 1011.0586600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US91-02942-12
Query Match 0.8%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 598 CATGGTGACGGCGTGGAGAGGCC 621
DB 24 CATGGTGGCGCTTCGAACCGGCC 1
RESULT 45
US-08-261-822A-55
Sequence 55, Application US/08261822A
Patent No. 5650553
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R. et al.
TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5650553ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,822A
FILING DATE: 17-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-261-822A-55

Query Match          0.8%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1405 GAAAAAGAGAAAGCCCG 1423
DB 2 GAAGAGAGAAAGACTCAG 20

RESULT 46
US-09-780-045-26/c
; Sequence 26, Application US/09780045
; Patent No. 6602713
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT B
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0130
; CURRENT APPLICATION NUMBER: US/09/780,045
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-780-045-26

Query Match          0.8%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1338 GGAGGGAGAGGGGGCGC 1356
DB 19 GGGGGAGAGGGGAGCGGC 1

RESULT 47
PCT-US95-07744A-55
; Sequence 55, Application PC/TUS9507744A
; GENERAL INFORMATION:
; APPLICANT: Trustees of The University of Pennsylvania
; TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
; TITLE OF INVENTION: and Pathogens
; NUMBER OF SEQUENCES: 82
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07744A
; FILING DATE: 15-JUNE-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/261,822

```

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 559 TATCACCAGAGGTCGTGT 577
Db 2 TCTCACCAGAGGTCGTGT 20

RESULT 49

US-08-920-919A-54
; Sequence 54, Application US/08920919A
; Patent No. 6114119
; GENERAL INFORMATION:
; APPLICANT: Aeschlimann, Daniel
; APPLICANT: Mosher, Deane F
; TITLE OF INVENTION: Transglutaminase and Gene Encoding Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/920,919A
; APPLICATION NUMBER: US/08/920,919A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berson, Bennett J
; REGISTRATION NUMBER: 37094
; REFERENCE/DOCKET NUMBER: 960296.94509
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-920-919A-54

Query Match 0.8%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 559 TATCACCAGAGGTCGTGT 577
Db 2 TCTCACCAGAGGTCGTGT 20

RESULT 50

US-09-033-936-30/c
; Sequence 30, Application US/09033936
; Patent No. 6632976
; GENERAL INFORMATION:
; APPLICANT: TOMIZUKA, KAZUMA
; APPLICANT: YOSHIDA, HITOSHI
; APPLICANT: HANAKA, KAZUNORI
; APPLICANT: OSHIMURA, MITSUO
; APPLICANT: ISHIDA, ISAO
; TITLE OF INVENTION: CHIMERIC ANIMAL AND METHOD FOR PRODUCING THE SAME
; FILE REFERENCE: 081356/0114
; CURRENT APPLICATION NUMBER: US/09/033,936
; CURRENT FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: PCT/JP96/02427
; PRIOR FILING DATE: 1996-08-29

; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-033-936-30

Query Match 0.8%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1459 AAGGAGCAGAGCCAGAG 1477
Db 20 AAGGAGTAGAAGCCAAAAG 2

RESULT 51

US-08-478-470-7/c
; Sequence 7, Application US/08478470
; Patent No. 5591607
; GENERAL INFORMATION:
; APPLICANT: GRYZNOV, SERGEI
; TITLE OF INVENTION: OLIGONUCLEOTIDE
; TITLE OF INVENTION: N3'-PS' PHOSPHORAMIDATES:
; TITLE OF INVENTION: HYBRIDIZATION AND NUCLEASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro
; ADDRESSEE: Huddleson & Tatum
; STREET: 5 Palo Alto Square
; STREET: 3000 El Camino Real
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,470
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: John D. Mendlein
; REGISTRATION NUMBER: 38,770
; REFERENCE/DOCKET NUMBER: LYNX-005/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5020
; TELEFAX: (415) 857-0663
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Oligonucleotide 7, Fig. 5
US-08-478-470-7

Query Match 0.8%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1599 TATTATATAAAATTTAT 1617


```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Oligonucleotide 7, Fig. 5
US-08-214-599-7

Query Match 0.8%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1599 TATTTATATAAAATTTAT 1617
||| ||||| ||||| |||||
Db 24 TATATATATAAAATATAT 6

RESULT 54
US-08-214-599-9/c
; Sequence 9, Application US/08214599
; Patent No. 5599922
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; TITLE OF INVENTION: Properties
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/214,599
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Oligonucleotide 9, Fig. 5
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..2
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 3..4

;
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 5..6
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 7..8
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 9..10
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 15..16
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 17..18
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 19..20
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 21..22
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 23..24
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
US-08-214-599-9

Query Match 0.8%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1599 TATTTATATAAAATTTAT 1617
||| ||||| ||||| |||||
Db 24 TATATATATAAAATATAT 6

RESULT 55
US-08-473-015-7/c
; Sequence 7, Application US/08473015
; Patent No. 5631135
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; TITLE OF INVENTION: Properties
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,015
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,599
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Oligonucleotide 7, Fig. 5
; US-08-473-015-7

```

```

Query Match      0.8%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1599 TATTATATATAAAATTTAT 1617
DB 24 TATATATATAAAATATAT 6

```

```

RESULT 56
US-08-473-015-9/c
; Sequence 9, Application US/08473015
; Patent No. 5631135
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5',
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,015
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,599
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880

```

```

; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Oligonucleotide 9, Fig. 5
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..2
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3..4
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 5..6
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7..8
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 9..10
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 15..16
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 17..18
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 19..20
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 21..22
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 23..24
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; US-08-473-015-9

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Query Match      0.8%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1599 TATTATATATAAAATTTAT 1617
DB 24 TATATATATAAAATATAT 6

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RESULT 57
US-08-465-368-7/c
; Sequence 7, Application US/08465368
; Patent No. 5726297
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Schultz, Ronald G.
; APPLICANT: Chen, Jer-kang
; TITLE OF INVENTION: OLIGODEOXYRIBONUCLEOTIDE
; TITLE OF INVENTION: N3'P5'PHOSPHORAMIDATES: USES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,368
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/210,505
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Oligonucleotide 7, Fig. 5
; NAME/KEY: misc_feature
; LOCATION: 1..2
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3..4
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 5..6
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7..8
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 9..10
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 15..16
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 17..18
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature

Query Match 0.8%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1599 TATTATATATAAAATTAT 1617
||| ||||| ||||| |||
Db 24 TATATATATAAAATATAT 6

RESULT 58
US-08-465-368-9/c
; Sequence 9, Application US/08465368
; Patent No. 5726297
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Schultz, Ronald G.
; APPLICANT: Chen, Jer-kang
; TITLE OF INVENTION: OLIGODEOXYRIBONUCLEOTIDE
; TITLE OF INVENTION: N3'P5'PHOSPHORAMIDATES: USES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
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; LOCATION: 19..20
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 21..22
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 23..24
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
;
; US-08-465-368-9
;
; Query Match
; Best Local Similarity 0.8%; Score 15.8; DB 1; Length 24;
; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1599 TATTATATATAAAATTTAT 1617
; DB 24 TATATATATAAAATATAT 6
;
; RESULT 60
; US-08-477-306-9/c
; Sequence 9, Application US/08477306
; Patent No. 5837835
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; TITLE OF INVENTION: Properties
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,306
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/214,599
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Oligonucleotide 9, Fig. 5
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..2
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3..4
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 5..6
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
;
; FEATURE:
; NAME/KEY: misc_feature
;
; US-08-477-306-7
;
; Query Match
; Best Local Similarity 0.8%; Score 15.8; DB 1; Length 24;
; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1599 TATTATATATAAAATTTAT 1617
; DB 24 TATATATATAAAATATAT 6
;
; RESULT 59
; US-08-477-306-7/c
; Sequence 7, Application US/08477306
; Patent No. 5837835
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; TITLE OF INVENTION: Properties
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,306
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/214,599
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Oligonucleotide 7, Fig. 5
;
; US-08-477-306-7
```

LOCATION: 7..8
OTHER INFORMATION: /note= "where the intersubunit bond
FEATURE:
NAME/KEY: misc_feature
LOCATION: 9..10
OTHER INFORMATION: /note= "where the intersubunit bond
OTHER INFORMATION: is "np"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 15..16
OTHER INFORMATION: /note= "where the intersubunit bond
OTHER INFORMATION: is "np"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 17..18
OTHER INFORMATION: /note= "where the intersubunit bond
OTHER INFORMATION: is "np"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19..20
OTHER INFORMATION: /note= "where the intersubunit bond
OTHER INFORMATION: is "np"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 21..22
OTHER INFORMATION: /note= "where the intersubunit bond
OTHER INFORMATION: is "np"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 23..24
OTHER INFORMATION: /note= "where the intersubunit bond
OTHER INFORMATION: is "np"
US-08-477-306-9

Query Match 0.8%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1599 TATTATATAAAATTTAT 1617
||| |||||
Db 24 TATATATAAAATATAT 6

RESULT 61
US-08-700-448-7/c
Sequence 7, Application US/08700448
Patent No. 5965720
GENERAL INFORMATION:
APPLICANT: Gryaznov, Sergei et al.
TITLE OF INVENTION: Oligonucleotide N3'-P5'
TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
TITLE OF INVENTION: Properties
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,448
FILING DATE: 01/10/97
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent M. Powers
REGISTRATION NUMBER: 36,246
REFERENCE/DOCKET NUMBER: 5525-0012.10
TELEPHONE: (650) 324-0960
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: DNA Oligonucleotide 9, Fig. 5
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..2

REFERENCE/DOCKET NUMBER: 5525-0012.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: DNA Oligonucleotide 7, Fig. 5
US-08-700-448-7

Query Match 0.8%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1599 TATTATATAAAATTTAT 1617
||| |||||
Db 24 TATATATAAAATATAT 6

RESULT 62
US-08-700-448-9/c
Sequence 9, Application US/08700448
Patent No. 5965720
GENERAL INFORMATION:
APPLICANT: Gryaznov, Sergei et al.
TITLE OF INVENTION: Oligonucleotide N3'-P5'
TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
TITLE OF INVENTION: Properties
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,448
FILING DATE: 01/10/97
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent M. Powers
REGISTRATION NUMBER: 36,246
REFERENCE/DOCKET NUMBER: 5525-0012.10
TELEPHONE: (650) 324-0960
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: DNA Oligonucleotide 9, Fig. 5
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..2

```
;
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 3..4
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 5..6
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 7..8
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 9..10
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 15..16
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 17..18
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 19..20
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 21..22
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 23..24
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
;
; US-08-700-448-9
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Query Match 0.8%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1599 TATTTATATAAAATTTAT 1617
Db |||||
24 TATATATATAAAATATAT 6
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RESULT 63

```
US-08-923-386A-7/c
; Sequence 7, Application US/08923386A
; Patent No. 6169170
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5',
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; TITLE OF INVENTION: Properties
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
```

```
;
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,386A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Oligonucleotide 7, Fig. 6
;
; US-08-923-386A-7
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Query Match 0.8%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1599 TATTTATATAAAATTTAT 1617
Db |||||
24 TATATATATAAAATATAT 6
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RESULT 64

```
US-08-923-386A-9/c
; Sequence 9, Application US/08923386A
; Patent No. 6169170
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5',
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; TITLE OF INVENTION: Properties
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,386A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
```

```

; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Oligonucleotide 9, Fig. 6
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..2
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3..4
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 5..6
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7..8
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 9..10
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 15..16
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 17..18
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 19..20
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 21..22
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 23..24
; OTHER INFORMATION: /note= "where the intersubunit bond
; OTHER INFORMATION: is "np"
;
US-08-923-386A-9

```

```

Query Match      0.8%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1599 TATTATATAAAATTAT 1617
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Db 24 TATATATATAAATAT 6

```

RESULT 65

```

US-09-033-936-69
; Sequence 69, Application US/09033936
; Patent No. 6632976
; GENERAL INFORMATION:
; APPLICANT: TOMIZUKA, KAZUMA
; APPLICANT: YOSHIDA, HITOSHI
; APPLICANT: HANAOKA, KAZUNORI
; APPLICANT: OSHIMURA, MITSUO
; APPLICANT: ISHIDA, ISAO
; TITLE OF INVENTION: CHIMERIC ANIMAL AND METHOD FOR PRODUCING THE SAME
; FILE REFERENCE: 081356/0114
; CURRENT APPLICATION NUMBER: US/09/033,936
; CURRENT FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: PCT/JP96/02427
; PRIOR FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 69
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-033-936-69

Query Match      0.8%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1350 GGGCGCGCAAGAACTCTTCC 1368
    ||| ||||| |||||
Db 1 GAGCTGCAAGAACTCTTCC 19

RESULT 66
US-07-814-964-2/c
; Sequence 2, Application US/07814964
; Patent No. 5359047
; GENERAL INFORMATION:
; APPLICANT: Donahue, Brian A.
; APPLICANT: Toney, Jeffrey H.
; APPLICANT: Bruhn, Suzanne L.
; APPLICANT: Pil, Pieter M.
; APPLICANT: Brown, Steven
; APPLICANT: Kelleff, Patti
; APPLICANT: Essigmann, John M.
; APPLICANT: Lippard, Stephen J.
; TITLE OF INVENTION: DNA Structure Specific Recognition
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: 2 Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/814,964
; FILING DATE: 19911226
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/539,906
; FILING DATE: 18-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-4787AAA

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Synthetic oligonucleotide
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(11..12)
OTHER INFORMATION: /label= Pt-DNA
OTHER INFORMATION:
OTHER INFORMATION: Platinated DNA Structural Motif"
US-07-814-964-2
Query Match 0.7%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1447 GAGGAGAAACCAAGAGGAGA 1468
DB 22 GAGAAGAGAACTAAGAAGGAGA 1
RESULT 67
US-07-814-964-5/c
Sequence 5, Application US/07814964
Patent No. 5359047
GENERAL INFORMATION:
APPLICANT: Donahue, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Pil, Pieter M.
APPLICANT: Brown, Steven
APPLICANT: Kellert, Patti
APPLICANT: Essigmann, John M.
APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,964
FILING DATE: 19911226
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-9540
TELEFAX: 617-861-6240
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Synthetic oligonucleotide
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(11..12)
OTHER INFORMATION: /label= Pt-DNA
OTHER INFORMATION:
OTHER INFORMATION: Platinated DNA Structural Motif"

LENGTH: 22 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Synthetic oligonucleotide
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(12)
OTHER INFORMATION: /label= Pt-DNA
OTHER INFORMATION:
OTHER INFORMATION: monofunctional Platinated DNA Structural Motif"
US-07-814-964-5
Query Match 0.7%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1447 GAGGAGAAACCAAGAGGAGA 1468
DB 22 GAGAAGAGAACTAAGAAGGAGA 1
RESULT 68
US-08-238-963A-10
Sequence 10, Application US/08238963A
Patent No. 5625047
GENERAL INFORMATION:
APPLICANT: Been, Michael D.
APPLICANT: Rosenstein, Sarah P.
APPLICANT: Perrotta, Anne T.
TITLE OF INVENTION: ENZYMAIC RNA MOLECULES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,963A
FILING DATE: May 5, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/821,155
FILING DATE: January 13, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 207/093
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-238-963A-10
Query Match 0.7%; Score 15.6; DB 1; Length 22;
Best Local Similarity 68.2%; Pred. No. 1.7e+02;

Patent No. 6410323
GENERAL INFORMATION:
APPLICANT: Roberts, M. Luisa
APPLICANT: Cowsett, Lex M.
TITLE OF INVENTION: Antisense Modulation of Human Rho Family Gene
FILE REFERENCE: ISPH-0404
CURRENT APPLICATION NUMBER: US/09/387,341
EARLIER FILING DATE: 1999-08-31
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 233
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 197
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-387-341-197

Query Match 0.7%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1450 GAGAAACCAAGAGGAGGAGC 1471
||||| ||||| ||||| |||||
Db 22 GAGAAACTGAAGAGGAGGAGC 1

RESULT 72
US-10-134-890-3
Sequence 3, Application US/10134890
Patent No. 6660737
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Almstead, Ji-In
APPLICANT: Jones, David
APPLICANT: Kawamoto, Richard
APPLICANT: Izzo, Nicholas
TITLE OF INVENTION: Medicinal Uses of Hydrazones
FILE REFERENCE: 8543P
CURRENT APPLICATION NUMBER: US/10/134,890
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 22
TYPE: DNA
ORGANISM: Homo sapien
US-10-134-890-3

Query Match 0.7%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 482 ACCATGCAAGAAAGTCCGAGGC 503
||||| ||||| ||||| |||||
Db 1 ACCATGCCAAGTGTCCGAGGC 22

RESULT 73
PCT-US92-11107-2/c
Sequence 2, Application PC/TUS9211107
GENERAL INFORMATION:
APPLICANT: Donahue, Brian A.

Patent No. 6410323
GENERAL INFORMATION:
APPLICANT: Roberts, M. Luisa
APPLICANT: Cowsett, Lex M.
TITLE OF INVENTION: Antisense Modulation of Human Rho Family Gene
FILE REFERENCE: ISPH-0404
CURRENT APPLICATION NUMBER: US/09/387,341
EARLIER FILING DATE: 1999-08-31
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 233
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 197
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-387-341-197

Query Match 0.7%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1450 GAGAAACCAAGAGGAGGAGC 1471
||||| ||||| ||||| |||||
Db 22 GAGAAACTGAAGAGGAGGAGC 1

RESULT 72
US-10-134-890-3
Sequence 3, Application US/10134890
Patent No. 6660737
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Almstead, Ji-In
APPLICANT: Jones, David
APPLICANT: Kawamoto, Richard
APPLICANT: Izzo, Nicholas
TITLE OF INVENTION: Medicinal Uses of Hydrazones
FILE REFERENCE: 8543P
CURRENT APPLICATION NUMBER: US/10/134,890
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 22
TYPE: DNA
ORGANISM: Homo sapien
US-10-134-890-3

Query Match 0.7%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 482 ACCATGCAAGAAAGTCCGAGGC 503
||||| ||||| ||||| |||||
Db 1 ACCATGCCAAGTGTCCGAGGC 22

RESULT 73
PCT-US92-11107-2/c
Sequence 2, Application PC/TUS9211107
GENERAL INFORMATION:
APPLICANT: Donahue, Brian A.

Patent No. 6410323
GENERAL INFORMATION:
APPLICANT: Roberts, M. Luisa
APPLICANT: Cowsett, Lex M.
TITLE OF INVENTION: Antisense Modulation of Human Rho Family Gene
FILE REFERENCE: ISPH-0404
CURRENT APPLICATION NUMBER: US/09/387,341
EARLIER FILING DATE: 1999-08-31
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 233
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 197
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-387-341-197

Query Match 0.7%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1450 GAGAAACCAAGAGGAGGAGC 1471
||||| ||||| ||||| |||||
Db 22 GAGAAACTGAAGAGGAGGAGC 1

RESULT 72
US-10-134-890-3
Sequence 3, Application US/10134890
Patent No. 6660737
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Almstead, Ji-In
APPLICANT: Jones, David
APPLICANT: Kawamoto, Richard
APPLICANT: Izzo, Nicholas
TITLE OF INVENTION: Medicinal Uses of Hydrazones
FILE REFERENCE: 8543P
CURRENT APPLICATION NUMBER: US/10/134,890
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 22
TYPE: DNA
ORGANISM: Homo sapien
US-10-134-890-3

Query Match 0.7%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 482 ACCATGCAAGAAAGTCCGAGGC 503
||||| ||||| ||||| |||||
Db 1 ACCATGCCAAGTGTCCGAGGC 22

RESULT 73
PCT-US92-11107-2/c
Sequence 2, Application PC/TUS9211107
GENERAL INFORMATION:
APPLICANT: Donahue, Brian A.

Patent No. 6410323
GENERAL INFORMATION:
APPLICANT: Roberts, M. Luisa
APPLICANT: Cowsett, Lex M.
TITLE OF INVENTION: Antisense Modulation of Human Rho Family Gene
FILE REFERENCE: ISPH-0404
CURRENT APPLICATION NUMBER: US/09/387,341
EARLIER FILING DATE: 1999-08-31
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 233
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 197
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-387-341-197

Query Match 0.7%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1450 GAGAAACCAAGAGGAGGAGC 1471
||||| ||||| ||||| |||||
Db 22 GAGAAACTGAAGAGGAGGAGC 1

RESULT 72
US-10-134-890-3
Sequence 3, Application US/10134890
Patent No. 6660737
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Almstead, Ji-In
APPLICANT: Jones, David
APPLICANT: Kawamoto, Richard
APPLICANT: Izzo, Nicholas
TITLE OF INVENTION: Medicinal Uses of Hydrazones
FILE REFERENCE: 8543P
CURRENT APPLICATION NUMBER: US/10/134,890
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 22
TYPE: DNA
ORGANISM: Homo sapien
US-10-134-890-3

Query Match 0.7%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 482 ACCATGCAAGAAAGTCCGAGGC 503
||||| ||||| ||||| |||||
Db 1 ACCATGCCAAGTGTCCGAGGC 22

RESULT 73
PCT-US92-11107-2/c
Sequence 2, Application PC/TUS9211107
GENERAL INFORMATION:
APPLICANT: Donahue, Brian A.

Patent No. 6410323
GENERAL INFORMATION:
APPLICANT: Roberts, M. Luisa
APPLICANT: Cowsett, Lex M.
TITLE OF INVENTION: Antisense Modulation of Human Rho Family Gene
FILE REFERENCE: ISPH-0404
CURRENT APPLICATION NUMBER: US/09/387,341
EARLIER FILING DATE: 1999-08-31
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 233
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 197
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-387-341-197

Query Match 0.7%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1450 GAGAAACCAAGAGGAGGAGC 1471
||||| ||||| ||||| |||||
Db 22 GAGAAACTGAAGAGGAGGAGC 1

RESULT 72
US-10-134-890-3
Sequence 3, Application US/10134890
Patent No. 6660737
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Almstead, Ji-In
APPLICANT: Jones, David
APPLICANT: Kawamoto, Richard
APPLICANT:

```
;
; TITLE OF INVENTION: DNA Structure Specific Recognition
;
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: 2 Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/11107
; FILING DATE: 19921218
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/539,906
; FILING DATE: 18-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-4787AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Synthetic oligonucleotide
; FEATURE:
; NAME/KEY: misc difference
; LOCATION: replace(12, "")
; OTHER INFORMATION: /label= Pt-DNA
; OTHER INFORMATION: /note= "cis-[Pt (NH3)2 (N3-cytosine)] dG
;
; OTHER INFORMATION: monofunctional Platinated DNA Structural Motif"
;
PCT-US92-11107-5

Query Match 0.7%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1447 GAGGAGAAACCAAGGAGGAGA 1468
Db 22 GAGAAGAGAACGAGAGGAGA 1

RESULT 75
US-08-390-850-574
; Sequence 574, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,850
; FILING DATE: February 17, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5612215ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 574:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-390-850-574

Query Match 0.7%; Score 15.4; DB 1; Length 17;
Best Local Similarity 35.3%; Pred. No. 1e+02;
Matches 6; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 2041 GATACTATTTCATTTT 2057
Db 1 GAUACUGUUUCAUUU 17

RESULT 76
US-08-390-850-575
; Sequence 575, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,850
```

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 211/084
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 574:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-390-850-575

Query Match 0.7%; Score 15.4; DB 1; Length 17;
Best Local Similarity 29.4%; Pred. No. 1e+02;
Matches 5; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 2042 ATACTATTTCATTTT 2058
||:||||:||||:||||:
DB 1 AUACUGUUUUCAUUUU 17

RESULT 77
US-08-435-634-574
Sequence 574, Application US/08435634
Patent No. 5731295
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Gustofson, John
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
OF ARTHRITIC CONDITIONS
NUMBER OF SEQUENCES: 1151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,634
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/390,850
FILING DATE: February 17, 1995
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 211/084
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 211/084
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 574:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-634-574

Query Match 0.7%; Score 15.4; DB 1; Length 17;
Best Local Similarity 35.3%; Pred. No. 1e+02;
Matches 6; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 2041 GATCTATTTCATTTT 2057
||:||||:||||:||||:
DB 1 GAUACUGUUUUCAUUUU 17

RESULT 78
US-08-435-634-575
Sequence 575, Application US/08435634
Patent No. 5731295
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Gustofson, John
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
OF ARTHRITIC CONDITIONS
NUMBER OF SEQUENCES: 1151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,634
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/390,850
FILING DATE: February 17, 1995
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 211/084
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 575:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-435-634-575

Query Match 0.7%; Score 15.4; DB 1; Length 17;
Best Local Similarity 29.4%; Pred. No. 1e+02;
Matches 5; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

Qy 2042 ATACTATTTCATTTT 2058

Db 1 AUACUGUUUUCAUUUU 17

RESULT 79

US-08-390-850-1130

; Sequence 1130, Application US/08390850

; Patent No. 5612215

; GENERAL INFORMATION:

; APPLICANT: Draper, Kenneth G.

; APPLICANT: Pavco, Pamela

; APPLICANT: McSwiggen, James

; APPLICANT: Gustofson, John

; APPLICANT: Stinchcomb, Dan T.

; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT

; OF ARTHRITIC CONDITIONS

; NUMBER OF SEQUENCES: 1151

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/390,850

; FILING DATE: February 17, 1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/354,920

; FILING DATE: December 13, 1994

; APPLICATION NUMBER: 08/152,487

; FILING DATE: No. 5612215ember 12, 1993

; APPLICATION NUMBER: 07/989,848

; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 211/084

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 1130:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-390-850-1130

Query Match

Best Local Similarity 0.7%; Score 15.4; DB 1; Length 18;

Best Local Similarity 35.3%; Pred. No. 1.2e+02;

Matches 6; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 2041 GATACTATTTCATTTT 2057

Db 2 GAUACUGUUUUCAUUUU 18

RESULT 80

US-08-435-634-1130

; Sequence 1130, Application US/08435634

; Patent No. 5731295

; GENERAL INFORMATION:

; APPLICANT: Draper, Kenneth G.

; APPLICANT: Pavco, Pamela

; APPLICANT: McSwiggen, James

; APPLICANT: Gustofson, John

; APPLICANT: Stinchcomb, Dan T.

; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT

; OF ARTHRITIC CONDITIONS

; NUMBER OF SEQUENCES: 1151

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/435,634

; FILING DATE: 05-MAY-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/390,850

; FILING DATE: February 17, 1995

; APPLICATION NUMBER: 08/354,920

; FILING DATE: December 13, 1994

; APPLICATION NUMBER: 08/152,487

; FILING DATE: No. 5731295ember 12, 1993

; APPLICATION NUMBER: 07/989,848

; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 211/084

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 1130:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-435-634-1130

Query Match

Best Local Similarity 0.7%; Score 15.4; DB 1; Length 18;

Best Local Similarity 35.3%; Pred. No. 1.2e+02;

Matches 6; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 2041 GATACTATTTCATTTT 2057

Db 2 GAUACUGUUUUCAUUUU 18

RESULT 81

US-09-255-912-44/c

; Sequence 44, Application US/09255912
; Patent No. 6037142

; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia

; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD2 EXPRESSION

; FILE REFERENCE: RTS-0044

; CURRENT APPLICATION NUMBER: US/09/255,912

; CURRENT FILING DATE: 1999-02-23

; NUMBER OF SEQ ID NOS: 47

; SEQ ID NO 44

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-255-912-44

Query Match 0.7%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 1.2e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1510 TGAATGGACCTCTCAG 1526

Db 18 TGAATGGACCTCTACAG 2

RESULT 82

US-09-422-978-6129/c

; Sequence 6129, Application US/09422978

; Patent No. 6537751

; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta

; APPLICANT: Chumakov, Ilya

; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

; FILE REFERENCE: GENSET.020CP1

; CURRENT APPLICATION NUMBER: US/09/422,978

; CURRENT FILING DATE: 1999-10-20

; EARLIER APPLICATION NUMBER: US 09/298,850

; EARLIER FILING DATE: 1999-04-21

; EARLIER APPLICATION NUMBER: US 60/109,732

; EARLIER FILING DATE: 1998-11-23

; EARLIER APPLICATION NUMBER: US 60/082,614

; EARLIER FILING DATE: 1998-04-21

; NUMBER OF SEQ ID NOS: 11796

; SEQ ID NO 6129

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: primer_bind

; LOCATION: 1..19

; OTHER INFORMATION: upstream amplification primer 99-9204 for SEQ 2195,

US-09-422-978-6129

Query Match 0.7%; Score 15.4; DB 1; Length 19;

Best Local Similarity 94.1%; Pred. No. 1.4e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1987 TCTGTCTCTCTCTAATT 2003

Db 18 TCTGTCTCTCTCTAAAT 2

RESULT 83

US-08-203-905B-17/c

; Sequence 17, Application US/08203905B

; Patent No. 5646249

; GENERAL INFORMATION:

; APPLICANT: KAYE, FEDERIC J.

; APPLICANT: OTTERSON, GREGORY A.

; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF A

; TITLE OF INVENTION: NOVEL CHAPERONE PROTEIN

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR

; STREET: 620 NEWPORT CENTER DRIVE, SIXTEENTH FLOOR

; CITY: NEWPORT BEACH

; STATE: CA

; COUNTRY: USA

; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/203,905B

; FILING DATE: February 28, 1994

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: KIRKPATRICK, ANITA M.

; REGISTRATION NUMBER: 32,617

; REFERENCE/DOCKET NUMBER: NIH089.001A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-235-8550

; TELEFAX: 619-235-0176

; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 22 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-08-203-905B-17

Query Match 0.7%; Score 15.4; DB 1; Length 22;

Best Local Similarity 94.1%; Pred. No. 2e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1383 CAAGAGAGTCAAAACAG 1399

Db 18 CAGGAGAGTCAAAACAG 2

RESULT 84

US-09-686-179A-20/c

; Sequence 20, Application US/09686179A

; Patent No. 6350580

; GENERAL INFORMATION:

; APPLICANT: Sorge, Joseph

; TITLE OF INVENTION: Methods for Detection of a Target Nucleic Acid Using a

; FILE REFERENCE: 25436/1140

; CURRENT APPLICATION NUMBER: US/09/686,179A

; CURRENT FILING DATE: 2000-10-11

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 20

; LENGTH: 23

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: synthetic oligonucleotide primer

US-09-686-179A-20

Query Match 0.7%; Score 15.4; DB 1; Length 23;

Best Local Similarity 94.1%; Pred. No. 2.2e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 761 ATGACGAGTCTTATGAG 777

```
Db      23  ATGACGAGTCTTATGAG  7

RESULT 85
US-09-422-978-5835/c
; Sequence 5835, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSER.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5835
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..23
; OTHER INFORMATION: upstream amplification primer 99-72 for SEQ 1901,
US-09-422-978-5835

Query Match      0.7%; Score 15.4; DB 1; Length 23;
Best Local Similarity 94.1%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1754  GGTGAAGGATGACTTT 1770
Db      17  GGTGAAGGATGACTTT 1
|||||
|

RESULT 86
US-09-981-621-20/c
; Sequence 20, Application US/09981621
; Patent No. 6589743
; GENERAL INFORMATION:
; APPLICANT: Soize, Joseph
; TITLE OF INVENTION: Methods for Detection of a Target Nucleic Acid Using a
; FILE REFERENCE: 25436/1140
; CURRENT APPLICATION NUMBER: US/09/981,621
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: US/09/686,179
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 20
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: synthetic oligonucleotide primer
US-09-981-621-20

Query Match      0.7%; Score 15.4; DB 1; Length 23;
Best Local Similarity 94.1%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      761  ATGACGAGTCTTATGAG  777
Db      23  ATGACGAGTCTTATGAG  7
|||||
|

RESULT 87
US-09-429-323-36
; Sequence 36, Application US/09429323A
; Patent No. 6140126
; Patent No. 6140126 6140123
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF Y-BOX BINDING PROTEIN 1 EXPRESSION
; FILE REFERENCE: RTS-0092
; CURRENT APPLICATION NUMBER: US/09/429,323A
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-429-323-36

Query Match      0.7%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1716  CCGTTCCTTACTTTGAACCA 1735
Db      1  CCGTTCCTTACTTTGAACCA 20
|||||
|

RESULT 88
US-08-857-076-4/c
; Sequence 4, Application US/08857076C
; Patent No. 6225120
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Kimura, Koutarou
; APPLICANT: Patterson, Garth
; APPLICANT: Ogg, Scott
; APPLICANT: Paradis, Suzanne
; APPLICANT: Tissenbaum, Heidi
; APPLICANT: Morris, Jason
; APPLICANT: Kowsek, Allison
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE REFERENCE: 00786/351001
; CURRENT APPLICATION NUMBER: US/08/857,076C
; CURRENT FILING DATE: 1997-05-15
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer/probe derived from C. elegans
US-08-857-076-4

Query Match      0.7%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      806  TAATGGAGATGTTCCAGCCT 825
Db      20  TAATGTAGATGATCCAGCCT 1
|||||
|

RESULT 89
US-09-428-583-74/c
; Sequence 74, Application US/09428583
; Patent No. 6271029
; GENERAL INFORMATION:
```

Query Match 0.7%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CGGAGCCGCGCGCGGAGGG 23
DB 20 CGGGCGCGGGCGGGTGG 1

RESULT 92
US-08-219-842-53/c
; Sequence 53, Application US/08219842
; Patent No. 5565323
; GENERAL INFORMATION:
; APPLICANT: Parker, W. D.
; APPLICANT: Herntstadt, Corinna
; TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
; TITLE OF INVENTION: for Alzheimer's Disease
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,842
; FILING DATE: 30-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-AG 9504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-219-842-53

Query Match 0.7%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1243 GCGATGAGGACGAGACGA 1262
DB 21 GCGATGAGGACTAGGATCA 2

RESULT 93
US-08-219-842-86
; Sequence 86, Application US/08219842
; Patent No. 5565323
; GENERAL INFORMATION:
; APPLICANT: Parker, W. D.
; APPLICANT: Herntstadt, Corinna
; TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
; TITLE OF INVENTION: for Alzheimer's Disease
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego

APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF CYTOSIN-2 EXPRESSION
FILE REFERENCE: RTS-0096
CURRENT APPLICATION NUMBER: US/09/428,583
CURRENT FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 74
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-428-583-74

Query Match 0.7%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 620 CTTCTACACCGGACCGG 639
DB 20 CTTCTACACCGGACCGG 1

RESULT 90
US-09-198-452A-1484
; Sequence 1484, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1484
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1484

Query Match 0.7%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1209 GCGATTCTGAGGACGCA 1228
DB 1 GCGATTCTGAAGACTA 20

RESULT 91
US-09-780-045-31/c
; Sequence 31, Application US/09780045
; Patent No. 6602713
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0130
; CURRENT APPLICATION NUMBER: US/09/780,045
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-780-045-31


```
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,842
; FILING DATE: 30-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-AG 9504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-219-842-86

Query Match          0.7%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1243 GCGGATGAGGACGAGCA 1262
DB 1 GCGGATGAGGACTAGGATGA 20

RESULT 94
US-08-451-096-53/c
; Sequence 53, Application US/08451096
; Patent No. 5760205
; GENERAL INFORMATION:
; APPLICANT: Parker, W. D.
; APPLICANT: Herrnstadt, Corinna
; TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
; TITLE OF INVENTION: for Alzheimer's Disease
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,096
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/219,842
; FILING DATE: 30-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-AG 9504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-451-096-86

Query Match          0.7%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1243 GCGGATGAGGACGAGCA 1262
DB 1 GCGGATGAGGACTAGGATGA 20

RESULT 94
US-08-451-096-53/c
; Sequence 53, Application US/08451096
; Patent No. 5760205
; GENERAL INFORMATION:
; APPLICANT: Parker, W. D.
; APPLICANT: Herrnstadt, Corinna
; TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
; TITLE OF INVENTION: for Alzheimer's Disease
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,096
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/219,842
; FILING DATE: 30-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-AG 9504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 53:
```

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-451-096-53

Query Match          0.7%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1243 GCGGATGAGGACGAGCA 1262
DB 21 GCGGATGAGGACTAGGATGA 2

RESULT 95
US-08-451-096-86
; Sequence 86, Application US/08451096
; Patent No. 5760205
; GENERAL INFORMATION:
; APPLICANT: Parker, W. D.
; APPLICANT: Herrnstadt, Corinna
; TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
; TITLE OF INVENTION: for Alzheimer's Disease
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,096
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/219,842
; FILING DATE: 30-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-AG 9504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-451-096-86

Query Match          0.7%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1243 GCGGATGAGGACGAGCA 1262
DB 1 GCGGATGAGGACTAGGATGA 20

RESULT 96
US-08-413-740A-14/c
; Sequence 14, Application US/08413740A
; Patent No. 6171859
```

GENERAL INFORMATION:
APPLICANT: HERNSTADT, CORINNA
APPLICANT: PARKER, WILLIAM D.
APPLICANT: DAVIS, ROBERT
APPLICANT: MILLER, SCOTT W.
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
TITLE OF INVENTION: Animal Models for Diseases Associated with Mitochondrial
NUMBER OF SEQUENCES: 206
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,740A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: 08/413,740
FILING DATE: 30-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2105/7
TELEPHONE: (202) 429-0796
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-413-740A-14

Query Match 0.7%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1243 GCGGATGAGGACGACGA 1262
DB 21 GCGGATGAGGACTAGGATGA 2

RESULT 97
US-09-367-007C-9
Sequence 9, Application US/09367007C
Patent No. 6416987
GENERAL INFORMATION:
APPLICANT: Bertino, Joseph R.
APPLICANT: Banerjee, Debabrata
APPLICANT: Tong, Youzhi
APPLICANT: Liu-Chen, Xinyue
TITLE OF INVENTION: Mutants of Thymidylate Synthase and Uses Thereof
FILE REFERENCE: D5978
CURRENT APPLICATION NUMBER: US/09/367,007C
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/US98/02145
PRIOR FILING DATE: 1998-01-03

NUMBER OF SEQ ID NOS: 39
SEQ ID NO 9
LENGTH: 21
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: primer_bind
LOCATION: 97..117
OTHER INFORMATION: Sense primer HTS-4A for PCR amplification of part
OTHER INFORMATION: of 890 base pair fragment of human TS gene
OTHER INFORMATION: from nucleotide 50 to the C-terminus
US-09-367-007C-9

Query Match 0.7%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1135 TACCTGGAGAGATCAACA 1154
DB 1 TACCTGGGCGAGATCCAACA 20

RESULT 98
PCT-US95-04063-14/c
Sequence 14, Application PC/TUS9504063
GENERAL INFORMATION:
APPLICANT: HERNSTADT, CORINNA
APPLICANT: PARKER, WILLIAM D.
APPLICANT: DAVIS, ROBERT
APPLICANT: MILLER, SCOTT W.
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
TITLE OF INVENTION: Animal Models for Diseases Associated with Mitochondrial
NUMBER OF SEQUENCES: 206
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2105/7
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-04063-14

Query Match 0.7%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1243 GCGGATGAGGACGACGA 1262

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Db 21 GCGCATGAGGACTAGGATGA 2
|||||
RESULT 99
US-08-338-579A-79
; Sequence 79, Application US/08338579A
; Patent No. 6068975
; GENERAL INFORMATION:
; APPLICANT: Gilliam, T. Conrad
; APPLICANT: Tanzi, Rudolph E.
; TITLE OF INVENTION: ISOLATION AND USES OF A WILSON'S
; TITLE OF INVENTION: DISEASE GENE
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,579A
; FILING DATE: June 17, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/44011-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
US-08-338-579A-79
Query Match 0.7%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1519 CTCCTCCAGCTCTGGCTTCCT 1538
|||||
Db 1 CTCCTCCAGCTCAGGCTTCIT 20

RESULT 100
PCT-US94-05388-28
; Sequence 28, Application PC/TUS9405388
; GENERAL INFORMATION:
; APPLICANT: Jack L. Leonard
; APPLICANT: Peter E. Newburger
; TITLE OF INVENTION: POST-TRANSCRIPTIONAL GENE
; TITLE OF INVENTION: REGULATION BY TRACE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.

; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05388
; FILING DATE: 16 May 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/066,680
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04020/026001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US94-05388-28
Query Match 0.7%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1621 ATATAAATATCCCCAGGGAC 1640
|||||
Db 2 ATATATATATCCCCGGGTC 21

RESULT 101
PCT-US94-09851-79
; Sequence 79, Application PC/TUS9409851
; GENERAL INFORMATION:
; APPLICANT: Gilliam, T. Conrad
; APPLICANT: Tanzi, Rudolph E.
; TITLE OF INVENTION: ISOLATION AND USES OF A WILSON'S
; TITLE OF INVENTION: DISEASE GENE
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09851
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/44011-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
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;
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US94-09851-79

Query Match          0.7%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1519 CTCTCCAGCTCTGGCTTCT 1538
Db 1 CTCTCCAGTTCAGGCTTCT 20

RESULT 102
US-08-192-942-1
; Sequence 1, Application US/08192942
; Patent No. 5989906
; GENERAL INFORMATION:
; APPLICANT: JAMES D. THOMPSON
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING P-GLYCOPROTEIN mdr-
; TITLE OF INVENTION: 1 GENE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/192,942
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/882,885
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 197/173
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-192-942-1

Query Match          0.7%; Score 15.2; DB 1; Length 23;
Best Local Similarity 65.0%; Pred. No. 2.4e+02;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1363 TCTTCAACTTCAAAAAGC 1382
Db 1 UCUUCCAAGCUCAAGAAGC 20

RESULT 103
US-09-052-469-9
; Sequence 9, Application US/09052469
; Patent No. 6380360
; GENERAL INFORMATION:
; APPLICANT: Harris et al.
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE 1 GENE
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: One Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,469
; FILING DATE: Concurrently herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/422,582
; FILING DATE: 14-April-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9507766.5
; FILING DATE: 13-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411900.5
; FILING DATE: 14-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB94/02822
; FILING DATE: 23-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9326470.3
; FILING DATE: 24-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3265/74165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..23
; OTHER INFORMATION: /function= "AH3 F9 primer"
US-09-052-469-9

Query Match          0.7%; Score 15.2; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1266 TGACAAGCGCATCTCGATCT 1285
Db 3 TGACAAGCACATCTGGCTCT 22

RESULT 104
US-08-422-582-9
; Sequence 9, Application US/08422582
; Patent No. 6485960
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; GENERAL INFORMATION:
; APPLICANT: Harris et al.
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE 1 GENE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,582
; FILING DATE: 14-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411900.5
; FILING DATE: 14-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB94/02822
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: GB 9507766.5
; FILING DATE: 13-APR-1995
; APPLICATION NUMBER: GB 9326470.3
; FILING DATE: 24-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3265/53313 (MRC-006xx)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..23
; OTHER INFORMATION: /function= "AH3 F9 primer"
; US-08-422-582-9

Query Match 0.7%; Score 15.2; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1266 TGACAGCGCATCTCGATCT 1285
Db 3 TGACAGCACATCTGGCTCT 22

RESULT 105
US-09-052-262-9
; Sequence 9, Application US/09052262
; Patent No. 6656681
; GENERAL INFORMATION:
; APPLICANT: Harris et al.
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE 1 GENE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: One Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,262
; FILING DATE: Concurrently herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/422,582
; FILING DATE: 14-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9507766.5
; FILING DATE: 13-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411900.5
; FILING DATE: 14-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB94/02822
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: GB 9326470.3
; FILING DATE: 24-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3265/74118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..23
; OTHER INFORMATION: /function= "AH3 F9 primer"
; US-09-052-262-9

Query Match 0.7%; Score 15.2; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1266 TGACAGCGCATCTCGATCT 1285
Db 3 TGACAGCACATCTGGCTCT 22

RESULT 106
US-08-250-856A-22/c
; Sequence 22, Application US/08250856A
; Patent No. 5563255
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P. and Boggs, Russell T.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill

```

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; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,856A
; FILING DATE: May 31, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0094
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-08-250-856A-22

Query Match 0.7%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1460 AGGAGGAGAGCCAG 1474
DB 15 AGGAGGAGAGCCAG 1

RESULT 107
US-08-468-037A-12/c
; Sequence 12, Application US/08468037A
; Patent No. 5859221
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: A. Kawasaki
; TITLE OF INVENTION: 2'-Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859221ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,973A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 835,932
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; US-08-471-973A-12

Query Match 0.7%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1460 AGGAGGAGAGCCAG 1474
DB 15 AGGAGGAGAGCCAG 1

RESULT 108
US-08-471-973A-12/c
; Sequence 12, Application US/08471973A
; Patent No. 5872232
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: Andrew Kawasaki
; TITLE OF INVENTION: Sugar Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5872232ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,973A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 835,932
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; US-08-471-973A-12

Query Match 0.7%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1460 AGGAGGAGAGCCAG 1474
DB 15 AGGAGGAGAGCCAG 1

RESULT 109
US-08-468-037A-12/c
; Sequence 12, Application US/08468037A
; Patent No. 5859221
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: A. Kawasaki
; TITLE OF INVENTION: 2'-Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859221ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,037A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 835,932
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2004
; TELECOMMUNICATION INFORMATION:
```

RESULT 109

US-08-756-806A-22/c
 ; Sequence 22, Application US/08756806A
 ; Patent No. 5952229
 ; GENERAL INFORMATION:
 ; APPLICANT: Monia, Brett P. and Boggs, Russell T.
 ; TITLE OF INVENTION: Antisense Oligonucleotide Modulation
 ; TITLE OF INVENTION: of raf Gene Expression
 ; NUMBER OF SEQUENCES: 65
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Law Offices of Jane Massey Licata
 ; STREET: 66 East Main Street
 ; CITY: Marlton
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08053

COMPUTER READABLE FORM:
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/756.806A

FILING DATE: No. 5952229 September 26, 1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/07111

FILING DATE: May 31, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/250,856

FILING DATE: May 31, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPH-0200

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 810-1454

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 20

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

ANTI-SENSE: Yes

US-08-756-806A-22

Query Match 0.7%; Score 15; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1460 AGGAGGAGAGCCAG 1474

Db 15 AGGAGGAGAGCCAG 1

RESULT 110

US-08-465-880-12/c
 ; Sequence 12, Application US/08465880
 ; Patent No. 5955589
 ; GENERAL INFORMATION:
 ; APPLICANT: Philip Dan Cook
 ; TITLE OF INVENTION: Gapped 2' Modified Oligonucleotides
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5955589ris
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: U.S.A.
 ; ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk, 720 Kb

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/465.880
 FILING DATE: Herewith
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 244,993
 FILING DATE: 21-JUN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Joseph Lucci
 REGISTRATION NUMBER: 33,307
 REFERENCE/DOCKET NUMBER: ISIS-2002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-568-3100
 TELEFAX: 215-568-3439
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 bases
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 ANTI-SENSE: Yes
 US-08-465-880-12

Query Match 0.7%; Score 15; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1460 AGGAGGAGAGCCAG 1474

Db 15 AGGAGGAGAGCCAG 1

RESULT 111

US-09-035-357-12/c
 ; Sequence 12, Application US/09035357
 ; Patent No. 6005087
 ; GENERAL INFORMATION:
 ; APPLICANT: Phillip Dan Cook
 ; APPLICANT: A. Kawasaki
 ; TITLE OF INVENTION: 2'-Modified Oligonucleotides
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6005087ris
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: U.S.A.
 ; ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk, 720 Kb

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/035,357

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/468,037

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Joseph Lucci

REGISTRATION NUMBER: 33,307

REFERENCE/DOCKET NUMBER: ISIS-2004

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 bases

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-09-035-357-12

Query Match 0.7%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1460 AGGAGGAGAGCCAG 1474
Db 15 AGGAGGAGAGCCAG 1

RESULT 112

US-09-143-214-22/c
Sequence 22, Application US/09143214
Patent No. 6090626

GENERAL INFORMATION:
APPLICANT: Monia, Brett P. and Boggs, Russell T.
TITLE OF INVENTION: Antisense Oligonucleotide Modulation
TITLE OF INVENTION: of raf Gene Expression
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
STATE: NJ
COUNTRY: USA
ZIP: 08053

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/143,214
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/756,806
FILING DATE: No. 6090626member 26, 1996

APPLICATION NUMBER: PCT/US95/07111
FILING DATE: May 31, 1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/250,856
FILING DATE: May 31, 1994

ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPR-0200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400

TELEFAX: (609) 810-1454
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:

LENGTH: 20

TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes

US-09-143-214-22

Query Match 0.7%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1460 AGGAGGAGAGCCAG 1474
Db 15 AGGAGGAGAGCCAG 1

RESULT 113

US-09-000-136-8/c
Sequence 8, Application US/09000136
Patent No. 6096720

GENERAL INFORMATION:

APPLICANT: Love, William G
APPLICANT: Shatman, Thomas
APPLICANT: Phillips, Judith A
APPLICANT: Nicklin, Paul L
APPLICANT: Hamilton, Karen O
TITLE OF INVENTION: Liposomal Oligonucleotide Compositions
FILE REFERENCE: 4-20536/A/MA 2112
CURRENT APPLICATION NUMBER: US/09/000,136
CURRENT FILING DATE: 1998-04-23
EARLIER APPLICATION NUMBER: GB 9515743.4
EARLIER FILING DATE: 1995-08-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide

OTHER INFORMATION: alternative oligonucleotide with uniform

OTHER INFORMATION: phosphorothioate backbones and nucleotides 7-20

OTHER INFORMATION: being substituted by methoxy at the 2' position of

OTHER INFORMATION: the sugar moiety

US-09-000-136-8

Query Match 0.7%; Score 15; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1460 AGGAGGAGAGCCAG 1474

Db 15 AGGAGGAGAGCCAG 1

RESULT 114

US-09-702-251-47/c

Sequence 47, Application US/09702251

Patent No. 6372492

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Lex M. Cowser

TITLE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION

FILE REFERENCE: RTS-0199

CURRENT APPLICATION NUMBER: US/09/702,251

CURRENT FILING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 89

SEQ ID NO 47

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-702-251-47

Query Match 0.7%; Score 15; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 413 CTGTGGCAAGTGTCTG 427

Db 19 CTGTGGCAAGTGTCTG 5

RESULT 115

US-09-135-202-12/c

Sequence 12, Application US/09135202

Patent No. 6399754


```
;
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: Andrew Kawasaki
; TITLE OF INVENTION: Sugar Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6399754ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,202
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/471,973
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucchi
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; US-09-135-202-12

Query Match 0.7%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1460 AGGAGGAGAGCCAG 1474
Db 15 AGGAGGAGAGCCAG 1

RESULT 116
US-09-506-073-22/c
; Sequence 22, Application US/09506073
; Patent No. 6410518
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/506,073
; CURRENT FILING DATE: 2000-02-18
; EARLIER APPLICATION NUMBER: US 09/143,214
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: PCT/US98/13961
; EARLIER FILING DATE: 1998-07-06
; EARLIER APPLICATION NUMBER: US 08/888,982
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US 08/756,806
; EARLIER FILING DATE: 1996-11-26
; EARLIER APPLICATION NUMBER: PCT/US95/07111
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/250,856
; EARLIER FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 22
```

```
;
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
; US-09-506-073-22

Query Match 0.7%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1460 AGGAGGAGAGCCAG 1474
Db 15 AGGAGGAGAGCCAG 1

RESULT 117
US-08-802-331-12/c
; Sequence 12, Application US/08802331
; Patent No. 6451991
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D.
; APPLICANT: Monia, Brett
; APPLICANT: Martin, Pierre
; APPLICANT: Altman, Karl-Heinz
; TITLE OF INVENTION: Sugar-Modified Gapped Oligonucleotides
; FILE REFERENCE: ISNO0083
; CURRENT APPLICATION NUMBER: US/08/802,331
; CURRENT FILING DATE: 1997-02-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6451991el Sequence
; US-08-802-331-12

Query Match 0.7%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1460 AGGAGGAGAGCCAG 1474
Db 15 AGGAGGAGAGCCAG 1

RESULT 118
US-09-389-283-12/c
; Sequence 12, Application US/09389283
; Patent No. 6531584
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: A. Kawasaki
; TITLE OF INVENTION: 2'-Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6531584ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/389,283
; FILING DATE:
; CLASSIFICATION:
```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/035,357
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; US-09-389-283-12

Query Match 0.7%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1460 AGGAGGAGAGCCAG 1474
Db 15 AGGAGGAGAGCCAG 1

RESULT 119
PCT-US95-07111A-22/c
; Sequence 22, Application PC/TUS950711A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P. and Boggs, Russell T.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation
; TITLE OF INVENTION: of raf Gene Expression
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07111A
; FILING DATE: May 31, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250,856
; FILING DATE: May 31, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0135
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: yes
; PCT-US95-07111A-22

Query Match 0.7%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/035,357
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; US-09-389-283-12

Query Match 0.7%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1460 AGGAGGAGAGCCAG 1474
Db 15 AGGAGGAGAGCCAG 1

RESULT 120
US-09-431-480-21/c
; Sequence 21, Application US/09431480
; Patent No. 6235708
; GENERAL INFORMATION:
; APPLICANT: Holloway, James L.
; APPLICANT: Feldhaus, Andrew
; TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T
; FILE REFERENCE: 98-72
; CURRENT APPLICATION NUMBER: US/09/431,480
; CURRENT FILING DATE: 1999-11-01
; EARLIER APPLICATION NUMBER: 60/109,217
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: 60/156,382
; EARLIER FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC17516
; US-09-431-480-21

Query Match 0.7%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1692 GAGCCACCTTGCCACCCATTCTT 1714
Db 23 GGGACACCTTGCCACCTTACTT 1

RESULT 121
US-09-617-302-21/c
; Sequence 21, Application US/09617302
; Patent No. 6245529
; GENERAL INFORMATION:
; APPLICANT: Holloway, James L.
; APPLICANT: Feldhaus, Andrew
; TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T
; FILE REFERENCE: 98-72 C1
; CURRENT APPLICATION NUMBER: US/09/617,302
; CURRENT FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/431,480
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/109,217
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/156,382
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC17516
; US-09-617-302-21

Query Match 0.7%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1692 GAGCCACCTTGCCACCCATTCTT 1714
```


COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.125
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,197C
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0410000
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-282-197C-14

Query Match 0.7%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 642 CATGACTGTGCTCTTCA 659
DB 18 CATGGCTGGCCCTTCA 1

RESULT 126
US-08-906-517-60/c
Sequence 60, Application US/08906517
Patent No. 6180774
GENERAL INFORMATION:
APPLICANT: Brown, Sherri M.
APPLICANT: Dean, Duff A.
APPLICANT: Fromm, Michael E.
APPLICANT: Sanders, Patricia R.
TITLE OF INVENTION: Synthetic DNA Sequences Having Enhanced
TITLE OF INVENTION: Expression in Monocytoidonous Plants and Method For
TITLE OF INVENTION: Preparation Thereof
NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,517
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-906-517-60

Query Match 0.7%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 599 ATGGTGACGGCGTGAAG 616
DB 18 ATGGTGCGCGCTGAAG 1

RESULT 127
US-09-522-217-23
Sequence 23, Application US/09522217
Patent No. 6307024
GENERAL INFORMATION:
APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAIL LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-522-217-23

Query Match 0.7%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 464 ATGGGCTGGGGCGCTGC 481
DB 1 ACTGGGCTGGGGCGCTGC 18

RESULT 128
US-09-404-641-22
Sequence 22, Application US/09404641
Patent No. 6576744
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Conklin, Darrell C.
APPLICANT: No. 6576744ak, Julia E.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHAIL
FILE REFERENCE: 98-55
CURRENT APPLICATION NUMBER: US/09/404,641
CURRENT FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/100,896
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: US 60/123,546
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/142,574

```
; PRIOR FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-404-641-22
```

```
Query Match      0.7%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 464 ATTGGGCTGGGGGCTGC 481
Db 1 ACTGGGCTGGGGGACTGC 18
```

```
RESULT 129
US-09-404-641-39
; Sequence 39, Application US/09404641
; Patent No. 6576744
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. 6576744a, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLH11
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/09/404,641
; CURRENT FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-404-641-39
```

```
Query Match      0.7%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 464 ATTGGGCTGGGGGCTGC 481
Db 1 ACTGGGCTGGGGGACTGC 18
```

```
RESULT 130
US-09-923-246-23
; Sequence 23, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272a, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
```

```
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-923-246-23
```

```
Query Match      0.7%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 464 ATTGGGCTGGGGGCTGC 481
Db 1 ACTGGGCTGGGGGACTGC 18
```

```
RESULT 131
US-10-295-723-23
; Sequence 23, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178a, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-295-723-23
```

```
Query Match      0.7%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 464 ATTGGGCTGGGGGCTGC 481
Db 1 ACTGGGCTGGGGGACTGC 18
```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-305-856B-79

Query Match      0.7%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

QY 1783 AGACAACTCTCTGAAATG 1800
Db 18 AACAACTCTCTGCAATG 1

RESULT 134
US-08-157-235-12/c
; Sequence 12, Application US/08157235
; Patent No. 5550016
; GENERAL INFORMATION:
; APPLICANT: OKAMOTO, Hiroaki
; TITLE OF INVENTION: OLIGONUCLEOTIDES OF HCV, PRIMERS AND
; TITLE OF INVENTION: PROBES THEREFROM, METHOD OF DETERMINING HCV GENOTYPES,
; TITLE OF INVENTION: AND METHOD OF DETECTING HCV IN SAMPLES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beveridge, DeGrandi, Weilacher & Young
; STREET: 1850 M Street N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY:
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,235
; FILING DATE: 24-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 354370/92
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert G. Weilacher
; REGISTRATION NUMBER: 20,531
; REFERENCE/DOCKET NUMBER: 06/87-49206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-659-2811
; TELEFAX: 202-659-1462
; TELEX: 64470
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-157-235-12

Query Match      0.7%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1388 GAGTCAAAACAGAGATG 1405
Db 20 GAGTCAAAACAGCGGTG 3

RESULT 135
US-09-132-028-3
; Sequence 3, Application US/09132028
; Patent No. 6222014

```

; GENERAL INFORMATION:
; APPLICANT: Wilding, Edwina Imogen
; APPLICANT: Black, Michael Trevor
; APPLICANT: Traini, Christopher M.
; TITLE OF INVENTION: nrde
; FILE REFERENCE: GM10162
; CURRENT APPLICATION NUMBER: US/09/132,028
; CURRENT FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: staphylococcus aureus
US-09-132-028-3

Query Match 0.7%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1452 GAAACCAAGGAGGAGAA 1469
|||||
Db 3 GAAACCAAGGAGGAGAA 20
|||||

RESULT 136
US-09-210-748A-12/c
; Sequence 12, Application US/09210748A
; Patent No. 6335156
; GENERAL INFORMATION:
; APPLICANT: Hermeking, Heiko
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
; FILE REFERENCE: 1107.77810
; CURRENT APPLICATION NUMBER: US/09/210,748A
; CURRENT FILING DATE: 1998-12-15
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER
US-09-210-748A-12

Query Match 0.7%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1131 TGAGTACCTGGAGAAGT 1148
|||||
Db 18 TGAGTACCGGAGAAGT 1
|||||

RESULT 137
US-09-844-525A-23
; Sequence 23, Application US/09844525A
; Patent No. 6468796
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BIFUNCTIONAL APOPTOSIS REGULATOR EXPRES
; FILE REFERENCE: R1S-0230
; CURRENT APPLICATION NUMBER: US/09/844,525A
; CURRENT FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-844-525A-23

Query Match 0.7%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1223 ACGCATCCCTGAGGAGA 1240
|||||
Db 3 ATGCATCCCTGAGGAGA 20
|||||

RESULT 138
US-09-198-452A-1656/c
; Sequence 1656, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1656
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1656

Query Match 0.7%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 59 GCAAGATGGCGGACGC 76
|||||
Db 19 GCAAGATGGCGGACGC 2
|||||

RESULT 139
US-09-198-452A-6144/c
; Sequence 6144, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6144
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6144

Query Match 0.7%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 519 CGTCAATGATATCGCTT 536
|||||
Db 20 CATCAATGATATCGCTT 3
|||||

RESULT 140
US-09-009-913-112/c
; Sequence 112, Application US/09009913

Patent No. 6087485
GENERAL INFORMATION:
APPLICANT: Axys Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
FILING DATE: 21-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-4P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-009-913-112

Query Match 0.7%; Score 14.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1650 GGCCCGAGCTCAGGCGAGC 1669
DB 20 GGCCCGAGCTCAGGCGAGC 1

RESULT 141
US-09-428-583-6/c
Sequence 6, Application US/09428583
Patent No. 6271029
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF CYTOKINESIN-2 EXPRESSION
FILE REFERENCE: RTS-0096
CURRENT APPLICATION NUMBER: US/09/428,583
CURRENT FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 6
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Probe
US-09-428-583-6

Query Match 0.7%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 468 GGCTGGGGGCTGCACCA 485
DB 19 GCCTGAGGGGCTGCACCA 2

RESULT 142
US-09-434-066-15/c
Sequence 15, Application US/09434066
Patent No. 6465714
GENERAL INFORMATION:
APPLICANT: Luthman, L. Holger
APPLICANT: Galli, L.G. Joakim
TITLE OF INVENTION: Congenic Animal Models of No. 6465714-Insulin
TITLE OF INVENTION: Dependent Diabetes Mellitus
FILE REFERENCE: 09705/009001
CURRENT APPLICATION NUMBER: US/09/434,066
CURRENT FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer
US-09-434-066-15

Query Match 0.7%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1463 AGGAGAGCCGACGACCA 1480
DB 18 AGAGAGACAGACGACCA 1

RESULT 143
US-09-422-978-10680/c
Sequence 10680, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilva
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 10680
LENGTH: 21
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..21
OTHER INFORMATION: downstream amplification primer 99-19142 for SEQ 2815, in compl
US-09-422-978-10680

Query Match 0.7%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 914 GTGTGGAATTGTCAGA 931
DB 21 GTGTGGAATTGTCAGA 4

Query Match	Score	DB	Length	Indels	Gaps
US-09-102-830-15/c	0.7%	14	22	0	0
Sequence 15, Application US/09102830	88.9%	14	22	0	0
Patent No. 6001558	88.9%	14	22	0	0
GENERAL INFORMATION:		14	22	0	0
APPLICANT: BACKUS, JOHN W		14	22	0	0
APPLICANT: ATWOOD, SUSAN M		14	22	0	0
APPLICANT: CASEY, ANN E		14	22	0	0
APPLICANT: RASMUSSEN, ERIC B		14	22	0	0
APPLICANT: CUMMINS, THOMAS J		14	22	0	0
TITLE OF INVENTION: AMPLIFICATION AND DETECTION OF HIV-1		14	22	0	0
TITLE OF INVENTION: AND/OR HIV-2		14	22	0	0
NUMBER OF SEQUENCES: 34		14	22	0	0
CORRESPONDENCE ADDRESS:		14	22	0	0
ADDRESSEE: JOHNSON & JOHNSON		14	22	0	0
STREET: ONE JOHNSON & JOHNSON PLAZA		14	22	0	0
CITY: NEW BRUNSWICK		14	22	0	0
STATE: NEW JERSEY		14	22	0	0
COUNTRY: USA		14	22	0	0
ZIP: 08933		14	22	0	0
COMPUTER READABLE FORM:		14	22	0	0
MEDIUM TYPE: Floppy disk		14	22	0	0
COMPUTER: IBM PC compatible		14	22	0	0
OPERATING SYSTEM: PC-DOS/MS-DOS		14	22	0	0
SOFTWARE: PatentIn Release #1.0, Version #1.25		14	22	0	0
CURRENT APPLICATION DATA:		14	22	0	0
APPLICATION NUMBER: US/09/102,830		14	22	0	0
FILING DATE:		14	22	0	0
CLASSIFICATION:		14	22	0	0
ATTORNEY/AGENT INFORMATION:		14	22	0	0
NAME: OGDEN, STASIA L		14	22	0	0
REGISTRATION NUMBER: 36,228		14	22	0	0
REFERENCE/DOCKET NUMBER: CDS-137/SLO		14	22	0	0
TELECOMMUNICATION INFORMATION:		14	22	0	0
TELEPHONE: 908-524-2819		14	22	0	0
TELEFAX: 908-524-2808		14	22	0	0
INFORMATION FOR SEQ ID NO: 30:		14	22	0	0
SEQUENCE CHARACTERISTICS:		14	22	0	0
LENGTH: 22 base pairs		14	22	0	0
TYPE: nucleic acid		14	22	0	0
STRANDEDNESS: single		14	22	0	0
TOPOLOGY: linear		14	22	0	0
MOLECULE TYPE: DNA (genomic)		14	22	0	0
US-09-102-830-15		14	22	0	0
Query Match	0.7%	14	22	0	0
Best Local Similarity	88.9%	14	22	0	0
Matches	16; Conservative	14	22	0	0
QY	666 TGGAGAGTACTTCCCGG 683	14	22	0	0
Db	22 TGGAGAGACCTCCCGG 5	14	22	0	0
RESULT 145		14	22	0	0
US-09-102-830-30/c	0.7%	14	22	0	0
Sequence 30, Application US/09102830	88.9%	14	22	0	0
Patent No. 6001558	88.9%	14	22	0	0
GENERAL INFORMATION:		14	22	0	0
APPLICANT: BACKUS, JOHN W		14	22	0	0
APPLICANT: ATWOOD, SUSAN M		14	22	0	0
APPLICANT: CASEY, ANN E		14	22	0	0
APPLICANT: RASMUSSEN, ERIC B		14	22	0	0
APPLICANT: CUMMINS, THOMAS J		14	22	0	0
TITLE OF INVENTION: AMPLIFICATION AND DETECTION OF HIV-1		14	22	0	0
TITLE OF INVENTION: AND/OR HIV-2		14	22	0	0
NUMBER OF SEQUENCES: 34		14	22	0	0
CORRESPONDENCE ADDRESS:		14	22	0	0
ADDRESSEE: JOHNSON & JOHNSON		14	22	0	0
STREET: ONE JOHNSON & JOHNSON PLAZA		14	22	0	0
CITY: NEW BRUNSWICK		14	22	0	0
STATE: NEW JERSEY		14	22	0	0
ZIP: 08933		14	22	0	0
COMPUTER READABLE FORM:		14	22	0	0
MEDIUM TYPE: Floppy disk		14	22	0	0
COMPUTER: IBM PC compatible</					

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: no
ANTI-SENSE: yes
FRAGMENT TYPE: internal
ORIGINAL SOURCE: HIV
ORGANISM: HIV
FEATURE:
OTHER INFORMATION: amplification primer for HIV

US-08-938-641C-1

Query Match 0.7%; Score 14.8; DB 1; Length 22;
Best Local Similarity 77.3%; Pred. No. 2.8e+02;
Matches 17; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1985 TGTCTGCTCTCTCTTAATTCTG 2006
|||||:|||||
Db 22 TGTCTWTCGCTCTCGYTTCTG 1

RESULT 147
US-09-050-516-32
; Sequence 32, Application US/09050516
; Patent No. 6627414
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HAYDEN, MARK
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE GASTROINTESTINAL
; TRACT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/278,547
; FILING DATE: 23-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/050,516
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/828,855
; FILING DATE: 31-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6065.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623

TELEX:
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-050-516-32

Query Match 0.7%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 491 AGAAGTCGAGGCATCTG 508
|||||:|||||
Db 2 AGAAGTCGAGGCATCTG 19

RESULT 148
US-10-278-547-32
; Sequence 32, Application US/10278547
; Patent No. 6660834
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HAYDEN, MARK
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE GASTROINTESTINAL
; TRACT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/278,547
; FILING DATE: 23-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/050,516
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/828,855
; FILING DATE: 31-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6065.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623

INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 32;

US-10-278-547-32

Query Match 0.7%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 491 AGAAGTCGAGGCATCTG 508
|||||||
Db 2 AGAAGTCCAGTCATCTG 19

RESULT 149

US-08-852-807-31
; Sequence 31, Application US/08852807
; Patent No. 5861298
; GENERAL INFORMATION:
; APPLICANT: Debouck, Christine
; APPLICANT: Drake, Fred
; APPLICANT: Gowen, Maxine
; APPLICANT: Rood, Julie
; APPLICANT: Hastings, Gregg
; APPLICANT: Adams, Mark
; APPLICANT: Fraser, Claire
; APPLICANT: Lee, No. 5861298man
; APPLICANT: Kirkness, Ewen
; APPLICANT: Blake, Judith
; APPLICANT: Fitzgerald, Lisa
; TITLE OF INVENTION: CATHEPSIN K GENE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,807
; FILING DATE: 07-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/019,942
; FILING DATE: 14-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/020,273
; FILING DATE: 17-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/026,273
; FILING DATE: 26-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50006-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:

US-08-852-807-31

Query Match 0.7%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 713 GCAAAGGCAAGTATTATGCTG 733
|||||||
Db 1 GCAAAGGTGTATTATGATG 21

RESULT 150

US-08-882-083-11/c
; Sequence 11, Application US/08882083
; Patent No. 5869292
; GENERAL INFORMATION:
; APPLICANT: VOORBERG, Johannes J.
; TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,083
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/558,107
; FILING DATE: 13-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 30472/212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-882-083-11
Query Match 0.7%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2025 CTAGTTTCCTTTTGAGATAC 2045

Db 21 CTGGTTTCCTTTTGATCTAC 1

RESULT 151

US-08-558-107-11/c
; Sequence 11, Application US/08558107
; Patent No. 5910481
; GENERAL INFORMATION:
; APPLICANT: VOORBERG, Johannes J.
; TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner

```

; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/558,107
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 30472/212
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-558-107-11
;
; Query Match 0.7%; Score 14.6; DB 1; Length 21;
; Best Local Similarity 81.0%; Pred. No. 2.8e+02;
; Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
;
QY 2025 CTAGTTTCCTTTTCAGATAC 2045
DB 21 CTGGTTTCCTCTTTGATCTAC 1
;
RESULT 152
US-08-63-639A-63
; Sequence 63, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-863-639A-75
;
; Query Match 0.7%; Score 14.6; DB 1; Length 21;
; Best Local Similarity 81.0%; Pred. No. 2.8e+02;
; Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
;
QY 1243 GCGGATGAGGACGACGAC 1263
DB 21 GACGACGACGACGACGAC 1
;
RESULT 154
US-08-594-452-63
; Sequence 63, Application US/08594452
;
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-863-639A-63
;
; Query Match 0.7%; Score 14.6; DB 1; Length 21;
; Best Local Similarity 81.0%; Pred. No. 2.8e+02;
; Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
;
QY 1243 GCGGATGAGGACGACGAC 1263
DB 21 GACGACGACGACGACGAC 1
;
RESULT 154
US-08-594-452-63
; Sequence 63, Application US/08594452
;
```

; Patent No. 6013639
; GENERAL INFORMATION:
; APPLICANT: PEYMAN, Anuschirwan
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: G CAP-STABILIZED OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,452
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 195 02 912.7
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 18748/264/HOCE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-594-452-63

Query Match 0.7%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1854 GGGTGGCTGGTCTCAAG 1874
Db 1 GGGTGGCTGGTCTTCGGG 21

RESULT 155
US-08-722-240-5
; Sequence 5, Application US/08722240
; Patent No. 6083905
; GENERAL INFORMATION:
; APPLICANT: Voorberg, Johannes Jacobus,
; APPLICANT: van Mourik, Jan Aart
; APPLICANT: Mertens, Koenraad
; TITLE OF INVENTION: Method and means for detecting and treating
; TITLE OF INVENTION: disorders in the blood coagulation cascade
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michaelson & Wallace
; STREET: 328 Newman Springs Road, P.O. Box 8489
; CITY: Red Bank
; STATE: New Jersey
; ZIP: 07701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk 3 1/2", 1.44 Mbyte
; COMPUTER: HP Vectra XU
; OPERATING SYSTEM: Windows NT 4 Workstation
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/722,240
; FILING DATE: January 27, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michaelson, Peter L.
; REGISTRATION NUMBER: 30090
; REFERENCE/DOCKET NUMBER: Stichting-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (732)530-6671
; TELEFAX: (732)530-6584
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; US-08-722-240-5

Query Match 0.7%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2025 CTAGTTTCCTTTTGAGATAC 2045
Db 1 CTGGTTTCCATTTCATCTAC 21

RESULT 156
US-08-722-240-6/c
; Sequence 6, Application US/08722240
; Patent No. 6083905
; GENERAL INFORMATION:
; APPLICANT: Voorberg, Johannes Jacobus,
; APPLICANT: van Mourik, Jan Aart
; APPLICANT: Mertens, Koenraad
; TITLE OF INVENTION: Method and means for detecting and treating
; TITLE OF INVENTION: disorders in the blood coagulation cascade
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michaelson & Wallace
; STREET: 328 Newman Springs Road, P.O. Box 8489
; CITY: Red Bank
; STATE: New Jersey
; ZIP: 07701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk 3 1/2", 1.44 Mbyte
; COMPUTER: HP Vectra XU
; OPERATING SYSTEM: Windows NT 4 Workstation
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,240
; FILING DATE: January 27, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michaelson, Peter L.
; REGISTRATION NUMBER: 30090
; REFERENCE/DOCKET NUMBER: Stichting-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (732)530-6671
; TELEFAX: (732)530-6584
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; US-08-722-240-6

Query Match 0.7%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
QY 2025 CTAGTTTCCTTTTGAGATAC 2045
    ||||||| ||||| |||
Db 21 CTGGTTCCATTGATCTAC 1

RESULT 157
US-09-258-408-63
; Sequence 63, Application US/09258408
; Patent No. 6121434
; GENERAL INFORMATION:
; APPLICANT: FREYMAN, Anuschirwan
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: G CAP-STABILIZED OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,408
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09258408
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 30472/212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-243-539-11

Query Match 0.7%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2025 CTAGTTTCCTTTTGAGATAC 2045
    ||||||| ||||| |||
Db 21 CTGGTTTCCTTTTGATCTAC 1

RESULT 159
US-08-991-840A-12/c
; Sequence 12, Application US/08991840A
; Patent No. 6261570
; GENERAL INFORMATION:
; APPLICANT: Michael D. Parker
; APPLICANT: Jonathan F. Smith
; APPLICANT: Bruce Crise
; APPLICANT: Mark Steve Oberste
; APPLICANT: Shannon Schmura
; TITLE OF INVENTION: Live Attenuated Virus Vaccines for Eastern Equine Encephalitis
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: USA MPMC - MPMC-JA
; CITY: FORT DETRICK, FREDERICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,840A
; FILING DATE: December 16, 1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: Provisional Application 60/047162,
; FILING DATE: May 20, 1997
; APPLICATION NUMBER: Provisional Application 60/053,652
; FILING DATE: July 24, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris

QY 1854 GGGGTGGCTGGGTCTTCAAGG 1874
    ||||||| ||||| |||
Db 1 GGGGTGCCGGGTCTTCGGGG 21

RESULT 158
US-09-243-539-11/c
; Sequence 11, Application US/09243539
; Patent No. 6130203
; GENERAL INFORMATION:
; APPLICANT: VOORBERG, Johannes J.
; TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
```

```

; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: 003/058/SAP RIID 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-5034
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: Unknown
; US-08-991-840A-12

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```

Query Match      0.7%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

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QY 475 GGCCTGCACCATGCAAGAAG 495
Db 21 GGCATGCAGCATGAAAAGCAG 1

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RESULT 160

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US-09-525-392-15
; Sequence 15, Application US/09525392
; Patent No. 6416997
; GENERAL INFORMATION:
; APPLICANT: BATES, Paul
; APPLICANT: MIR-SHEKARI, Yasamin
; TITLE OF INVENTION: RECEPTOR-BINDING MUTANTS OF INFLUENZA A VIRUS
; FILE OF INVENTION: HEMAGGLUTININ FOR USE IN TARGETED GENE DELIVERY
; FILE REFERENCE: 209596.0334/66U1
; CURRENT APPLICATION NUMBER: US/09/525,392
; CURRENT FILING DATE: 2000-03-15
; EARLIER APPLICATION NUMBER: 60/059,239
; EARLIER FILING DATE: 1997-09-18
; EARLIER APPLICATION NUMBER: PCT/US98/19552
; EARLIER FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primers
; OTHER INFORMATION: For Influenza Virus A Strain X-31 Hemagglutinin
; US-09-525-392-15

```

```

Query Match      0.7%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 780 CATTTCAGCCGTCATGTC 800
Db 1 CATTTCGACCATGAGGTC 21

```

RESULT 161

```

US-09-422-978-9046
; Sequence 9046, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732

```

```

; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9046
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-2094 for SEQ 1181, in complement
; US-09-422-978-9046

```

```

Query Match      0.7%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1405 GAAAAAGAGAAAGACCCAGAG 1425
Db 1 GATAATGAGAGGACCCAGAG 21

```

RESULT 162

```

US-08-338-509B-5
; Sequence 5, Application US/08338509B
; Patent No. 5712152
; GENERAL INFORMATION:
; APPLICANT: DEQUIN, SYLVIE
; APPLICANT: BARRE, PIERRE
; TITLE OF INVENTION: YEAST STRAINS EXPRESSING THE LACTIC LDH
; TITLE OF INVENTION: GENE AND VECTORS WHICH CAN BE USED FOR OBTAINING SAID
; TITLE OF INVENTION: STRAINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,509B
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR PCT/FR93/00618
; FILING DATE: 22-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/07632
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 384-40-0PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-338-509B-5

```

```

Query Match      0.7%; Score 14.6; DB 1; Length 22;

```



```
/ FILING DATE: 14-OCT-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BAKER, HOLLIE L.
/ REGISTRATION NUMBER: 31,321
/ REFERENCE/DOCKET NUMBER: 102.378.120DV-2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-526-6110
/ TELEFAX: 617-526-5000
/ INFORMATION FOR SEQ ID NO: 82:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 1..22
/ OTHER INFORMATION: /product= "BB10195 oligomer"
US-08-450-905B-82

Query Match          0.7%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 918 GGAATTGTCAGAGCTTTAA 938
Db 1 GGAATTGTCAGAGGTTAA 21

RESULT 166
US-08-450-905B-167
/ Sequence 167, Application US/08450905B
/ Patent No. 5856301
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: Stem Cell Inhibiting Proteins
/ NUMBER OF SEQUENCES: 178
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: HALE and DORR
/ STREET: 60 State Street
/ CITY: Boston
/ STATE: MA
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/450,905B
/ FILING DATE: 26-MAR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/982,759
/ FILING DATE: 08-MAR-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9127319.3
/ FILING DATE: 23-DEC-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9221587.0
/ FILING DATE: 14-OCT-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BAKER, HOLLIE L.
/ REGISTRATION NUMBER: 31,321
/ REFERENCE/DOCKET NUMBER: 102.378.120DV-2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-526-6110
/ TELEFAX: 617-526-5000
/ INFORMATION FOR SEQ ID NO: 167:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
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/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 1..22
/ OTHER INFORMATION: /product= "BB10195 oligomer"
US-08-450-905B-167

Query Match          0.7%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 918 GGAATTGTCAGAGCTTTAA 938
Db 1 GGAATTGTCAGAGGTTAA 21

RESULT 167
US-08-770-544-28/c
/ Sequence 28, Application US/08770544
/ Patent No. 5907085
/ GENERAL INFORMATION:
/ APPLICANT: Gonsalves, Dennis
/ APPLICANT: Ling, Kai-Shu
/ TITLE OF INVENTION: GRAPEVINE LEAPROLL VIRUS PROTEINS AND
/ TITLE OF INVENTION: THEIR USES
/ NUMBER OF SEQUENCES: 32
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
/ STREET: Clinton Square, P.O. Box 1051
/ CITY: Rochester
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 14603
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/770,544
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60009008
/ FILING DATE: 21-DEC-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Goldman, Michael L.
/ REGISTRATION NUMBER: 30,727
/ REFERENCE/DOCKET NUMBER: 19603/621
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (716) 263-1304
/ TELEFAX: (716) 263-1600
/ INFORMATION FOR SEQ ID NO: 28:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
US-08-770-544-28

Query Match          0.7%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 291 GCGCTCCATCCGTCAGATAA 311
Db 22 GCGTCCATCCGTCAGGTTAA 2

RESULT 168
US-07-982-759F-82
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```

STREET: 60 State Street
CITY: Boston
STATE: MA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/07/982,759F
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9127319.3
FILING DATE: 23-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9221587.0
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, HOLLIE L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 102378.120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-526-6000
TELEFAX: 617-526-5000
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..22
OTHER INFORMATION: /product= "BB10195 oligomer"
US-07-982-759F-167

Query Match 0.7%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.2e+02;
Matches 1; Conservative 0; Mismatches 4; Indels

Qy 918 GGAATTTGTCAGAGCTTAA 938
Db 1 GGAATTTGTCAGAGGTGTA 21
|||||
|||||

RESULT 170
US-08-781-891-1
Sequence 1, Application US/08/781891
Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

```

```
/ APPLICATION NUMBER: US/08/781,891
/ FILING DATE: 27-DEC-1996
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6090620tenburg Ph.D., Carol
/ REGISTRATION NUMBER: 39,317
/ REFERENCE/DOCKET NUMBER: 240052.419
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-781-891-1
Query Match 0.7%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1138 CTGGAGAGATCAACAGCGA 1158
Db 1 CTGGCAAGGATCAACAGAGA 21

RESULT 171
US-08-781-891-167
/ Sequence 167, Application US/08781891
/ Patent No. 6090620
/ GENERAL INFORMATION:
/ APPLICANT: Fu, Ying-Hui
/ APPLICANT: Yu, Chang-En
/ APPLICANT: Oshima, Junko
/ APPLICANT: Mulligan, John T.
/ APPLICANT: Schellenberg, Gerald D.
/ TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
/ TITLE OF INVENTION: WERNER'S SYNDROME
/ NUMBER OF SEQUENCES: 209
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED AND BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE: 27-DEC-1996
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6090620tenburg Ph.D., Carol
/ REGISTRATION NUMBER: 39,317
/ REFERENCE/DOCKET NUMBER: 240052.419
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 167:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-781-891-167
Query Match 0.7%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1138 CTGGAGAGATCAACAGCGA 1158
Db 1 CTGGCAAGGATCAACAGAGA 21

RESULT 172
US-09-010-641-19
/ Sequence 19, Application US/09010641
/ Patent No. 6121023
/ GENERAL INFORMATION:
/ APPLICANT: ROMANO, JOSEPH W.
/ APPLICANT: SHURTLIFF, ROXANNE
/ APPLICANT: WILLIAMS, KIMBERLY G.
/ TITLE OF INVENTION: ISOTHERMAL AMPLIFICATION BASED ASSAY FOR
/ TITLE OF INVENTION: THE DETECTION AND QUANTIFICATION OF CHEMOKINES RANTES,
/ TITLE OF INVENTION: MIP-1ALPHA AND MIP-1BETA
/ NUMBER OF SEQUENCES: 45
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: AKZO NOBEL PATENT DEPARTMENT
/ STREET: 1300 PICCARD DRIVE, SUITE 206
/ CITY: ROCKVILLE
/ STATE: MARYLAND
/ COUNTRY: USA
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010,641
/ FILING DATE: 22-JAN-1998
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KLESNER, SHARON N.
/ REGISTRATION NUMBER: 36,335
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 301-948-7400
/ TELEFAX: 301-948-9751
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/
US-09-010-641-19
Query Match 0.7%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1583 TTCTATTCTCTGTGTTT 1603
Db 1 TTTCGATTCACAGTGTGTTT 21

RESULT 173
US-09-356-281-19
/ Sequence 19, Application US/09356281
/ Patent No. 6218154
/ GENERAL INFORMATION:
/ APPLICANT: ROMANO, JOSEPH W.
/ APPLICANT: SHURTLIFF, ROXANNE
/ APPLICANT: WILLIAMS, KIMBERLY G.
/ TITLE OF INVENTION: ISOTHERMAL AMPLIFICATION BASED ASSAY FOR
/ TITLE OF INVENTION: THE DETECTION AND QUANTIFICATION OF CHEMOKINES RANTES,
/ TITLE OF INVENTION: MIP-1ALPHA AND MIP-1BETA
/ NUMBER OF SEQUENCES: 45
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: AKZO NOBEL PATENT DEPARTMENT
/
```

STREET: 1300 PICCARD DRIVE, SUITE 206

CITY: ROCKVILLE

STATE: MARYLAND

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/356,281

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/010,641

FILING DATE: 22-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: KLESNER, SHARON N.

REGISTRATION NUMBER: 36,335

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-948-7400

TELEFAX: 301-948-9751

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-09-356-281-19

Query Match 0.7%; Score 14.6; DB 1; Length 22;

Best Local Similarity 81.0%; Pred. No. 3.2e+02;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1583 TTTCATTTCTGCTGTTT 1603

Db 1 TTTCGATTTTCAGTGTGTTT 21

RESULT 174

US-09-240-918-10/c

; Sequence 10, Application US/09240918

; Patent No. 6265165

; GENERAL INFORMATION:

; APPLICANT: Gruenert, Dieter C.

; APPLICANT: Xu, Zhidong

; TITLE OF INVENTION: METHODS FOR EST-SPECIFIC FULL LENGTH cDNA CLONING

; FILE REFERENCE: 480.85.1(HV)

; CURRENT APPLICATION NUMBER: US/09/240,918

; CURRENT FILING DATE: 1999-01-29

; PRIOR APPLICATION NUMBER: 60/108,183

; PRIOR FILING DATE: 1998-11-12

; NUMBER OF SEQ ID NOS: 96

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer

US-09-240-918-10

Query Match

Best Local Similarity 0.7%; Score 14.6; DB 1; Length 22;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1409 AAGAGAAAGACCCAGAGGAGA 1429

Db 22 AAGAGAAATGAGTGAGAGGAGA 2

RESULT 175

US-09-367-206-25/c

; Sequence 25, Application US/09367206

; Patent No. 6326482

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; TITLE OF INVENTION: NSP Molecules

; FILE REFERENCE: P1223R1E

; CURRENT APPLICATION NUMBER: US/09/367,206

; CURRENT FILING DATE: 1999-08-09

; PRIOR APPLICATION NUMBER: PCT/US99/08847

; PRIOR FILING DATE: 1999-04-23

; PRIOR APPLICATION NUMBER: US 60/082,767

; PRIOR FILING DATE: 1998-04-23

; PRIOR APPLICATION NUMBER: US 60/113,296

; PRIOR FILING DATE: 1998-12-22

; NUMBER OF SEQ ID NOS: 35

; SEQ ID NO 25

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide Probe

US-09-367-206-25

Query Match

Best Local Similarity 0.7%; Score 14.6; DB 1; Length 22;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1420 CCAGAGGAGAGAAAGAGTC 1440

Db 22 CCAGAGGAGACCAAGGAGTC 2

RESULT 176

US-09-043-149-9

; Sequence 9, Application US/09043149

; Patent No. 6355418

; GENERAL INFORMATION:

; APPLICANT: Schmidt, Gunter

; TITLE OF INVENTION: Chimeric Oligonucleotides and Uses Thereof in the

; FILE REFERENCE: 020600-272

; CURRENT APPLICATION NUMBER: US/09/043,149

; CURRENT FILING DATE: 1998-03-13

; PRIOR APPLICATION NUMBER: PCT/GB96/02275

; PRIOR FILING DATE: 1996-09-13

; PRIOR APPLICATION NUMBER: GB 9518864.5

; PRIOR FILING DATE: 1995-09-14

; NUMBER OF SEQ ID NOS: 54

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: primer

US-09-043-149-9

Query Match

Best Local Similarity 0.7%; Score 14.6; DB 1; Length 22;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1393 AAAACAGAGGATGAAAAAGAG 1413

Db 2 AAAACGGAGGCTGAACAATAG 22

RESULT 177

US-09-638-509C-12/c

; Sequence 12, Application US/09638509C

; Patent No. 6372435

; GENERAL INFORMATION:

```

; APPLICANT: Tang, Jianming
; APPLICANT: Kaslow, Richard A.
; TITLE OF INVENTION: Methods of Surveying For CC (Beta) Chemokine
; TITLE OF INVENTION: Receptor Variants and Their Association With HIV-1
; TITLE OF INVENTION: Transmission and/or Disease Progression
; FILE REFERENCE: D6217
; CURRENT APPLICATION NUMBER: US/09/638,509C
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/148,530
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 12
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: primer_bind
; OTHER INFORMATION: CCR5P-3/6S, primer used for typing major
; OTHER INFORMATION: polymorphism in CCR2b, CCR5 and the CCR5 downstream
; OTHER INFORMATION: promoter region
US-09-638-509C-12

```

```

Query Match          0.7%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1312 GAGGAGAGTTCCTCCGATTCT 1332
      ||||| ||||| ||||| |||||
Db 21 GAAGAACTGTCCTGATTCT 1

```

```

RESULT 178
US-09-638-509C-13/c
; Sequence 13, Application US/09638509C
; Patent No. 6372435
; GENERAL INFORMATION:
; APPLICANT: Tang, Jianming
; APPLICANT: Kaslow, Richard A.
; TITLE OF INVENTION: Methods of Surveying For CC (Beta) Chemokine
; TITLE OF INVENTION: Receptor Variants and Their Association With HIV-1
; TITLE OF INVENTION: Transmission and/or Disease Progression
; FILE REFERENCE: D6217
; CURRENT APPLICATION NUMBER: US/09/638,509C
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/148,530
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 13
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: primer_bind
; OTHER INFORMATION: CCR5P-3/7S, primer used for typing major
; OTHER INFORMATION: polymorphism in CCR2b, CCR5 and the CCR5 downstream
; OTHER INFORMATION: promoter region
US-09-638-509C-13

```

```

Query Match          0.7%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1312 GAGGAGAGTTCCTCCGATTCT 1332
      ||||| ||||| ||||| |||||
Db 21 GAAGAACTGTCCTGATTCT 1

```

```

RESULT 179
US-09-579-259-28/c
; Sequence 28, Application US/09579259
; Patent No. 6558953
; GENERAL INFORMATION:
; APPLICANT: Gonsalves, Dennis
;

```

```

; Ling, Kai-Shu
; TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS
; TITLE OF INVENTION: PROTEINS AND THEIR USES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/579,259
; FILING DATE: 25-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60090008
; FILING DATE: 21-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-579-259-28

```

```

Query Match          0.7%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 291 GCGTCCATCCGTCACGATAA 311
      ||||| ||||| ||||| |||||
Db 22 GCGTCCATCCGTCACGATAA 2

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RESULT 180
US-09-618-166-1
; Sequence 1, Application US/09618166
; Patent No. 6583112
; GENERAL INFORMATION:
; APPLICANT: Fu, Ying-Hui
; Yu, Chang-En
; Oshima, Junko
; Mulligan, John T.
; Schellenberg, Gerald D.
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
; WERNER'S SYNDROME
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
;

```

US-09-618-166-1
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/618,166
; FILING DATE: 17-Jul-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 240052.419C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-618-166-1
; Query Match 0.7%; Score 14.6; DB 1; Length 22;
; Best Local Similarity 81.0%; Pred. No. 3.2e+02;
; Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1138 CTGGAGAAGATCAACACGCA 1158
| | | | | | | | | | | | | | | | | | | | | |
DB 1 CTGGCAAGGATCAACACAGAGA 21
; RESULT 181
US-09-618-166-167
; Sequence 167, Application US/09618166
; Patent No. 6583112
; GENERAL INFORMATION:
; APPLICANT: Fu, Ying-Hui
; Yu, Chang-En
; Oshima, Junko
; Mulligan, John T.
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/618,166
; FILING DATE: 17-Jul-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 240052.419C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 167:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 167:

US-09-618-166-167

Query Match 0.7%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1138 CTGGAGAAGATCAACACGCA 1158
| | | | | | | | | | | | | | | | | | | | | |
DB 1 CTGGCAAGGATCAACACAGAGA 21

RESULT 182

US-09-375-673B-62/c
; Sequence 62, Application US/09375673B
; Patent No. 6605431
; GENERAL INFORMATION:
; APPLICANT: GOURSE, RICHARD L.
; APPLICANT: ESTREM, SHAWN T.
; APPLICANT: ROSS, WILMA E.
; APPLICANT: GAAL, TAMAS
; TITLE OF INVENTION: PROMOTER ELEMENTS AND METHODS OF USE
; FILE REFERENCE: 11900130101
; CURRENT APPLICATION NUMBER: US/09/375,673B
; CURRENT FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: combined
; OTHER INFORMATION: accessory promoter element
US-09-375-673B-62

Query Match 0.7%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2031 TCCITTTTGAGATACATATTT 2051
| | | | | | | | | | | | | | | | | | | | | |
DB 22 TCCITTTTGAGAAATACTTT 2

RESULT 183

US-09-650-324A-28/c
; Sequence 28, Application US/09650324A
; Patent No. 6638720
; GENERAL INFORMATION:
; APPLICANT: GONSALVES, DENNIS
; APPLICANT: LING, KAI-SHU
; TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND
; TITLE OF INVENTION: THEIR USES
; FILE REFERENCE: 07678/025006
; CURRENT APPLICATION NUMBER: US/09/650,324A
; CURRENT FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 09/579,259
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 09/224,898
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 08/770,544
; PRIOR FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: US 60/009,008
; PRIOR FILING DATE: 1995-12-21
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-650-324A-28

RESULT 187
US-08-435-634-576
; Sequence 576, Application US/08435634
; Patent No. 5731295

```
;
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,634
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,850
; FILING DATE: February 17, 1995
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5731295ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 576:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-634-576

Query Match 0.7%; Score 14.4; DB 1; Length 17;
Best Local Similarity 25.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 2043 TACTATTTTCATTTT 2058
Db 1 UACUGUUUUCUUUU 16

RESULT 188
US-09-371-772B-4754
; Sequence 4754, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
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;
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4754
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-371-772B-4754

Query Match 0.7%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 1.9e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 470 CTGGGGCGCTGCACCA 485
Db 1 CUGGGAGCCUGCACCA 16

RESULT 189
US-09-866-108A-971/c
; Sequence 971, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 971
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-971

Query Match 0.7%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```


Qy 465 TTGGGCTGGGGCGCTG 480
|||||
Db 17 TTGGGCTGGGGCGCTG 2

RESULT 190
US-09-866-108A-972/c
; Sequence 972, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aemica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 972
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-972

Query Match 0.7%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 465 TTGGGCTGGGGCGCTG 480
|||||
Db 16 TTGGGCTGGGGCGCTG 1

RESULT 191
US-09-866-108A-8945/c
; Sequence 8945, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aemica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 8945
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-8945

Query Match 0.7%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1681 AGCTCTCCAGGAGCC 1696
|||||
Db 17 AGCTCTCCAGGAGCC 2

RESULT 192
US-09-866-108A-8946/c
; Sequence 8946, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 8946
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-8946

Query Match 0.7%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1681 AGCTCTCCAGGAGCC 1696
|||||
DB 16 AGCTCTCCAGGAGCC 1

RESULT 193
US-08-943-087-4/c
; Sequence 4, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other
IMMEDIATE SOURCE:

; CLONE: ZC11107
US-08-943-087-4

Query Match 0.7%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1408 AAAGAGAAAGACCCAG 1423
|||||
DB 17 AAAGAGAAACACCCAG 2

RESULT 194

US-09-207-388-46
; Sequence 46, Application US/09207388
; Patent No. 6497880
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Jan
; TITLE OF INVENTION: HEAT SHOCK GENES AND PROTEINS FROM
; TITLE OF INVENTION: NEISSERIA MENINGITIDIS, CANDIDA GLABRATA AND ASPERGILLUS
; FILE REFERENCE: 870109.411
; CURRENT APPLICATION NUMBER: US/09/207,388
; CURRENT FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer Used to clone Neisseria meningitidis Hsp70
; OTHER INFORMATION: Gene and to construct Neisseria meningitidis Hsp70
; OTHER INFORMATION: expression vectors
US-09-207-388-46

Query Match 0.7%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 236 AAGCCAATGCTCAGGA 251
|||||
DB 2 AAGCCAATGCCAGGA 17

RESULT 195

US-09-422-978-9179
; Sequence 9179, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9179
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-2275 for SEQ 1314, in complemen
US-09-422-978-9179

Query Match 0.7%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 2.2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1410 AGAGAAAGACCCAG 1425
 DB 1 AGAGAAAGACCCAG 16

RESULT 196

US-09-861-779-4/c
 ; Sequence 4, Application US/09861779
 ; Patent No. 6586448
 ; GENERAL INFORMATION:
 ; APPLICANT: Lok, Si
 ; APPLICANT: Kho, Choon J.
 ; APPLICANT: Jelmsberg, Anna C.
 ; APPLICANT: Adams, Robyn L.
 ; APPLICANT: Whitmore, Theodore E.
 ; APPLICANT: Farrish, Theresa M.
 ; TITLE OF INVENTION: Class II Cytokine Receptor-7
 ; FILE REFERENCE: 96-24C2
 ; CURRENT APPLICATION NUMBER: US/09/861,779
 ; CURRENT FILING DATE: 2001-05-21
 ; PRIOR APPLICATION NUMBER: 08/943,087
 ; PRIOR FILING DATE: 1997-10-02
 ; PRIOR APPLICATION NUMBER: 08/803,305
 ; PRIOR FILING DATE: 1997-02-20
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-861-779-4

Query Match 0.7%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 2.2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1408 AAAGAAAGACCCAG 1423
 DB 17 AAAGAAAGACCCAG 2

RESULT 197

US-09-422-978-6157/c
 ; Sequence 6157, Application US/09422978
 ; Patent No. 6537751
 ; GENERAL INFORMATION:
 ; APPLICANT: Cohen, Daniel
 ; APPLICANT: Blumenfeld, Marta
 ; APPLICANT: Chumakov, Ilva
 ; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
 ; FILE REFERENCE: GENSSET.020CP1
 ; CURRENT APPLICATION NUMBER: US/09/422,978
 ; CURRENT FILING DATE: 1999-10-20
 ; EARLIER APPLICATION NUMBER: US 09/298,850
 ; EARLIER FILING DATE: 1999-04-21
 ; EARLIER APPLICATION NUMBER: US 60/109,732
 ; EARLIER FILING DATE: 1998-11-23
 ; EARLIER APPLICATION NUMBER: US 60/082,614
 ; EARLIER FILING DATE: 1998-04-21
 ; NUMBER OF SEQ ID NOS: 11796
 ; SEQ ID NO 6157
 ; LENGTH: 19
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: primer_bind
 ; LOCATION: 1..19
 ; OTHER INFORMATION: upstream amplification primer 99-9420 for SEQ 2223,

US-09-422-978-6157

Query Match 0.7%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1582 TTTTCTATTCTCTGT 1597
 DB 17 TTTTCTATTCTCTCT 2

RESULT 198

US-07-959-119A-12/c
 ; Sequence 12, Application US/07959119A
 ; Patent No. 5487985
 ; GENERAL INFORMATION:
 ; APPLICANT: McClelland, Michael
 ; APPLICANT: Welsh, John T.
 ; APPLICANT: Sorge, Joseph A.
 ; TITLE OF INVENTION: Arbitrarily Primed Polymerase Chain
 ; TITLE OF INVENTION: Reaction Method For Fingerprinting Genomes
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 2730 Sand Hill Road
 ; CITY: Menlo Park
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/959,119A
 ; FILING DATE: 09-OCT-1992
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Halluin, Albert P.
 ; REGISTRATION NUMBER: 25,227
 ; REFERENCE/DOCKET NUMBER: 8142-021
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 854-3660
 ; TELEFAX: (415) 854-3694
 ; TELEX: 66141PENNIE
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 US-07-959-119A-12

Query Match 0.7%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 2.9e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 639 GGTCATGACTGTGTC 654
 DB 16 GGTCATGACTGTGTC 1

RESULT 199

US-09-444-053-60/c
 ; Sequence 60, Application US/09444053A
 ; Patent No. 6165728
 ; GENERAL INFORMATION:
 ; APPLICANT: Donna T. Ward
 ; APPLICANT: Lex M. Cowser
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF NCK-2 EXPRESSION
 ; FILE REFERENCE: RFS-0122

; CURRENT APPLICATION NUMBER: US/09/444,053A
; CURRENT FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-444-053-60

Query Match 0.7%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1437 AGTCACCGAGGAGGAG 1452
DB 16 AGTCACCGAGGAGGAG 1

RESULT 200
US-08-154-364-18/c
; Sequence 18, Application US/08154364
; Patent No. 6207810
; GENERAL INFORMATION:
; APPLICANT: McCelland, Michael
; APPLICANT: Welsh, John T.
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: ARBITRARILY PRIMED
; TITLE OF INVENTION: POLYMERASE CHAIN
; TITLE OF INVENTION: REACTION METHOD FOR FINGER PRINTING
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Limbach and Limbach
; STREET: 2001 Perry Building
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION NUMBER: US/08/154,364
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bortner, Scott R.
; REGISTRATION NUMBER: 34,298
; REFERENCE/DOCKET NUMBER: STRG-20142 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-433-4150
; TELEFAX: 414-433-8716
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-154-364-18

Query Match 0.7%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 639 GGTGATGACTGTGTCC 654

DB 16 GGTGATGACTGTGTCC 1

RESULT 201
US-09-629-645A-33
; Sequence 33, Application US/09629645A
; Patent No. 6365354
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF LYSOPHOSPHOLIPASE I EXPRESSION
; FILE REFERENCE: RTS-0137
; CURRENT APPLICATION NUMBER: US/09/629,645A
; CURRENT FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 164
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-629-645A-33

Query Match 0.7%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1572 AGTTTATATTTTCT 1587
DB 2 AGTTTATATTTTCT 17

RESULT 202
US-09-422-978-10071/c
; Sequence 10071, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilva
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10071
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-9355 for SEQ 2206, in complement
US-09-422-978-10071

Query Match 0.7%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1402 GATGAAAGAGAGAAAG 1417
DB 16 GATGAAAGAGAGAAAG 1

RESULT 203
US-09-705-267A-61

```
; Sequence 61, Application US/09705267A
; Patent No. 6551826
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF RAIDD EXPRESSION
; FILE REFERENCE: RTS-0211
; CURRENT APPLICATION NUMBER: US/09/705,267A
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 177
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-705-267A-61

Query Match          0.7%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1000 ACATATGAGACAGCTG 1015
Db 2 ACATATGAGACACCTG 17

RESULT 204
US-09-198-452A-6177
; Sequence 6177, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6177
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6177

Query Match          0.7%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1093 CACATCAGTCCTCCCA 1108
Db 1 CACATCAGTCCTCCCA 16

RESULT 205
US-09-112-580-57
; Sequence 57, Application US/09112580
; Patent No. 6610539
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping
; APPLICANT: DUGOURD, Dominique
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE SEQUENCES AS INHIBITORS OF MICROORGANISMS
; FILE REFERENCE: 032396-016
; CURRENT APPLICATION NUMBER: US/09/112,580
; CURRENT FILING DATE: 1998-07-09
; EARLIER APPLICATION NUMBER: US 60/052,160
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 265
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-112-580-57

Query Match          0.7%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 GCCTTCTACACACCG 634
Db 3 GCCTTCCACACACCG 18

RESULT 206
US-09-445-283C-43/c
; Sequence 43, Application US/09445283C
; Patent No. 6624296
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Silhavy, Daniel
; APPLICANT: Sriraman, Priya
; TITLE OF INVENTION: Plasmid Promoters for Transgene Expression in the Plasmids of Higher Plants
; FILE REFERENCE: Rut 97-0097
; CURRENT APPLICATION NUMBER: US/09/445,283C
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: PCT/US98/11437
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/058,670
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/048,376
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-445-283C-43

Query Match          0.7%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 754 GGGATTGATGACGAGT 769
Db 16 GGGATTGATGACGAGT 1

RESULT 207
US-08-639-501-56/c
; Sequence 56, Application US/08639501
; Patent No. 5837492
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Kamb, Alexander
; APPLICANT: Simard, Jacques
; APPLICANT: Couch, Fergus
; APPLICANT: Rommens, Johanna
; APPLICANT: Weber, Barbara
; TITLE OF INVENTION: Chromosome 13-Linked Breast Cancer Susceptibility Gene
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1001
; CITY: Washington
; STATE: DC
; COUNTRY: USA
```

ZIP: 22204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,501
FILING DATE: 29-APR-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/585,391
FILING DATE: 11-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/576,559
FILING DATE: 21-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/575,359
FILING DATE: 20-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/573,779
FILING DATE: 18-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-116802-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-639-501-56

Query Match 0.7%; Score 14.4; DB 1; Length 21;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1402 GATGAAAAGAGAAAG 1417
|||||
Db 21 GATGAAAAGAGCAAG 6

RESULT 208
US-09-044-946-56/c
Sequence 56, Application US/09044946
Patent No. 6033857
GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Kamb, Alexander
APPLICANT: Simard, Jacques
APPLICANT: Couch, Fergus
APPLICANT: Rommens, Johanna
APPLICANT: Weber, Barbara
TITLE OF INVENTION: Chromosome 13-Linked Breast Cancer
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1001
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 22204
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/044,946
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/639,501
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/576,559
FILING DATE: 21-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/575,359
FILING DATE: 20-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/573,779
FILING DATE: 18-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-116802-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-044-946-56

Query Match 0.7%; Score 14.4; DB 1; Length 21;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1402 GATGAAAAGAGAAAG 1417
|||||
Db 21 GATGAAAAGAGCAAG 6

RESULT 209
US-08-755-587-182
Sequence 182, Application US/08755587
Patent No. 6045997
GENERAL INFORMATION:
APPLICANT: Futreal, Phillip A
APPLICANT: Wooster, Richard F
APPLICANT: Ashworth, Alan
APPLICANT: Stratton, Michael R
TITLE OF INVENTION: Materials and methods relating to the
TITLE OF INVENTION: identification and sequencing of the BRCA2 cancer
TITLE OF INVENTION: susceptibility gene and uses thereof.
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park & Gibson
STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
CITY: Raleigh
STATE: NC
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,587
; FILING DATE: 25-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9523959.6
; FILING DATE: 23-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525555.0
; FILING DATE: 14-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9617961.9
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenneth D Sibley
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5405-135
; INFORMATION FOR SEQ ID NO: 182:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-755-587-182

Query Match 0.7%; Score 14.4; DB 1; Length 21;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1991 TCTTCTCCTAATTCG 2006
Db 1 TCTTCTCCTAATTCG 16

RESULT 210
US-09-044-908-56/c
; Sequence 56, Application US/09044908
; Patent No. 6124104
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Kamb, Alexander
; APPLICANT: Simard, Jacques
; APPLICANT: Couch, Feigus
; APPLICANT: Rommens, Johanna
; APPLICANT: Weber, Barbara
; TITLE OF INVENTION: Chromosome 13-Linked Breast Cancer
; TITLE OF INVENTION: Susceptibility Gene
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1001
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 22204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,908
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/639,501
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/576,559
; FILING DATE: 21-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/575,359
; FILING DATE: 20-DEC-1995
; PRIOR APPLICATION DATA:
```

```
;
; APPLICATION NUMBER: US 08/573,779
; FILING DATE: 18-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-116802-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-044-908-56

Query Match 0.7%; Score 14.4; DB 1; Length 21;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1402 GATGAAAAAGAGAAAG 1417
Db 21 GATGAAAAAGAGCAAG 6

RESULT 211
US-08-899-367-16
; Sequence 16, Application US/08899367
; Patent No. 6472170
; GENERAL INFORMATION:
; APPLICANT: Yang et al.
; TITLE OF INVENTION: BCL-X{SYMBOL 103 \f "Symbol"}, A NOVEL BCL-X
; TITLE OF INVENTION: ISOFORM, AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,367
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-899-367-16
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```
Query Match          0.7%; Score 14.4; DB 1; Length 21;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1084 TTCAGCTCCACATCA 1099
Db 1 TTCAGCTCCACTCA 16

RESULT 212
US-09-111-667C-3/c
; Sequence 3, Application US/09111667C
; Patent No. 6501003
; GENERAL INFORMATION:
; APPLICANT: Messing, Albee
; APPLICANT: Zhuo, Lang
; APPLICANT: Murphy, Christopher J.
; TITLE OF INVENTION: TRANSGENIC MOUSE EXPRESSING GREEN FLUORESCENT PROTEIN IN ASTROCYTES
; FILE REFERENCE: 96429-9017
; CURRENT APPLICATION NUMBER: US/09/111,667C
; CURRENT FILING DATE: 2002-07-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Aequorea victoria
US-09-111-667C-3

Query Match          0.7%; Score 14.4; DB 1; Length 21;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 594 TCACCATGGTGACGCG 609
Db 21 TCACCATGGTGCGGCG 6

RESULT 213
US-09-422-978-10830/c
; Sequence 10830, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPl
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10830
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-21244 for SEQ 2965, in complete
US-09-422-978-10830

Query Match          0.7%; Score 14.4; DB 1; Length 21;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1910 AGCCATTTTAGATTG 1925
```

```
Db 16 AGACATTTTAGATTG 1

RESULT 214
US-08-242-664-37
; Sequence 37, Application US/08242664
; Patent No. 5571937
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Weil, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,664
; FILING DATE: May 12, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-242-664-37

Query Match          0.7%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1334 AAGAGGAGGAGGAGGGGG 1352
Db 1 AAGAGGAGGAGGAGGTGGG 19

RESULT 215
US-08-484-138-37
; Sequence 37, Application US/08484138
; Patent No. 5652350
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Weil, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: 3.5 inch 1.44MB
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,138
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683-Z/JPW/WJG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-484-138-37

Query Match          0.7%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1334 AAGAGGAGGAGGAGGGGG 1352
Db 1 AAGAGGAGGAGGAGGTGGG 19

RESULT 216
US-09-305-856B-77/c
; Sequence 77, Application US/09305856B
; Patent No. 6479236
; GENERAL INFORMATION:
; APPLICANT: Penny, Laura
; APPLICANT: Galvin, Margaret
; TITLE OF INVENTION: Genotyping the Human
; FILE REFERENCE: 4389-7 (formerly SEQ-17CIP)
; CURRENT APPLICATION NUMBER: US/09/305,856B
; CURRENT FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: 60/084,807
; PRIOR FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; US-09-305-856B-77

Query Match          0.7%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1780 ATAAGACAAACTCTGAAA 1798
Db 19 ATTAACAAACTCTGCAA 1

RESULT 217
US-09-422-978-11276
; Sequence 11276, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
```

```

; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11276
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: downstream amplification primer 99-3789 for SEQ 3411, in complete
; US-09-422-978-11276

Query Match          0.7%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 914 GTGTGAATTGTCAAGAG 932
Db 1 GTGTGAATATGTGAAGAG 19

RESULT 218
PCT-US95-06379-37
; Sequence 37, Application PC/TUS9506379
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Weil, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44MB
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06379
; FILING DATE: May 13, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US95-06379-37

Query Match          0.7%; Score 14.2; DB 1; Length 19;
```

```
Best Local Similarity 84.2%; Pred No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1334 AAGAGGAGGAGGAGGGGG 1352
      ||||| ||||| |||||
Db 1 AAGAGGAGGAGGAGGTGG 19

RESULT 219
US-07-838-264-7/c
; Sequence 7, Application US/07838264
; Patent No. 5348876
; GENERAL INFORMATION:
; APPLICANT: MICHAELSEN, Terje
; APPLICANT: SANDLIE, Inger
; TITLE OF INVENTION: IgG3 Antibodies With Shortened Hinge
; TITLE OF INVENTION: Region And A Complement Activation Test
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/838,264
; FILING DATE: 19920312
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP90/01172
; FILING DATE: 17-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8916400.8
; FILING DATE: 18-JUL-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16787/156/DFBC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-838-264-7

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 376 GGCCTGTTGAGTCTGTC 394
      ||||| ||||| |||||
Db 19 GGCATGTTGAGTCTGTC 1

RESULT 220
US-08-029-327-3
; Sequence 3, Application US/08029327
; Patent No. 5424189
; GENERAL INFORMATION:
; APPLICANT: Oberst, Richard
; APPLICANT: Hays, Michael T.
; TITLE OF INVENTION: Specific DNA Primers and Method To Use

; TITLE OF INVENTION: Same to Detect Bovine Respiratory Syncytial Virus
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
; STREET: 100 South Wacker Drive, Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,327
; FILING DATE: 19930305
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fentress, Susan B.
; REGISTRATION NUMBER: 31,327
; REFERENCE/DOCKET NUMBER: 92062A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)-456-8000
; TELEFAX: (312)-456-7776
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-029-327-3

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1483 GGGGTCAAGGAGGAGGTCA 1501
      ||||| ||||| |||||
Db 1 GTGTCACAGAGAGAGGTCA 19

RESULT 221
US-08-222-177A-261/c
; Sequence 261, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dc-da)n.(dg-dt)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DeWitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
```

REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
TELEX:
INFORMATION FOR SEQ ID NO: 261:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: mfd74p1
US-08-222-177A-261

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1451 AGAAACCAAGGAGGAGAA 1469
DB 20 ACAAGCCCAAGGAGGTGAA 2

RESULT 222
US-08-750-532-13
Sequence 13, Application US/08750532
Patent No. 5756339
GENERAL INFORMATION:
APPLICANT: MITTA, Masanori
APPLICANT: YAMAMOTO, Katsuhiko
APPLICANT: MORISHITA, Mio
APPLICANT: ASADA, Kiyozo
APPLICANT: TSUNASAWA, Susumu
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,532
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01095
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1994/130236
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1994/173912
FILING DATE: 26-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: MITTA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-750-532-16

LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-750-532-13

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1119 CCAGAACACGAATGAGTAC 1137
DB 1 CCAGAACACGAATGAGTAC 19

RESULT 223
US-08-750-532-16/c
Sequence 16, Application US/08750532
Patent No. 5756339
GENERAL INFORMATION:
APPLICANT: MITTA, Masanori
APPLICANT: YAMAMOTO, Katsuhiko
APPLICANT: MORISHITA, Mio
APPLICANT: ASADA, Kiyozo
APPLICANT: TSUNASAWA, Susumu
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,532
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01095
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1994/130236
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1994/173912
FILING DATE: 26-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: MITTA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-750-532-16

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1119 CCAGAACACGATGAGTAC 1137
Db 20 CCAGAACACGATGAGTAC 2

RESULT 224

US-08-147-843-1
; Sequence 1, Application US/08147843
; Patent No. 5766948
; GENERAL INFORMATION:
; APPLICANT: Gage, Fred H.
; APPLICANT: Ray, Jasodhara
; TITLE OF INVENTION: METHOD FOR PRODUCTION OF NEUROBLASTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Juba & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,843
; FILING DATE: 03-NOV-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-3107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: Nfn Forward Primer
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..20
US-08-147-843-1

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 247 GAGGAGATGACCAAGTACC 265
Db 1 GAGGAGATACTGAGTACC 19

RESULT 225

US-08-602-203-7
; Sequence 7, Application US/08602203
; Patent No. 5770414
; GENERAL INFORMATION:
; APPLICANT: Gage et al., Fred H.
; TITLE OF INVENTION: REGULATABLE RETROVIRUS SYSTEM FOR
; TITLE OF INVENTION: GENETIC MODIFICATION OF CELLS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,203
; FILING DATE: 20-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/024001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-602-203-7

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 247 GAGGAGATGACCAAGTACC 265
Db 1 GAGGAGATACTGAGTACC 19

RESULT 226

US-08-465-485A-26
; Sequence 26, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.

```
;
;
;   REGISTRATION NUMBER: 34,600
;   REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (408) 436-2070
;   TELEFAX: (408) 436-2075
;   INFORMATION FOR SEQ ID NO: 26:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 20 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: Other nucleic acid;
;   DESCRIPTION: Synthetic DNA
;   ANTI-SENSE: YES
;   FEATURE:
;   NAME/KEY: Modified_base
;   LOCATION: 18..19
;   OTHER INFORMATION: Last two internucleoside linkages are
;   OTHER INFORMATION: phosphorothioates
;
US-08-465-485A-26

Query Match          0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      6 GAGCGCGGGCGGGAGGGC 24
DB      1 GCGCGCGGGCGGGCGGGC 19

RESULT 227
US-08-975-211-6/c
; Sequence 6, Application US/08975211
; Patent No. 5948902
; GENERAL INFORMATION:
; APPLICANT: Honkanen, Richard E
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF
; TITLE OF INVENTION: HUMAN SERINE/THREONINE PROTEIN PHOSPHATASE GENE EXPRESSION
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jaecle Fleischmann & Mugel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,211
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Braham, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87647.97R407
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; ANTI-SENSE: YES
;
US-08-975-211-6
```

```
;
;
;   Query Match          0.7%; Score 14.2; DB 1; Length 20;
;   Best Local Similarity 84.2%; Pred. No. 3.2e+02;
;   Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      246 TGAGGAGATGACCAAGTAC 264
DB      19 TGAGGTGAGGCCAAGTAC 1

RESULT 228
US-08-837-201C-78
; Sequence 78, Application US/08837201C
; Patent No. 5985558
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; APPLICANT: Miraglia, Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; TITLE OF INVENTION: Compositions and Methods for the Modulation of
; TITLE OF INVENTION: Activating Protein 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,201C
; FILING DATE: April 14, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
;
US-08-837-201C-78

Query Match          0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1554 TTTCTTCCCAACCCCTCA 1572
DB      2 TTTCTTCCACTGCCCTCA 20

RESULT 229
US-08-837-201C-95/c
; Sequence 95, Application US/08837201C
; Patent No. 5985558
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; APPLICANT: Miraglia, Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; TITLE OF INVENTION: Compositions and Methods for the Modulation of
```

;; TITLE OF INVENTION: Activating Protein 1
;; NUMBER OF SEQUENCES: 139
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Law Offices of Jane Massey Licata
;; STREET: 66 East Main Street
;; CITY: Marlton
;; STATE: NJ
;; COUNTRY: USA
;; ZIP: 08053
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
;; COMPUTER: IBM PS/2
;; OPERATING SYSTEM: WINDOWS 95
;; SOFTWARE: WORDPERFECT 6.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/837,201C
;; FILING DATE: April 14, 1997
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jane Massey Licata
;; REGISTRATION NUMBER: 32,257
;; REFERENCE/DOCKET NUMBER: ISPH-0209
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (609) 810-1515
;; TELEFAX: (609) 810-1454
;; INFORMATION FOR SEQ ID NO: 95:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20
;; TYPE: Nucleic Acid
;; STRANDEDNESS: Single
;; TOPOLOGY: Linear
;; ANTI-SENSE: Yes
;; US-08-837-201C-95

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1554 TTTCTTCCCAACCCCTCA 1572
|||||
Db 19 TTTCTTCCACTGCCCTCA 1

RESULT 230
US-09-065-858-1
; Sequence 1, Application US/09065858
; Patent No. 6013521
; GENERAL INFORMATION:
; APPLICANT: Gage, Fred H.
; TITLE OF INVENTION: METHOD FOR PRODUCTION OF NEUROBLASTS
; FILE REFERENCE: 07257/013003
; CURRENT APPLICATION NUMBER: US/09/065,858
; CURRENT FILING DATE: 1998-04-24
; EARLIER APPLICATION NUMBER: 08/147,843
; EARLIER FILING DATE: 1993-11-03
; EARLIER APPLICATION NUMBER: 08/001,543
; EARLIER FILING DATE: 1993-01-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotides for PCR
US-09-065-858-1

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 247 GAGGAGATGACCAAGTACC 265
|||||
Db 1 GAGGAGATAACTGAGTACC 19

RESULT 231
US-09-065-883-1
; Sequence 1, Application US/09065883
; Patent No. 6020197
; GENERAL INFORMATION:
; APPLICANT: Gage, Fred H.
; APPLICANT: Ray, Jasodhara
; TITLE OF INVENTION: METHOD FOR PRODUCTION OF NEUROBLASTS
; FILE REFERENCE: 07257/013004
; CURRENT APPLICATION NUMBER: US/09/065,883
; CURRENT FILING DATE: 1998-04-24
; EARLIER APPLICATION NUMBER: 08/147,843
; EARLIER FILING DATE: 1993-11-03
; EARLIER APPLICATION NUMBER: 08/001,543
; EARLIER FILING DATE: 1993-01-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotides for PCR
US-09-065-883-1

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 247 GAGGAGATGACCAAGTACC 265
|||||
Db 1 GAGGAGATAACTGAGTACC 19

RESULT 232
US-09-080-285-26
; Sequence 26, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: Synthetic DNA
; ANTI-SENSE: YES
; FEATURE:
; NAME/KEY: Modified_base
; LOCATION: 18..19
; OTHER INFORMATION: Last two internucleoside linkages are
; OTHER INFORMATION: phosphorothioates
; US-09-080-285-26

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 GAGCGCGGGCGGAGGGC 24
Db 1 GCGCGGGCGGGCGGGC 19

RESULT 233
US-09-095-769-1
; Sequence 1, Application US/09095769
; Patent No. 6045807
; GENERAL INFORMATION:
; APPLICANT: Gage, Fred H.
; APPLICANT: Ray, Jasodhara
; TITLE OF INVENTION: METHOD FOR PRODUCTION OF NEUROBLASTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,769
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/147,843
; FILING DATE: 03-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-3107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 1:
```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: NFh Forward Primer
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..20
; US-09-095-769-1

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 247 GAGGAGATGACCAAGTACC 265
Db 1 GAGGAGATAACTGAGTACC 19

RESULT 234
US-09-289-267-69
; Sequence 69, Application US/09289267A
; Patent No. 6046320
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF MDMX EXPRESSION
; FILE REFERENCE: RTS-0049
; CURRENT APPLICATION NUMBER: US/09/289,267A
; CURRENT FILING DATE: 1999-04-04
; NUMBER OF SEQ ID NOS: 166
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-289-267-69

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2016 GTTGCTAGTCTAGTTTCCT 2034
Db 1 GTTGCTTCTCAAGTTTCCT 19

RESULT 235
US-09-344-001-12/c
; Sequence 12, Application US/09344001
; Patent No. 6054440
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF Jun N-TERMINAL KINASE EXPRESSION
; FILE REFERENCE: RTS-0067
; CURRENT APPLICATION NUMBER: US/09/344,001
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-344-001-12

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
```

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 601 GGTGACGGCGTGGAGAGG 619
Db 19 GGTGGCGCGGGGAAGATG 1

RESULT 236

US-09-344-001-14/c

; Sequence 14, Application US/09344001

; Patent No. 6054440

; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia

; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF JUN N-TERMINAL KINASE

; FILE REFERENCE: RTS-0067

; CURRENT APPLICATION NUMBER: US/09/344,001

; CURRENT FILING DATE: 1999-06-24

; NUMBER OF SEQ ID NOS: 47

; SEQ ID NO 14

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-344-001-14

Query Match

Best Local Similarity 0.7%; Score 14.2; DB 1; Length 20;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 51 GGAGCGGAGCAAGTGGCG 69

Db 20 GCGCGCGGGGAAGATGGCG 2

RESULT 237

US-09-009-913-312

; Sequence 312, Application US/09009913

; Patent No. 6087485

; GENERAL INFORMATION:

; APPLICANT: Axys Pharmaceuticals, Inc.

; TITLE OF INVENTION: Asthma Related Genes

; NUMBER OF SEQUENCES: 339

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bozicevic & Reed, LLP

; STREET: 285 Hamilton Ave, Suite 200

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/009,913

; FILING DATE: 21-JAN-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Sherwood, Pamela J

; REGISTRATION NUMBER: 36,677

; REFERENCE/DOCKET NUMBER: SEQ-4P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-327-3231

; TELEFAX: 650-327-3231

; TELEX:

; INFORMATION FOR SEQ ID NO: 312:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-009-913-312

Query Match

Best Local Similarity 0.7%; Score 14.2; DB 1; Length 20;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2033 CTTTTCAGATACTATT 2051

Db 2 CTTTTCAGATACTACTAT 20

RESULT 238

US-08-666-221B-32

; Sequence 32, Application US/08666221B

; Patent No. 6136544

; GENERAL INFORMATION:

; APPLICANT: Kamboj, Rajender

; APPLICANT: Nutt, Stephen

; TITLE OF INVENTION: GLUTAMATE RECEPTOR (OR EAA RECEPTOR)

; TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USES

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/666,221B

; FILING DATE: 20-JUN-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Bent, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 016777/0308

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "primer"

US-08-666-221B-32

Query Match

Best Local Similarity 0.7%; Score 14.2; DB 1; Length 20;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1242 TGCGATGAGCAGAGGAC 1260

Db 2 TGCGATGAGCAGAGGAC 20

RESULT 239

US-09-490-692-151/c

; Sequence 151, Application US/09490692
; Patent No. 6180353
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
; FILE REFERENCE: RTS-0120
; CURRENT APPLICATION NUMBER: US/09/490,692
; CURRENT FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 151
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-490-692-151

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1245 CGATGAGGACGAGACGAC 1263
||||| ||||| |||||
Db 20 CGATGATGACGATGAC 2

RESULT 240
US-09-927-219-65/c
; Sequence 65, Application US/08927219
; Patent No. 6187533
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamagata, Kazuya
; APPLICANT: Oda, Naohisa
; APPLICANT: Kaisaki, Pamela J.
; APPLICANT: Furuta, Hiroto
; APPLICANT: Horikawa, Yukio
; APPLICANT: Menzel, Stephen
; TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
; TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
; TITLE OF INVENTION: AND HNF-4ALPHA
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,219
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/029,679
; FILING DATE: 30-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,056
; FILING DATE: 02-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/025,719
; FILING DATE: 10-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD-272
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-927-219-65

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 GGAGCGCGGCGGAGGG 23
||||| ||||| |||||
Db 19 GGAGCAGCTGACGGAGGG 1

RESULT 241
US-09-311-260-179/c
; Sequence 179, Application US/09311260
; Patent No. 6214555
; GENERAL INFORMATION:
; APPLICANT: Leushner, James
; APPLICANT: Hui, May
; APPLICANT: Dunn, James M.
; APPLICANT: LaCroix, Jean-Michel
; TITLE OF INVENTION: METHOD, COMPOSITIONS AND KIT FOR DETECTION OF
; TITLE OF INVENTION: MICROORGANISMS AND BI-DIRECTIONAL SEQUENCING OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 189
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson LLP
; STREET: P.O. Box 5270
; CITY: Frisco
; STATE: CO
; COUNTRY: US
; ZIP: 80443-5270
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/311,260
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Larson, Marina T.
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-058-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (970) 668-2050
; TELEFAX: (970) 668-2082
; TELEX:
; INFORMATION FOR SEQ ID NO: 179:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: yes
; FRAGMENT TYPE: internal
US-09-311-260-179
Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 948 GCTGATGCTGGAGGCGGT 966
|||
Db 19 GCTGATGTTGGAGTAGGT 1

RESULT 242

US-09-282-736-6/c
; Sequence 6, Application US/09282736A
; Patent No. 6235891
; GENERAL INFORMATION:
; APPLICANT: Honkanen, Richard E.
; TITLE OF INVENTION: Glucocorticoid Receptor Agonist and Decreased PP5
; FILE REFERENCE: 004.00220
; CURRENT APPLICATION NUMBER: US/09/282,736A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-282-736-6

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 246 TGAGGATGACCAAGTAC 264
|||
Db 19 TGAGGTGAGGCCAGTAC 1

RESULT 243

US-09-377-309-76
; Sequence 76, Application US/09377309B
; Patent No. 6258790
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Condon, Tom P.
; APPLICANT: Cowsett, Lex M.
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN 4 EXPRESSION
; CURRENT APPLICATION NUMBER: US/09/377,309B
; CURRENT FILING DATE: 1999-08-19
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-309-76

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 296 CCATCCGTCACAGATAACAT 314
|||
Db 1 CCAGCCTCCACATAACAT 19

RESULT 244

US-08-884-427-1
; Sequence 1, Application US/08884427A
; Patent No. 6265175
; GENERAL INFORMATION:
; APPLICANT: Gage, Fred H.
; APPLICANT: Ray, Jasodhara

; TITLE OF INVENTION: Method for Production of Neuroblasts
; FILE REFERENCE: 072577/013002
; CURRENT APPLICATION NUMBER: US/08/884,427A
; CURRENT FILING DATE: 1997-06-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: sequence
US-08-884-427-1

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 247 GAGGAGTGACCAAGTACC 265
|||
Db 1 GAGGAGATAACTGAGTACC 19

RESULT 245

US-09-488-744A-14
; Sequence 14, Application US/09488744A
; Patent No. 6287860
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Donna T. Ward
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF MEK2 EXPRESSION
; FILE REFERENCE: RTS-0108
; CURRENT APPLICATION NUMBER: US/09/488,744A
; CURRENT FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-09-488-744A-14

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1137 CCTGGAGAAGATCAACAG 1155
|||
Db 1 CCGTGAGAAGATAAACAG 19

RESULT 246

US-09-364-416-78
; Sequence 78, Application US/09364416
; Patent No. 6312900
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; APPLICANT: Miraglia, Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; TITLE OF INVENTION: Compositions and Methods for the Modulation of
; TITLE OF INVENTION: Activating Protein 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA

```
;
;
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,416
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,201
; FILING DATE: April 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-09-364-416-78

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1554 TTCTTCCCAACCCCTCA 1572
Db 2 TTCTTCCACTGCCCTCA 20

RESULT 247
US-09-364-416-95/c
; Sequence 95, Application US/09364416
; Patent No. 6312900
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; APPLICANT: Miraglia, Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; TITLE OF INVENTION: Compositions and Methods for the Modulation of
; TITLE OF INVENTION: Activating Protein 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,416
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,201
; FILING DATE: April 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0209
; TELECOMMUNICATION INFORMATION:
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;
;
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-09-364-416-95

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1554 TTCTTCCCAACCCCTCA 1572
Db 19 TTCTTCCACTGCCCTCA 1

RESULT 248
US-09-326-186B-178/c
; Sequence 178, Application US/09326186B
; Patent No. 6319906
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein
; FILE REFERENCE: ISPH-0376
; CURRENT APPLICATION NUMBER: US/09/326,186B
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-09-326-186B-178

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1277 TCTCGATCTGCTCCTCTGA 1295
Db 19 TCTGCTGCTCCTCTCTGA 1

RESULT 249
US-09-079-812E-3
; Sequence 3, Application US/09079812E
; Patent No. 6340575
; GENERAL INFORMATION:
; APPLICANT: Bollag, Gideon
; APPLICANT: Crompton, Anne
; APPLICANT: No. 6340575th, Anne
; APPLICANT: Sharma, Sanju
; APPLICANT: Roscoe, William
; TITLE OF INVENTION: Methods and Compositions for Treating Abnormal Cell
; TITLE OF INVENTION: Growth Related to Unwanted Guanine Nucleotide Exchange
; TITLE OF INVENTION: Factor Activity
; FILE REFERENCE: 1028-US
; CURRENT APPLICATION NUMBER: US/09/079,812E
; CURRENT FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/049,879
; PRIOR FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
```

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; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Oligo
US-09-079-812E-3

Query Match      0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 775 GAGGCCATTTTCAAGCCGG 793
Db 2 GAGGCCATGTCGAGCTGG 20

RESULT 250
US-09-659-791A-22/c
; Sequence 22, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-22

Query Match      0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1401 GGATGAAAAGAGAAGAC 1419
Db 19 GGGTGAACAGATAAAGAC 1

RESULT 251
US-09-798-096-75
; Sequence 75, Application US/09798096
; Patent No. 6399378
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL2 EXPRESSION
; FILE REFERENCE: RTS-0207
; CURRENT APPLICATION NUMBER: US/09/798,096
; CURRENT FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 75
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-798-096-75

Query Match      0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 575 TGTACATTGACATTGATAT 593
Db 1 TGGTCATTGGCATTGATAT 19

RESULT 252
US-09-724-426-26
; Sequence 26, Application US/09724426
; Patent No. 6414134
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
; FILE REFERENCE: 10412-024
; CURRENT APPLICATION NUMBER: US/09/724,426
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-426-26

Query Match      0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6 GAGCCGCGCGCGGAGGGC 24
Db 1 GCGCGCGCGCGCGGCGGC 19

RESULT 253
US-09-640-101-100/c
; Sequence 100, Application US/09640101
; Patent No. 6448079
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; APPLICANT: McKay, Robert
; TITLE OF INVENTION: Antisense Modulation of p38 Mitogen
; FILE REFERENCE: ISPH-0488
; CURRENT APPLICATION NUMBER: US/09/640,101
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 09/286,904
; PRIOR FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 100
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-640-101-100

Query Match      0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 784 TTCAGCCGCGTCATGTCCA 802
Db 20 TTCAGCCGCGCACGTCCA 2

RESULT 254
US-09-658-688A-45/c
; Sequence 45, Application US/09658688A
; Patent No. 6498035
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: William Gaarde
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF MEK3 EXPRESSION
; FILE REFERENCE: RTS-0143
```